

XX
DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

PS Example 2; SEQ ID NO 1439; 134pp; English.

The invention describes a purified polypeptide which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIP0 at [ftp.wipo.int/publ/published.pct.sequences](http://wipo.int/publ/published.pct.sequences)

SQ Sequence 839 AA;

Alignment Scores:

Alignment Scores:	
Pred. No.:	0
Score:	435.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	50.76%
DB:	6
Gaps:	0
Length:	839
Matches:	839
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-396-985B-1 (1-4868) X ABU04773 (1-839)

QY	104	ATGATGTCGCTCGGCGCTGGCTGGGACTTCGATGCCAGCCATGGCCCTTCCTCTG	153
Db	1	MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys	20
QY	164	GTGAGACCAAGAAAGCTGGAGGCCCTCGTGAGAGTGTTCTTAATATTAATTCAATGC	223
Db	21	ValArgProGlnSerThrGlnProCysValGluValValProAsnIleThrTrpGlnCys	40
QY	224	ATGAGCTGAATTTCTACAAATCCCCGACACCTCCCTTCTCAACCAAGAACTGGAC	283
Db	41	MetGluLeuAspPheTrpLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp	60
QY	284	CTGAGCTTAAATCCCTCGAGGCATTTAGGACGATTAGCTTTCAGTTTCCAGAACTG	343
Db	61	LeuSerPheAsnProLeuArgHisLeuGlySerTrpSerPheSerPheProGlnLeu	80
QY	344	CAGGTCTGATTTATCCAGGTGTGAATCCAGACATTTGAAGATGGGCATATCAGAGC	403
Db	81	GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTrpGlnSer	100
QY	404	CTAAGCACCTCTCTACCTTAATATTGACAGAAACCCCATCCAGATTAGGCCCTGGGA	463
Db	101	LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly	120
QY	464	GCCTTTTCTGACTATCAAGATTACAGAACTGTGGCTGTGAGACAAATCTAGCATCT	523
Db	121	AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValAlaGluThrAsnLeuAlaSer	140
QY	524	CTAGGAATTTCCCTCCCTTGGACATCTCAAAACTTTGAAGAATCTTAATGTGGCTCAAT	583
Db	141	LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn	160
QY	584	CTTATCCAATCTTTCAAAATTACCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTTG	643

[illegible]


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Db      521 SerLeuGlnValIleuAmeMetSerHisAsnAsnDnhePheSerLeuAapThrPheProTyr 540
QY      1724 AAGTGTGAACTCCCTCCAGAGTCTTGTATGATTAAGTCTCAATGACATTAATGATCTCCAAA 1783
Db      541 LysCysIleuAmeSerLeuGlnValIleuAapThrSerLeuAmeHisIleMetThrSerLys 560
QY      1784 AAACAGAACTACAGACATTTTCCAGAGTACTTCTTAAATCTTAATCTTAATCTCAAGATGAC 1843
Db      561 LysGlnGlnLeuGlnHisPheProSerSerLeuHisPheLeuAmeLeuThrGlnAsnAsp 580
QY      1844 TTTCCTTGATCTTGTGAACACACAGATTTCTGCAATGATGACAGACAGAGGACAGCTC 1903
Db      581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 600
QY      1904 TTGATGGAAGTTGAACGAATGGAATGCAACCTTCAATGAGGACGACCTGTG 1963
Db      601 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAapLysGlnGlnMetProVal 620
QY      1964 CTGAGTTGAATATCACCTGTCAAGATGAATGAACATCATTTGGTGTGCTGCTCAGT 2023
Db      621 LeuSerLeuAmeHisIleThrCysGlnMetAsnHisThrIleIleGlnValSerValLeuSer 640
QY      2024 GTGCTTGATGATCTGTTTGAGCAGTTCTGTGCTTAATGATTTTCACTGATGCTT 2083
Db      641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisIleuMetLeu 660
QY      2084 CTTCGTGAGTGCATAAAGTATGATGAGAGGAGAAACATCATGATGCTTGTATGATCTAC 2143
Db      661 LeuAlaCysIleLysTyrGlnArgGlnLysAsnHisIleTyrAapAlaPheValIleTyr 680
QY      2144 TCAAGCCAGATGAGAGCTGGGTAAAGATGAGCTAGTAAAGATTTTGAAGAAGAGGGGTG 2203
Db      681 SerSerGlnAspGlnAapThrValArgAsnGlnLeuValLysAsnLeuGlnGlnVal 700
QY      2204 CTTTCATTTGAGCTCTGCTTCACTAAGACATTTATCCCGGTGTGGCCATGCTGCC 2263
Db      701 ProProPheGlnLeuCysLeuHisIleTyrArgAapPheIleProGlnValAlaIleAla 720
QY      2264 AACATCATCATGAAGGTTTCCATAAAGCCGAAGGAGTGTGTGTGGTGTGCCACAC 2323
Db      721 AsnIleHisGlnGlnPheHisLysSerArgLysValIleValValSerGlnHis 740
QY      2324 TTTCATCCAGAGCCGCTGTGATATCTTGAATATGAGATTTCTCAGACCTGCGAGTTCTG 2383
Db      741 PheIleIleHisArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeu 760
QY      2384 AGCAGTGTGCTGTATCATCTTCAATTTCTGTCAGAAAGTGAAGAGACCTGCTCAGG 2443
Db      761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 780
QY      2444 CAGCAGGTGAGCTGTACCCGCTTCTGAGAGAAACCTTACCTGAGTGGAGAGACAGT 2503
Db      781 GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLysPheSer 800
QY      2504 GTTCCTGGGCGGACATCTTCTGAGAGACACTCAGAAAAGCCCTGATGATGTAATCA 2563
Db      801 ValLeuGlnLysArgHisIlePheThrPArgArgLeuArgLysAlaLeuAapGlnLysSer 820
QY      2564 TGAATTCAGAAAGACAGTGGGTACAGATGCAATTTGCGAAGAAAGCAATCATTC 2620
Db      821 TrpAsnProGlnGlnThrValGlnTyrGlnCysAsnThrProlGlnGlnAlaThrSerIle 839

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RESULT 2

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ABU04774
ID      ABU04774 standard; protein; 839 AA.
XX
AC      ABU04774;
XX
DT      29-JAN-2003 (first entry)
DE      Human expressed protein tag (EPT) #1440.
XX
KW      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

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KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KM      receptor; transcription factor; cancer; MHC;
KM      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS      Homo sapiens.
XX
PN      WO200278524-A2.
XX
PD      10-OCT-2002.
XX
PF      28-MAR-2002; 2002WO-US009671.
XX
PR      28-MAR-2001; 2001US-0279495P.
PR      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
XX
PA      (ZYCO-) ZYCOS INC.
XX
PI      Chicz RM, Tomlinson AJ, Urban RG;
XX
DR      WPI; 2003-040607/03.
XX
PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukemia.
XX
PS      Example 2; SEQ ID NO 1440; 134pp; English.
XX
CC      The invention describes a purified polypeptide, which comprises a
CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
CC      transporter, cytoskeletal protein, receptor or transcription factor. The
CC      polypeptide is useful as an immunogenic composition for eliciting in a
CC      mammal an immunogenic response directed against any of the purified
CC      polypeptide. The purified polypeptide, or the antibody that binds to this
CC      polypeptide, is useful for treating cancer. The polypeptide is also
CC      useful for identifying compounds that binds to a naturally processed
CC      class I or class II MHC-binding polypeptide. The polypeptides and
CC      polynucleotides are particularly useful for treating or preventing
CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC      lymphoma or leukaemia. These are also useful for screening agents for
CC      treating the above mentioned diseases. This sequence represents an
CC      expressed protein tag (EPT) isolated from human tissue for translational
CC      profiling. Note: This sequence does not appear in the printed
CC      specification but was obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 839 AA;

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Alignment Scores:

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Pred. No.: 0
Score: 4355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 50.76%
DB: 6
Gaps: 0

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US-09-396-985B-1 (1-4868) x ABU04774 (1-839)

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QY      104 ATGATGTCTGCTCGGCGCTGTGAGACTTGATCCAGACATGAGCCTTCTCTCTGTC 163
Db      1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY      164 GTGAGACCGAAGCGGAGAGCCCTGCGAGAGTGTCTTCAATTAATCAATGC 223
Db      21 ValArgProGlnUserTyrProlProCysValGlnValAlaProAsnIleThrTyrGlnCys 40
QY      224 ATGAGCTGAATTTCTACAAATCCCGCAACCTCCCTTCAACCAAGAACCTGGAC 283

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Db 41 MetGluLeuAsnPhenylrlyslleProAspAsnLeuProPheSerThrlysaenLeuAsp 60
QY 284 CTGAGCTTTAATCCCGGAGGCAATTTAGGAGCTATGCTTCTTCAAGTTCCCGAAGACTG 343
Db 61 LeuSerPheAsnProLeuAlaGlnlySerlySerPhePheSerPheProGluLeu 80
QY 344 CAGGTGCTGGAATTTATCCAGGTGTGAATCCAGACAAATTGAGAGGCGCATACAGAC 403
Db 81 GlnValLeuAsnProLeuSerArgCysGluileGlnThrileGluAsnProGlyAlaTyrglnSer 100
QY 404 CTAGAGCACTCTCTACCTTAATTTAGACGAAACCCCATCCAGAGTTAGCCCTGGGA 463
Db 101 LeuSerThrileuSerThrileuThrileuThrlyAsnProileGlnSerleuAlaLeuGly 120
QY 464 GCCCTTTCTGACTATCAAGTTTACAGAGCTGTGCTGTGAGAGCAAACTTGAATCTGACTC 523
Db 121 AlaPheSerGlyLeuSerSerleuGlnlyLeuValAlaValGlnThrAsnLeuAlaSer 140
QY 524 CTAGAGAACTTCCCGATTTGACATCTCAAAACTTTGAGAACTTAAATGTGGCTCACAA 583
Db 141 LeuGluAsnPhenProileGlyHisleuLyThrleuLyseGluLeuAsnValAlaHisAsn 160
QY 584 CTATTCGAATCTTTCAAAATTAACCTGAGATTTTCTATCTGACCAATCTTGAGCACTTG 643
Db 161 LeuileGlnSerPheLyseuProGluTyPheSerAsnLeuThrAsnLeuGluHisleu 180
QY 644 GACCTTTCCAGCAACAGATTTCAAAATTTATTTAGCAGACTGGGGGTCTACATCAA 703
Db 181 AspLeuSerSerAsnLyseuThrileGlnSerThrileTyCysThrAsnLeuAlaGValLeuHisGln 200
QY 704 ATGCCCTTACTCAATCTCTCTTTAGACCTGTCCCTGAATCTTGAACCTTTATCCAAACA 763
Db 201 MetProLeuAsnLeuAsnLeuSerleuAsnProleuSerleuAsnProMetAsnPhenileGlnPro 220
QY 764 GGTGCACTTTAAAGAAATTTAGGCTTCATAGCTGACTTTAAGAAATTTTGTATGATTGA 823
Db 221 GlyAlaPheLyseGluThrleuGlnlyAsnleuThrleuThrleuThrleuThrleuThrleu 240
QY 824 AATGTAATGAAGAACTTGTATTTCAAGCTGCTGCTGTTAGAGGCTCATCGTTGGTCTG 883
Db 241 AsnValMetLyseThrCysileGlnGlyLeuAlaGlyLeuGluValHisArgleuValLeu 260
QY 884 GGAAGATTTTGAAGAAATTTGAGAACTTTGAGAAAGTTTGAACAACTTGTCTTGAAGGCTG 943
Db 261 GlyGluPheArgAsnGlnGlyAsnLeuGluLyPheAsnProlyseSerAlaLeuGluGlyLeu 280
QY 944 TGCATTTTGAACATTTGAGAAATTTCCGATTTAGCATTTAGCATCTTCTCCGATGATAT 1003
Db 281 CysAsnLeuThrThrileGlnGluPheArgLeuAlaTyrgleuAsnProTyrglyLeuAsnAspIle 300
QY 1004 ATTGACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGAATTT 1063
Db 301 IleAsnProPheAsnProleuThrAsnValSerSerPheSerleuValSerValThrIle 320
QY 1064 GAAAGGTTAAAGACTTTTCTTATTAATTTGAGTGAACAACTTTAGAAATTTAGTTAACTGT 1123
Db 321 GlnArgValLyseAsnPhenSerTyrgAsnPhenGlyTyrglnHisleuGluLeuValAsnCys 340
QY 1124 AAATTTGAGACGTTTCCCACTTGAACCTCAAAATCTCTCAAAAGGCTTACTTTGACTTCC 1183
Db 341 LysePheGlyGlnPheProThrleuLyseuLyseuSerleuLyseuArgleuThrPheThrSer 360
QY 1184 AACAAAGGTGGGAATGCTTTTCTTGAAGTTGATCTACCAAGCTTGAATTTCTGATCTC 1243
Db 361 AsnLyseGlyGlnAlaPheSerGluValAsnProSerleuGluPheLeuAsnPro 380
QY 1244 AGTAGAATGGCTTGAATTTCAAAAGTTGCTGTCTCAAAAGTGAATTTTGGGACAAACGAC 1303
Db 381 SerArgAsnGlyLeuSerPheLyseGlyCysCysSerGlnSerArgPheGlyThrThrSer 400
QY 1304 CTAAAGTATTTAGTCTGAGCTTCAATGCTGTATTTACCATGAGTCTCAAACTTCTTGAGC 1363
Db 401 LeuLyseTyrgleuAsnProleuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420

QY 1364 TTAGAACAACTAGAACATCTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATTT 1423
Db 421 LeuGluGlnLeuGluHisleuAsnProPheGlnHisSerAsnLeuLyseGlnMetSerGluPhe 440
QY 1424 TCGAGTTCCTTATCTACAGAAACCTCATTTACCTTGACATTTCTCATCTCACACCAAA 1483
Db 441 SerValPheLeuSerleuAsnProleuThrlyleuAsnProIleSerThrThrThrArg 460
QY 1484 GTTGCTTCAATGGCACTTCAATGAGCTGTGCTGCTGAGAGTCTTGAAGTCTTGAAGTGGCTGC 1543
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGluValLeuLyseThrAlaGly 480
QY 1544 AATTTCTTCCAGGAAACTTCTTCCAGATATCTTCAAGACTGAGACTGAGAACTTGACTTC 1603
Db 481 AsnSerPheGlnGluAsnPhenProAsnProIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1604 CTGAGACCTCTCTCAGGTGTCACTGAGGCACTGTGTCTCAACAGCATTTAACTCATCTGC 1663
Db 501 LeuAsnProleuSerGlnCysGlnleuGlnGlnleuSerProThrAlaPheAsnSerleuSer 520
QY 1664 AGTCTCAGGTACTAAATATGAGCCCAACAACTTCTTCAATGATGATGATGATGATGATGAT 1723
Db 521 SerleuGlnValLeuAsnMetSerHisAsnAsnPhenPheSerleuAsnProThrPheProTyrg 540
QY 1724 AAGTGTGTAACCTCCCTCCAGGTTCTTGATTAACAGTCTCAATCACTAAATGACTTCCAA 1783
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QY 1784 AAACAGAACTACAGCAATTTTCCAGATGCTTGAATCTTGAATCTTGAATCTTGAATGAC 1843
Db 561 LyseGlnGluLeuGlnHisPheProSerSerleuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGAATCTTGAACCAAGATTTCTGCAATGATGATGATGATGATGATGATGATGAT 1903
Db 581 PheAlaCysThrCysGlnHisleuGlnSerPheleuGlnThrIleLyseAsnProAlaGlnleu 600
QY 1904 TTGGTGAAGTTGAAGAAATGGAATGGAATGGAACCTTCAAGATGAGGAGGAGGAGCTGTG 1963
Db 601 LeuValGluValGluArgMetGlnCysValaThrProSerAsnProlyseGlnlyMetProVal 620
QY 1964 CTGAGTTTGAATTTCACTCTGTGACATGATGATGATGATGATGATGATGATGATGATGAT 2023
Db 621 LeuSerleuAsnIleThrCysGlnMetAsnLyseThrIleGlyValSerValLeuSer 640
QY 2024 GTGCTTGAATCTTGTGATGAGACTTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 2083
Db 641 ValLeuValValSerValValAlaValLeuValTyrglyPheThrPheHisleuMetLeu 660
QY 2084 CTGTGCTGCTGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2143
Db 661 LeuAlaGlyCysIleLyseTyrglyArgGlyGluAsnIleTyrgAsnAlaPheValIleTyrg 680
QY 2144 TCAAGCCAGATGAGAGCTGGGTAGAGAAATGAGCTGTAAGAAATTTAGAAAGGCGGTG 2203
Db 681 SerSerGlnAsnProGluAsnProValArgAsnGluLeuValLyseAsnleuGlnGlyVal 700
QY 2204 CTTCCATTTCAAGCTGCTGCTCACTCAAGACTTATTCCTGGGTGAGGCAATTTGCTGCC 2263
Db 701 ProProPheGlnleuCysleuHisTyrgArgAsnPhenIleProGlyValAlaIleAla 720
QY 2264 AACATCATCCATGAAGTTCATTAAGACCGAAAGTGAATTTGTTGGTGTCCAGAC 2323
Db 721 AsnIleIleHisGlnGlyPheHisLyseSerArglyValIleValValValSerGlnHis 740
QY 2324 TTGATCCAGAGCGGTGTGTATCTTGAATATGAGATTTGCTCAGACTTGCGAGTTTCTG 2383
Db 741 PheIleGlnSerArgTyrgPysIlePheGlnTyrgluileAlaGlnThrTyrglnPheLeu 760
QY 2384 AGCAGTCGTGCTGTATCATCTTCAATTTGCTGCGCAAGAGTGAAGAAAGCCGTGCTCAGG 2443
Db 761 SerSerArgAlaGlyIleIlePheIleValleuGlnlyValaGluLyseThrleuLeuArg 780

QY 2444 CAGCAGGTGAGCTGTACCGCCCTTCTCAGCAGGAACACTTACTGGAGTGGAGACAGT 2503
 DB 781 GlnGlnValGlnLeuValArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSer 800
 QY 2504 GTCTGGGGGGGACATCTTCTTGAGACGACTCAGAAAACCCCTGCTGGATGGTAATCA 2563
 DB 801 ValLeuGlnValArgHisLeuPheTyrArgArgLeuArgValAlaLeuLeuAspGlnLysSer 820
 QY 2564 TGGAAATCCAGAAAGAACAGTGGGTACAGATGCAATGGCAGGAAGCAATCATCTATC 2620
 DB 821 TrpAsnProGlnLeuGlnThrValGlnTyrGlnCysAsnTrpGlnGlnAlaTrpSerIle 839

RESULT 3
 ABU04775
 ID ABU04775 standard; protein; 839 AA.
 XX ABU04775;
 AC
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 XX
 PR 21-MAY-2001; 2001US-0292544P.
 XX
 PR 08-AUG-2001; 2001US-0310801P.
 XX
 PR 01-OCT-2001; 2001US-0326370P.
 XX
 PR 04-DEC-2001; 2001US-0336780P.
 XX
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134p; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0
 Score: 4355.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 50.76%
 DB: 6
 Gaps: 0

US-09-396-985b-1 (1-4868) x ABU04775 (1-839)

QY 104 ATGATGTCGCTCGCGCCCTGCGGAGCTGTATCCAGCCATGAGCCTTCCTCTGCG 163
 DB 1 MetMetSerAlaSerArgLeuAlaGlnThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 164 GTGAGACCAAGAAAGCTGGAGCCCTGCGTGGAGTGGTCTTAATTAATCAATGC 223
 DB 21 ValArgProGlnLeuSerTrpGlnProCysValGlnValAlaProAsnIleThrTyrGlnCys 40
 QY 224 ATGAGCTGAATTTCTACAAAATCCCGCAACCTCCCTTCCACCAAGACCTGGAC 283
 DB 41 MetGlnLeuAsnPheTyrIleProAspAlaLeuProPheSerThrLysAsnLeuAsp 60
 QY 284 CTGAGCTTAATCCCTGAGGCAATTTAGGCAAGCTTACGCTTCAAGTTCCAGAACTG 343
 DB 61 LeuSerPheAsnProLeuAlaArgHisLeuGlnSerTyrSerPhePheSerPheProGlnLeu 80
 QY 344 CAGGTGCTGAATTTATCCAGGTGTGAATCCAGACAAATGAAGATGGGCATATCAGAGC 403
 DB 81 GlnValLeuAsnProLeuSerArgCysGlnIleGlnThrIleGlnAspGlnAlaTyrGlnSer 100
 QY 404 CTGAGCCACTCTCTACCTTAATATTTGACAGAAACCCATCCAGAGTTTACGCTGGGA 463
 DB 101 LeuSerHisLeuSerThrLeuIleThrGlnAsnProIleGlnSerLeuAlaLeuGln 120
 QY 464 GCGTTTCTGAGACTATCAAGTTTACAGAGCTGTGGCTGGAGCAAAATCTAGCATCT 523
 DB 121 AlaPheSerGlnLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 140
 QY 524 CTAGAGAACTCCCATTTGAGACATCTCAAAACCTTTGAAAACCTTAATGTGGTCAAT 583
 DB 141 LeuGlnAsnPheProIleGlnHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 160
 QY 584 CTATATCAATCTTTCAATTAATCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTTG 643
 DB 161 LeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 644 GACCTTCCAGCAACAAGATTCAAGATTTATTTGACAGACTTGCGGGCTTACATCAA 703
 DB 181 AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
 QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGGAATCTATGAATCTTTATCCAAACA 763
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 764 GGTGCAATTTAAAGAAATTTAGCTTCAATAGCTGACTTTTAAGAAATTTGATAGTTTA 823
 DB 221 GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuAsnAsnPheAspSerLeu 240
 QY 824 AATGTAAATAAAACCTGTATTCAGAGCTGGGCTGTTTGAAGTCATGTTGGTTCG 883
 DB 241 AsnValMetLysThrCysIleGlnGlnLysLeuAlaGlnLysLeuValHisArgLeuValLeu 260
 QY 884 GGAGAAATTTAGAAATGAAGAAACTTGAAGAAATTTGACAAATCTGCTAGAGGCGCTG 943
 DB 261 GlyGlnPheArgAsnGlnLysLeuGlnLysLysPheAspLysSerAlaLeuGlnGlnLysLeu 280
 QY 944 TGCATTTTACCAATTTGAAGAAATTTCCGATTTAGCATTTAGACTTACTTCCATGATATT 1003
 DB 281 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspLysTyrLeuAspAspIle 300

QY 1004 ATTGATTATTAATTGTTGACAAATGTTCTTCAATTTCCCTGGTAGTGACTATT 1063
DB 301 ILeAspLeuPhehSenCySleuThrAnValSerSerPheSerLeuValSerValThrIle 320
QY 1064 GAAAGGGTAAAGACCTTTTCTTATTAATTTGGATGGCAATTTAGATTAAGTTAACTGT 1123
DB 321 GluArValAlaLysAspPheSerTyraSenPheGlyTyrGlnIhIbLeuGluLeuValaSenCyS 340
QY 1124 AAATTTGGACAGTTTCCCAATTTGAAATCAAAATCTCTCAAAAGGCTTACTTCACTGTC 1183
DB 341 LysPheGlyGlnPheProhIbLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
QY 1184 AACAAAGTGGGAATGCTTTTTCAGAAATGATCTACCAAGCTTGATGTTTTCAGATCTC 1243
DB 361 AsnLysGlyGlyLysAnIaPheSerGluValaAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1244 AGTAGAAATGGCTTGAATTCAAAGGTTGCTGTTCTCAAAAGTAAATTTGGACAAACGAC 1303
DB 381 SerArgAnGlyLeuSerPheLysGlyCySeSerSerInSerAspPheGlyThrThrSer 400
QY 1304 CTAAGATTATTAAGTCTGAGCTTCAATGGTGTATTAACATGAGTTCAAACTTGGGCG 1363
DB 401 LeuLysTyrLeuAspLeuSerPheAnGlyValIleThrMetSerSerAnPheLeuGly 420
QY 1364 TTAGAACAACTAGAACATCTGATTTTCCAGCATTTCCAAATTTGAAACAAATGAGTGAATT 1423
DB 421 LeuGlnGlnLeuGlnIhIbLeuAspPheGlnIhIbSerAnLeuLysGlnMetSerGluPhe 440
QY 1424 TCAGTATTCCTATACATCTAGAAACCTGATTTTACTGATCTTCTCATCTACACCA 1483
DB 441 SerValaPheLeuSerLeuArgAnLeuIleTyrLeuAspIleSerAnIbThrAnIbThrArg 460
QY 1484 GTTGCTTTCAATGGCATCTTCAATGGCTTCCAGTCTGCAAGTCTGAAAGTGGGCGG 1543
DB 461 ValaIaPheAnGlyIlePheAnGlyLeuSerSerLeuGluValaLeuLysMetAlaGly 480
QY 1544 AATTCCTTCCAGGAAATCTTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
DB 481 AsnSerPheGlnGlnIbAnPheLeuProAspIlePheThrGluLeuArgAnLeuThrPhe 500
QY 1604 CTGGACCTCTCTCAAGTCTCACTGAGAGAGTGTCTTCAACAGATTTAACTCACTCTCC 1663
DB 501 LeuAspLeuSerGlnCySglnLeuGlnLeuSerProThrIaPheAnSerLeuSer 520
QY 1664 AGTCTCAGGATCAAAATATGAGCCACAAACATCTTCTTCAATGATGATGTTTCTTAT 1723
DB 521 SerLeuGlnValaLeuAnMetSerAnIbAnPheSerLeuAspThrPheProTyr 540
QY 1724 AAGTCTGGAATCCCTCCAGTCTTGAATTAAGTCTCATCATCATATATGACTTCCAA 1783
DB 541 LysCySbLeuAnSerLeuGlnIbLeuAspTyrSerLeuAnIbIleMetThrSerLys 560
QY 1784 AAACAGAACTACAGCATTTTCCAGATGCTAGCTTCTTAAATCTTACTCAGAAATGAC 1843
DB 561 LysGlnGlnIbLeuGlnIhIbPheProSerSerLeuAnIaPheLeuAnLeuThrGlnAnAsp 580
QY 1844 TTGGCTTGTACTGTGTAACCAAGATTTCTGGAATGATGATGATGATGATGATGATG 1903
DB 581 PheIaCySbThrCySglnIhIbGlnSerPheLeuGlnIbIleLysAspGlnArgGlnLeu 600
QY 1904 TTGGTGAAGTGAACGAATGATGCAACATCTTCAATGAGAGGAGGAGGAGGAGGAGT 1963
DB 601 LeuValGlnValaGlnArgMetGlnCyAlaIbThrProSerAspLysGlnGlnMetProVal 620
QY 1964 CTGAGTTTGAATATCACCTGTCAAGATGAATGAACATCATGATGATGATGATGATG 2023
DB 621 LeuSerLeuAnIbThrCySglnMetAnLysThrIleIleGlyValSerValLeuSer 640
QY 2024 GTGGCTTGAATATCTGTGTAAGAGCTTGTGCTATATGATGATGATGATGATGATGAT 2083
DB 641 ValLeuValaValSerValaValaValaValaValaValaValaValaValaValaVala 660
QY 2084 CTTCCTGGCTGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2143

DB 661 LeuAlaGlyCySbIleLysTyrGlyArgGlyGluAnIleTyrAspAlaPheValIleTyr 680
QY 2144 TCAGCCAGAGATGAGGACCTGGGTAAAGGAATGAGCTAGTAAAGAAATTTAGAAAGAGCGG 2203
DB 681 SerSerGlnAspGlnAspTyrValaArgAnGlnLeuValaLysAnLeuGlnGlnGlyVala 700
QY 2204 CCTCATTTCACTGCTGCTTCACTACAGAGACTTAAATCCGAGTGGCCATTTGCTGCC 2263
DB 701 ProProPheGlnLeuCySbLeuIbTyrArgAspPheIleProGlyValaIleAlaIa 720
QY 2264 AACATCATCATGAAGTTCCTTCAATAAAGCCGAAAGTGAATTTGTGTGCTCCAGCAC 2323
DB 721 AsnIleIleIhIbGlnGlyPheIbIbLysSerArgLysValaIleValaValaSerGlnIh 740
QY 2324 TTCATCCAGAGCCGCTGGTGTATCTTTGAATATGAGATTCCTCAGACCTGGAGTTTCG 2383
DB 741 PheIleGlnSerArgTyrCySbIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheLeu 760
QY 2384 AGCAGTCGTGTGTATCATCTTCAATTTCTCTGCAAGAGTGGAGAACCTGTCTCAGG 2443
DB 761 SerSerArgAlaGlyIleIlePheIleValaLeuGlnLysValaGlnLysThrLeuLeuArg 780
QY 2444 CAGCAGTGAAGCTGTACCGCTTTCAGACAGAACATTTACTGAGTGGAGACAGT 2503
DB 781 GlnGlnValaGlnLeuTyrArgLeuLeuSerArgAnThrTyrLeuGlnTyrGlnAspSer 800
QY 2504 GTCCCTGGGGCGGACATCTTCTGGAAGACACTCAGAAAGCCCTGCTGATGGTAAATCA 2563
DB 801 ValLeuGlyArgIbIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 820
QY 2564 TGGATTCAGAAAGAACAGTGGGTACAGAGTCAATTTGGCAGAGAACATCTATC 2620
DB 821 TrpAnProGlnGlyThrValaGlnThrGlyCySbAnThrGlnGlnIbAlaThrSerIle 839

RESULT 4
ID ADC78785 standard; protein; 839 AA.
AC ADC78785;
DT 01-JAN-2004 (first entry)
XX XX
DE Human PRO protein #7.
XX XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX XX
OS Homo sapiens.
PN WO2003034984-A2.
XX XX
PD 01-MAY-2003.
XX XX
PF 15-OCT-2002; 2002WO-US033070.
XX XX
PR 19-OCT-2001; 2001US-0340083P.
XX XX
PA (GETH) GENENTECH INC.
XX XX
PI Goddard A, Gurney AL;
XX XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

XX Sequence 839 AA;

Alignment Scores:

Pred. No.:	Length:	839
Score:	4355.00	839
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	50.76%	Indels: 0
	7	Gaps: 0

US-09-396-985B-1 (1-4868) x ADC78785 (1-839)

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QY 104 ATGATGTCTGCGCTGGCGCTGGAGACTGTGATCCAGCATGGCCTTCCTCTCTGC 163
Db 1 MetMetSerLaserArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 164 GTGAGACCAAGAGCTGGAGCCCTGGTGAGAGTGCTTCTAATATTACTTATCATGC 223
Db 21 ValArgProGlnSerThrPgluProCysValGluValAlaProAsnIleThrTyrglnCys 40
QY 224 ATGAGAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 283
Db 41 MetGluLeuAsnPhetIryIysIleProAspAsnLeuProPheSerThrIysAsnLeuAsp 60
QY 284 CTGAGCTTAAATCCCTGAGGCAATTAGGAGCTTAAAGCTTTCAGTTTCCGAAACTG 343
Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGlnLeu 80
QY 344 CAGGTGTGATTTATTCAGAGTGTAATCCAGAACTTGAACATTTGAATGGGCGCATTCAGC 403
Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGluAspGlyAlaTyrglnSer 100
QY 404 CTAAAGCACTCTCTACTTAATATTGACAGAAACCCCACTCCAGAGTTAGCCCTGGGA 463
Db 101 LeuSerHisLeuSerThrLeuIleLeuThrClyAsnProIleGlnSerLeuAlaLeuGly 120
QY 464 GCGTTTTCGACTATCAAGTTTACAGAACTGGTGCTGTGAGAACAAATCTGACATCT 523
Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleLeuValAlaValGluThrAsnLeuAlaSer 140
QY 524 CTAGAGAACTTCCCACTTGACATCTTCAAACTTTGAAAACCTTAAATGTGGCTCAAT 583
Db 141 LeuGluAsnPhetIroIleGlyHisLeuIysThrLeuIysGluLeuAsnValAlaHisAsn 160
QY 584 CTATCCAACTCTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTG 643
Db 161 LeuIleGlnSerPheIysLeuProGlnIlyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
QY 644 GACCTTTCAGAACAAAGATTCAAAAGTATTATTGACAGACTTGGGGTTCTTACATCAA 703
Db 181 AspLeuSerSerAsnIysIleGlnSerIleTyCysThrAspLeuArgValLeuHisGln 200
QY 704 ATGCCCTTACTCATCTCTCTTTAGACCTGTCCCTGAAATCTTATGAACCTTATTCACCA 763
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 764 GGTGCAATTTAAAGAAATTAAGCTTCAATAGCTGACTTAAAGAAATATTATTGATAGTTA 823
Db 221 GlyHisPheIysGlnIleArgLeuHisIleIysLeuThrLeuArgAsnAsnPheAspSerLeu 240
QY 824 AATGTAATGAAGAACTTGATATCAAGTCTGGCTGGTTTGAAGTCCATCGTTTGGTTCTG 883
Db 241 AsnValMetIysThrCysIleGlnGlyLeuAlaGlyLeuGluIuValHisArgLeuValLeu 260
QY 884 GGAAGATTTGAAGTGAAGAACTTGAGAAAGTTTGAACAAATCTGCTTGAAGGGGCTG 943
Db 261 GlyIlePheArgAsnGlnGlyAsnLeuGlnIlyrPheAspIysSerAlaLeuGlnGlyLeu 280
QY 944 TGCAATTTGACATTTGAAGAAATTCGATAGCATTAAGTAACTGATGATATT 1003

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Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyLeuAspIyTyLeuAspAspIle 300
QY 1004 ATTGACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGGTGAAGTGAATATT 1063
Db 301 IleAspLeuPheAsnCysLeuThrAsnValIserSerPheSerLeuValSerValIthrIle 320
QY 1064 GAAAGGTAAGAACTTTCTTAAATTTCCGATGAGCAACATTTAGAAATAGTAATCTGT 1123
Db 321 GluArgValIlyAspPheSerIlyrAsnPheGlyTyrglnHisIleuGluLeuValAsnCys 340
QY 1124 AAATTTGACAGTTTCCCACTTGAAGTCAATCTCTGAAAAGCTTACTTTCACCTTCC 1183
Db 341 LysPheGlyGlnIlePheThrIleuIysLeuIysSerLeuIysArgLeuThrPheThrSer 360
QY 1184 AACAAAGTGGGAATGCTTTTTCAGAAAGTTGATCTTCAAGCTTGAAGTTTCAAGTCTC 1243
Db 361 AsnIlyGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeu 380
QY 1244 AGTGAAGATGGCTTGATTTCAAGGTTGCTGTCTCAAGTAAATTTGGGACCAACGACG 1303
Db 381 SerArgAsnGlyLeuSerPheIysGlyCysSerGlnSerAspPheGlyIthrThrSer 400
QY 1304 CTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTATTCAGATGATTCAAACTTGGGC 1363
Db 401 LeuIyTyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1364 TTAGAACAATGACATCTGCAATTTCCAGCATTCCTCAATTTGAACAAATGAGTGAATT 1423
Db 421 LeuGlnGluLeuIuHisLeuAspPheGlnHisSerAsnLeuIysGlnMetSerGluPhe 440
QY 1424 TCAGTATTCCTTCACTCGAAGAAACCTCAATTTACCTGACATTTCTGATCTCACACAGA 1483
Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrArg 460
QY 1484 GTTGCTTCAATGAGCATCTTCAATGAGCTTGTCCAGTCTGGAAGTCTGAAATGGCTGCG 1543
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIysMetAlaGly 480
QY 1544 AATTTCTTCAAGAAACTTCTTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1603
Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1604 CTGGAACCTCTCAGGTGCAACTGAGGAGTGTCTCCAAACGATTAATCACTCACTCC 1663
Db 501 LeuAspLeuSerClnIysGlnLeuGlnIleuGlnLeuSerProIthrAlaPheAsnSerLeuSer 520
QY 1664 AGTCTTCAGGTACTAATATAGAGCCACAACTTCTTTTCAATTTGATAGTTCCTTAT 1723
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnAsnPhePheSerLeuAspThrPheProTy 540
QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTTGAATACAGTCTCAATCACTCAATGACTCCAA 1783
Db 541 LysCysLeuAsnSerLeuGlnValIleAspIlyrSerLeuAsnHisIleMetThrSerIys 560
QY 1784 AAACAGAACTACAGATTTTCCAGTACTGATCTTCTTAAATCTTACTACGAAATGAC 1843
Db 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGTACTTGTGAACACCAAGATTTCTGCAATGATGATCAAGACGAGGACGCTC 1903
Db 581 PheAlaCysThrCysGlnIuHisGlnSerPheLeuGlnItrIlyAspGlnArgGlnLeu 600
QY 1904 TTGGTGAAGTGAAGCAATGGAATGGAACACTTCAAGATAGCAGGCGATGCTGTG 1963
Db 601 LeuValGluValGluArgMetGluCysAlaIthrProSerAspIysGlnIlyMetProVal 620
QY 1964 CTGAGTTTAATATCACTGTCAGATGATTAAGCAATATGAGTGTGCGGTCTCAAT 2023
Db 621 LeuSerLeuAsnIleThrCysGlnMetAsnIlyrThrIleIleGlyValSerValLeuSer 640
QY 2024 GTGCTGTAGTATCTGTTTACAGATTCGTGCTATTAAGTTCATTTTCAACCTGATGCTT 2083

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Db 641 ValIeuValIaSeValIaValIaValIeuValIyTrIlySpheTyRPhetiSleuMeIeu 660
Qy 2084 CTTGCTGGCTGCATTAAGTATGTAGAGGTGAAAAACATCTATGATGCTTTGTTATCTAC 2143
Db 661 LeuAlaGlyCysIleuTyRgIyArGgIyGluAsnIleTyRAspAlaPheValIleTyR 680
Qy 2144 TCAAGCAGAGATGAGACTGGGTAAAGATGAGCTAGTAAAGATTAGAAAGAGGGGTG 2203
Db 681 SerSerGlnAspGluAspTrpValIArgAsnIleuValIyAsnIleuGluGlyVal 700
Qy 2204 CTTGATTTAGCTCTGCTTCACTACAGAGACTTATTCCTGGGTGGCTATGCTGC 2263
Db 701 ProProPheGlnIleuCySleuHleTyRArgAspPheIleProGlyValAlaIleAla 720
Qy 2264 AACATCATTCATGAAAGTTTCCATTAAGCCGAAAGGTGATTTGTTGGTGTCCCGAC 2323
Db 721 AsnIleIleHleGluGlyPheHleSlySerArgIyValIleValIaValISerGlnHle 740
Qy 2324 TTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTG 2383
Db 741 PheIleGlnSerArgTrpCySlePheGlnTyRdIleAlaGlnThrTrpGlnPheIleu 760
Qy 2384 AGCAGTGTGTCTGTATCATCTTTCATTTGCTCTGAGAAAGGTGAGAAACCTGCTCAGG 2443
Db 761 SerSerArgIaGlyIleIlePheIleValIleuGlnIyValIeGluTyRThrLeuArg 780
Qy 2444 CAGCAGGTGAGACTGTACCCCTTCTGAGAGAAACCTTACCTGGAGTGGAGAGACT 2503
Db 781 GlnGlnIleValIeGluTyRArgLeuSerArgAsnThrTyRleuGlnTrpGluAspSer 800
Qy 2504 GTCTGTGGGGGCGACATCTTCTGAGAGAGACTCAGAAAGCCCTGCTGATGTAATCA 2563
Db 801 ValIeuGlyArgHleIlePheTrpArgIleuArgIyAlaIleuLeuAspGlyLysSer 820
Qy 2564 TGGATTCAGAAAGAGACAGTGGGTACAGATGCAATTGGCAGAAAGCAACATCTATC 2620
Db 821 TrpAsnProGlnGlyThrValIeGlyThrGlyCysAsnTrpGlnIleAlaThrSerIle 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX
DT 02-DEC-2004 (revised)
XX
DT 23-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAF05316.

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS
PS Example 1; Page; 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
SQ
Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4355.00 Matches: 839
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.76% Indels: 0
DB: 7 Gaps: 0

US-09-396-985b-1 (1-4868) x ADD48826 (1-839)

Qy 104 ATGATGTCCTGCTGCGCTGTGGAGCTTGATCCAGCAAGCCCTTCTCTCTGC 163
Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCyS 20
Qy 164 GTGAGACCAAGAAAGCTGGAGCCCTGCGAGGTGTTCTTAATTTACTTATCAATGC 223
Db 21 ValArgProGlnSerTrpGluProCySValIleValIaProAsnIleThrTyRgInCyS 40
Qy 224 ATGAGACTGAAATTTCTCAAAATCCCGCAACCTCCCTTCTCAACCAAGAACTTGAC 283
Db 41 MetGluLeuAsnPhetRlyTrIleProAspAenLeuProPheSerThrIySaenLeuAsp 60
Qy 284 CTGAGCTTTAATCCCTGAGGCACTTTAGAGCACTATAGCTTTCTTCAGTTCCAGAACTG 343
Db 61 LeuSerPheAsnProLeuArgHleSleuGlySerTySerPhePheSerPheProGluLeu 80
Qy 344 CAGGTGCTGATTTATCCAGGTGTGAAATCCAGAACTGAAGATGGGCGATTCAGAGC 403
Db 81 GlnValIeuAspLeuSerArgCySglnIleGlnThrIleGluAspIyAlaTyRgInSer 100
Qy 404 CTAAGCACCCTCTCTAATTTATTTAGACAGAAACCCATCCAGAGTTTGGCTTGGAG 463
Db 101 LeuSerHleLeuSerThrIleuIleuThrGlyAsnProIleGlnSerIleuAlaLeuGly 120
Qy 464 GCCTTTTCTGAGACTATCAAGATTACAGAAAGCTGTGGCTGTGGAGCAAACTTGAATCT 523
Db 121 AlaPheSerGlyLeuSerSerIleuGlnIySleuValIaValIeGlnThrAsnLeuAlaSer 140

QY 524 CTAGAGAACTTCCCATTTGACATCTGAAAATTGAAAGAACTTAATGTCACAAAT 583
 |||||
 Db 141 LeuGluAsnProIleGlyHisLeuHisThrLeuLysGluLeuAsnValAlaHisAsn 160
 |||||
 QY 584 CTTATCCAACTTTGAAATTAACCTGAGATTTTCTAATCTGACCAATCTTAAGCACTTG 643
 |||||
 Db 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180
 |||||
 QY 644 GACCTTCCAGCAACAGATTCAGAAATTAATTAATGACAGACTGGCGGTTCTACACAA 703
 |||||
 Db 181 AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAsnLeuAlaGluValLeuHisGln 200
 |||||
 QY 704 ATGCCCCCTACTCATCTCTCTTTAGACCTGCTCCGATCCCTATGAATTAATTCACAA 763
 |||||
 Db 201 MetProLeuLeuAsnLeuSerLeuAsnProMetAsnProMetAsnProMetAsnProMet 220
 |||||
 QY 764 GGTGCATTTTAAAGAAATTAAGCTTCATTAAGCTGCTTAAGAAATTAATTTGATAGTTTA 823
 |||||
 Db 221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnProMetAsnProMet 240
 |||||
 QY 824 AATGTAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 883
 |||||
 Db 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 |||||
 QY 884 GGAGAAATTTTGAATTAAGAAATTAAGAAATTTTGAACAAATGCTGCTTAAGAGGCGCTG 943
 |||||
 Db 261 GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAsnProMetAsnProMetAsnProMet 280
 |||||
 QY 944 TGCAATTTGACCATTTGAAGAAATTCGATTAAGCAATTAATTAATTAATTAATTAATTA 1003
 |||||
 Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAsnProMetAsnProMetAsnProMet 300
 |||||
 QY 1004 AATGACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1063
 |||||
 Db 301 IleAsnLeuPheAsnLysCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 |||||
 QY 1064 GAAAGGCTAAAGAACTTTCTTAATTAATTTGCGATGGCAACATTTAGTAATTAATTAAT 1123
 |||||
 Db 321 GlyArgValLysAsnProMetSerTyrAsnProMetSerTyrAsnProMetSerTyrAsnProMet 340
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 QY 1124 AAAATTTGACAGTTTCCCATTAAGAAATTCGATTAAGCAATTAATTAATTAATTAATTA 1183
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 Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
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 QY 1184 AACAAAGGTGGGAATGCTTTTTCAGAAATTCGATTAAGCAATTAATTAATTAATTAATTA 1243
 |||||
 Db 361 AsnLysGlyGlyAsnAlaPheSerGluValAsnProMetSerLeuGluPheLeuAsnProMet 380
 |||||
 QY 1244 AGTAAAGAAATGCTGAGTTTCAAAAGTTGCTGCTCAAAAGTGAATTTTGGGCAACACAGC 1303
 |||||
 Db 381 SerArgAsnGlnLysLeuSerPheLysGlyCysSerSerIleSerAsnProMetSerIleThrSer 400
 |||||
 QY 1304 CTAAGATTAATTAAGATTCGATTAAGCAATTCGATTAAGCAATTCGATTAAGCAATTCGAT 1363
 |||||
 Db 401 LeuLysLysLeuAsnProMetSerPheAsnGlyValIleThrMetSerSerAsnProMetSer 420
 |||||
 QY 1364 TTGGAACAACTTAAGCAATTCGATTAAGCAATTCGATTAAGCAATTCGATTAAGCAATTCGAT 1423
 |||||
 Db 421 LeuGlnGlnLeuGlnLysLeuAsnProMetSerPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
 |||||
 QY 1424 TCAGTATTTCTATCACTCAAGAAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 1483
 |||||
 Db 441 SerValPheLeuSerLeuAsnProMetSerPheLysGlyCysSerSerIleSerAsnProMetSer 460
 |||||
 QY 1484 GTTGCATTTCAATGATCTTCAATGATCTTCAATGATCTTCAATGATCTTCAATGATCTTCAAT 1543
 |||||
 Db 461 ValAlaPheAsnGlyLysPheAsnGlyLysSerSerLeuGluValLeuLysMetAlaGly 480
 |||||
 QY 1544 AATTTCTTTCAGAGAAATTCCTTTCAGATATCTTTCAGAGATCTTTCAGAGATCTTTCAGAGAT 1603
 |||||
 Db 481 AsnSerPheGlnGlnLeuAsnProMetSerPheAlaPheThrGlnLeuArgAsnLeuThrPhe 500

QY 1604 CTGAGACTTCTGAGTGTCACTGAGACAGTGTCTTCCAAACAGATTTAACTCATCTCC 1663
 |||||
 Db 501 LeuAsnProMetSerGlnCysGlnLeuGlnLysLeuSerProThrAlaPheAsnSerLeuSer 520
 |||||
 QY 1664 AGTCTCAGGTACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1723
 |||||
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnProMetSerLeuAsnProMetSerLeu 540
 |||||
 QY 1724 AAGTGTGAACTCCCTCCAGGTTCTTGAATTAAGTCAATGATTAAGCAATTAAGCAATTAAG 1783
 |||||
 Db 541 LysCysLeuAsnSerLeuGlnValLeuAsnProMetSerLeuAsnProMetSerLeuAsnProMet 560
 |||||
 QY 1784 AAACAGAACTACAGCAATTTCCAGATGATCTTGAATTAATTAATTAATTAATTAATTAATTA 1843
 |||||
 Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsn 580
 |||||
 QY 1844 TTTGCTTGTACTTGTGAACACAGAGTTCTTCAATGATTAAGCAATTAAGCAATTAAGCAAT 1903
 |||||
 Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrPheLysAsnGlnArgGlnLeu 600
 |||||
 QY 1904 TTGCTGGAAGTTGAAGAAATGAATGAGAACTTCAAGCAATTAAGCAATTAAGCAATTAAG 1963
 |||||
 Db 601 LeuValGluValGluArgMetGlnCysAlaThrProSerAsnProMetSerLeuProVal 620
 |||||
 QY 1964 CTGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2023
 |||||
 Db 621 LeuSerLeuAsnLysThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 640
 |||||
 QY 2024 GTGCTGTGATATCTGTTGATGAGATTCGCTGATTAATTAATTAATTAATTAATTAATTA 2083
 |||||
 Db 641 ValLeuValValSerValValAlaValLeuValLysPheThrPheHisLysMetLeu 660
 |||||
 QY 2084 CTTGCTGCTGCACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2143
 |||||
 Db 661 LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnLysThrAsnAlaPheValIleTyr 680
 |||||
 QY 2144 TCAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2203
 |||||
 Db 681 SerSerGlnAsnProMetSerPheValArgAsnProMetSerPheValArgAsnProMetSer 700
 |||||
 QY 2204 CTTCAATTTCAAGTCTGCTTCACTCAAGCAATTAATTAATTAATTAATTAATTAATTAAT 2263
 |||||
 Db 701 ProProPheGlnLeuCysLysHisTyrArgAsnProMetSerPheValArgAsnProMetSer 720
 |||||
 QY 2264 AACATGATCCATGAAGTTTCCATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 2323
 |||||
 Db 721 AsnIleIleIleGlnLysPheHisLysSerArgGlyValIleValValValSerGlnHis 740
 |||||
 QY 2324 TTGATCCAGAGCGGCTGATGATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 2383
 |||||
 Db 741 PheIleGlnSerArgTyrPheHisLysSerArgGlyValIleValValValSerGlnHis 760
 |||||
 QY 2384 AGCAGTCTGCTGATCACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2443
 |||||
 Db 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArg 780
 |||||
 QY 2444 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGAACTTAATTAATTAATTAATTAATTAATTA 2503
 |||||
 Db 781 GlnGlnValGluLeuLysArgLeuLeuSerArgAsnThrTyrLeuGlnLysArgGlnLeuSer 800
 |||||
 QY 2504 GTGCTGAGGCGGCAATCTTTCAGAGCACTCAGAAAGCCCTGCTGATGATTAATCA 2563
 |||||
 Db 801 ValLeuGlyArgHisIlePheThrPheArgLeuArgLysAlaLeuLeuAsnProMetSer 820
 |||||
 QY 2564 TGGAACTCAGAAAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2620
 |||||
 Db 821 TrpAsnProGlnLysThrValGlyThrGlyCysAsnThrGlnLysAlaThrSerIle 839

RESULT 6

AAW86361 standard; protein; 837 AA.

ID AAW86361
XX AAW86361;
AC AAW86361;

XX 15-MAR-1999 (first entry)
DT Human DNAX toll-1-like receptor DTLR4.
XX
DE DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
KM modulate inflammatory function; morphological effect;
KW immunological disorder.
OS Homo sapiens.
XX
PN W09850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
DR WPI; 1999-059670/05.
DR N-PSDB; AAV80675.
XX
PT Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Claim 3; Page 147-149; 171pp; English.
XX
CC The present invention specifically describes human DNAX toll-1-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 837 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 4335.50 Matches: 837
Percent Similarity: 99.88% Conservative: 0
Best Local Similarity: 99.88% Mismatches: 0
Query Match: 50.54% Indels: 1
DB: 2 Gaps: 1
US-09-396-985b-1 (1-4868) x AAW86361 (1-837)
QY 107 ATGCTGCGCTCGGCGCTGGGAGCTGTATCCAGCAATGAGCTTCTCTCGTGAGTG 166
DB 1 MesSerIaSerIaGluAaGlyThrLeuIleProIaMetIaIaPheLeuSerCysVal 20
QY 167 AGACAGAAAGCTGGAGCCCTGCGTGAGGTGGTTCCTAATATTACTTATCATGATG 226
DB 21 ArgProGluSerTrpGluProCysValGlu---ValProAsnIleThrTrpGlnCysMet 39
QY 227 GAGCTGAATTTCTACAAAATCCCGACAACTCCCTTTCTACACAGAACTGGAGCTG 286
DB 40 GluLeuAsnPheTrpIleProAspAsnLeuProPheSerThrIleAsnLeuAspLeu 59

QY 287 AGCTTAAATCCCTGAGGAGCATTTAGGCACTATAGCTTCTTCAGTTTCCAGAACTGACG 346
DB 60 SerPheAsnProLeuAsnIleGluIleuGlySerTrpSerPheSerPheProGluLeuGln 79
QY 347 GTGCTGGATTTATCCAGGTGTGAATCCAGACAAATGGAATGGGGCATATTCAGAGCTTA 406
DB 80 ValIleAspLeuSerArgGlyGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 99
QY 407 AGCCACTCTTACCTTAATATTGACAGGAAACCCCATCCAGAGTTTAGCCCTGGAGGCC 466
DB 100 SerIleSerThrLeuIleuThrGlyAsnProIleGlnSerLeuIleuGlyIle 119
QY 467 TTTTCGACTATCAAGTTTACAGAGCTGTGTGCTGTGAGACAAATCTAGACATCTCTTA 526
DB 120 PheSerGlyLeuSerSerLeuGlnIleuValIleValGluThrAsnLeuIleuSerLeu 139
QY 527 GAGAACTTCCCATTTGGACATCTCAAACTTTGAAAGAACTTAATGTGGCTCAAACTCTT 586
DB 140 GluAsnPheProIleGlyIleuIleuSerThrLeuIleuGlyGluLeuAsnValIleIle 159
QY 587 ATCCATCTTTGAAATTTACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTGGAC 646
DB 160 IleGlnSerPheLeuProGluTrpPheSerAsnLeuThrAsnLeuGlnIleuAsp 179
QY 647 CTTTCAGACAAAGATTCAAAGTATTTATTCACACAGCTTCGGGTTCTACATCAATG 706
DB 180 LeuSerSerAsnIleGlnIleuSerIleuTrpCysIleThrAspLeuArgValLeuIleGln 199
QY 707 CCCCTACTCAATCTCTCTTTAAGCTGTGCTCGGATCTTATGAACTTTATCCAACTGAGT 766
DB 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGly 219
QY 767 GCAATTAAGAAATTAAGCTTCATTAAGCTTACACTTTAGAAATTAATGATTGTTAAAT 826
DB 220 AlaPheLeuGluIleArgLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 239
QY 827 GTAATGAAACTGTATTCAGAGCTGCTGTGCTTTAGAACTCATGTTGTTCTGGAG 886
DB 240 ValMetLeuThrCysIleGlnIleuValIleGlnIleuValIleArgLeuValIleuGly 259
QY 887 GAATTTAGAAATGAGAAACTTTGAAAGTTTGACAAATCTGCTTTAGAGGCTGTGC 946
DB 260 GluPheArgAsnGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 279
QY 947 AATTTGACATTTGAAAGAAATTCGATTTAGACTTACCTGATGATGATTTATTT 1006
DB 280 AsnLeuThrIleGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 299
QY 1007 GACTTATTTAATGTTTGACAAATGTTCTCTCAATTTCCCTGAGTGTGACTATTTGAA 1066
DB 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
QY 1067 AGGTAAAGACTTTTCTTAATAATTTGAGATGGCAACTTTAGAAATTAGTTAACTGTAAA 1126
DB 320 ArgValIleAspPheSerTrpAsnPheGlyTrpGlnIleuGlnIleuValIleuValIle 339
QY 1127 TTGTGACAGTTTCCCATTTGAAACTCAATCTCTGAAAGGCTTACTTCTTCCAC 1186
DB 340 PheGlyGlnPheProThrLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 359
QY 1187 AAAGTGGGAATGCTTTTCAAGATTTGATCTTCAAGAGCTTGAAGTTTCTAGATCTCAGT 1246
DB 360 LysGlyGlyAsnIlePheSerGlyValIleAspLeuProSerLeuGlnIleuAspLeuSer 379
QY 1247 AGAAATGCTTGAAGTTTCAAGGTTCTGTCTCAAGATTTTGGACAACTGAGCTTA 1306
DB 380 ArgAsnGlyLeuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1307 AAGTATTTGATGATGATCTTCAATGATTTATTTACATAGTTCAAGTTCTTGGGCTTA 1366
DB 400 LysIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1367 GAACAACCTAGAACATCTGATTTCCAGCAATTCATTTGAAACAAATGAGTGAAGTTTCA 1426

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Db      420  G|G|I|n|e|u|g|i|n|u|s|e|u|a|p|h|e|g|i|n|h|s|e|r|s|e|n|e|u|y|s|g|i|n|e|s|e|r|g|i|u|p|h|s|e|r 439
Oy      1427  G|T|A|T|C|C|A|T|C|A|C|G|A|A|A|C|C|T|T|A|C|T|T|G|A|C|A|T|T|C|T|C|A|T|C|A|C|C|A|G|G|T 1486
Db      440  V|a|P|h|e|u|s|e|r|e|u|a|g|a|n|l|e|u|l|e|r|y|l|e|u|a|s|p|i|l|e|s|e|r|h|s|t|r|h|s|t|r|h|g|v|a|l 459
Oy      1487  G|C|T|T|C|A|A|T|G|C|A|T|T|C|A|A|T|G|G|C|T|T|G|C|A|G|T|C|C|A|G|T|T|G|A|A|A|T|G|G|T|G|C|A|T 1546
Db      460  A|l|e|h|e|a|n|s|c|i|y|l|e|h|e|a|n|g|i|l|e|u|s|e|r|s|e|r|i|e|u|i|v|a|l|e|u|y|m|e|t|a|a|g|i|y|a|n 479
Oy      1547  T|C|T|T|C|C|A|G|A|A|A|C|T|T|C|T|C|C|A|G|A|T|T|C|T|C|C|A|G|A|G|C|T|G|A|A|A|C|T|T|G|A|C|T|T|G|C 1606
Db      480  S|e|r|p|h|e|g|i|n|u|s|e|r|p|h|e|u|P|r|o|a|s|p|i|l|e|h|e|r|h|g|i|u|e|r|u|a|g|e|n|l|e|u|r|h|P|h|e|u 499
Oy      1607  G|A|C|C|T|C|T|C|A|G|G|T|C|A|C|T|G|A|G|C|A|G|T|G|T|C|C|C|A|C|A|G|C|A|T|T|T|A|C|T|C|T|C|C|A|G|T 1666
Db      500  A|s|p|h|e|u|s|e|r|i|n|C|y|s|i|n|l|e|u|g|i|n|l|e|u|s|e|r|t|h|r|a|l|a|h|e|a|n|s|e|r|l|e|u|s|e|r|s|e|r 519
Oy      1667  C|T|T|C|A|G|G|T|A|T|A|T|A|T|G|A|C|C|A|C|A|C|A|C|T|T|C|T|T|C|A|T|G|A|T|G|A|T|G|A|T|G|T|C|T|T|A|G 1726
Db      520  L|e|u|g|i|n|V|a|l|e|u|s|m|e|t|s|e|r|h|s|a|n|a|n|h|e|p|h|e|s|e|r|e|u|a|s|p|h|r|p|h|e|r|o|t|y|l|y|s 539
Oy      1727  T|G|T|G|A|A|C|T|C|C|T|C|C|A|G|G|T|T|T|G|A|T|T|A|C|A|G|T|C|A|T|C|A|T|C|A|T|A|T|G|A|C|T|T|C|A|A|A|A 1786
Db      540  C|y|s|e|u|a|n|s|e|r|l|e|u|g|i|n|V|a|l|l|e|u|a|p|t|y|S|e|r|l|e|u|a|n|h|i|s|t|l|e|w|e|t|h|r|s|e|r|y|e|y|s 559
Oy      1787  C|A|G|A|A|C|T|A|G|A|C|A|T|T|T|C|C|A|G|A|G|T|C|T|T|C|T|T|A|A|T|C|T|A|T|C|T|A|C|G|A|T|G|A|T|T 1846
Db      560  G|i|n|g|i|l|e|u|g|i|n|h|s|h|e|P|r|o|s|e|r|S|e|r|l|e|u|a|l|a|h|e|u|a|n|e|u|r|h|g|i|n|a|n|a|s|p|h|e 579
Oy      1847  G|C|T|T|G|A|C|T|T|G|A|A|C|C|A|G|A|G|T|T|C|C|T|C|A|T|G|A|T|G|A|C|A|G|A|G|C|A|G|C|A|G|C|T|T|G 1906
Db      580  A|l|e|C|y|e|h|r|h|y|s|g|i|u|h|s|i|n|s|e|r|P|h|e|u|e|i|g|i|n|t|r|i|l|e|y|s|a|p|g|i|n|a|g|i|n|l|e|u 599
Oy      1907  G|T|G|A|A|G|T|G|A|C|G|A|T|G|A|T|G|C|A|C|C|T|T|C|A|G|A|T|A|G|A|G|G|C|A|G|C|T|G|T|G|C|T|G 1966
Db      600  V|a|l|g|i|u|a|l|u|a|r|g|m|e|t|g|i|u|c|y|a|l|a|h|r|P|r|o|s|e|r|a|s|p|y|s|i|n|g|i|y|m|e|t|P|r|o|v|a|l|l|e|u 619
Oy      1967  A|G|T|T|G|A|A|T|C|A|C|C|T|G|C|A|G|A|T|G|A|A|A|C|A|C|A|T|C|T|G|T|G|T|G|T|G|T|T|A|T|C|T|A|C|T|C|A 2026
Db      620  S|e|r|l|e|u|a|n|h|e|r|h|C|y|s|i|n|e|t|A|s|h|u|y|s|h|r|i|l|l|e|g|i|y|a|l|s|e|r|V|a|l|l|e|u|s|e|r|V|a|l 639
Oy      2027  C|T|T|G|A|T|C|T|G|T|G|A|G|A|G|T|T|C|T|G|T|A|T|A|G|T|T|C|A|T|T|T|A|C|C|G|A|T|G|C|T|T|C|T 2086
Db      640  L|e|u|V|a|l|s|e|r|V|a|l|a|a|v|a|l|l|e|u|V|a|l|l|y|s|h|e|r|h|y|r|h|e|h|s|l|e|m|e|l|e|u 659
Oy      2087  G|C|T|G|C|T|G|C|A|T|A|A|G|T|A|G|T|A|G|G|T|G|A|A|A|C|A|T|C|T|A|T|G|C|T|T|T|A|T|C|T|A|C|T|C|A 2146
Db      660  A|l|a|g|i|C|y|e|i|l|e|y|r|g|i|y|a|g|i|y|l|u|a|n|h|l|e|r|h|a|s|h|a|p|h|e|V|a|l|l|e|r|y|s|e|r 679
Oy      2147  A|G|C|A|G|A|T|A|G|A|C|T|G|G|T|A|G|A|G|A|T|G|A|C|T|G|T|A|A|A|A|T|T|A|G|A|A|G|G|G|T|G|C|T 2206
Db      680  S|e|r|g|i|a|s|p|i|u|a|s|p|r|V|a|l|a|r|g|a|n|g|i|u|d|e|u|V|a|l|y|s|a|n|e|u|g|i|u|g|i|y|V|a|l|P|r|o 699
Oy      2207  C|A|T|T|C|A|G|C|T|G|C|T|C|A|C|A|G|A|C|T|T|A|T|T|C|C|G|G|T|G|G|C|A|T|T|G|G|C|A|C 2266
Db      700  P|r|o|h|e|i|n|e|u|c|y|s|e|h|i|s|t|r|y|r|a|r|g|a|s|h|p|h|e|i|l|e|r|o|l|y|a|l|a|h|a|i|e|a|a|h|a|a|h 719
Oy      2267  A|T|C|A|T|C|A|T|G|A|G|G|T|T|C|A|T|A|A|A|G|C|G|A|A|G|G|T|G|T|G|T|G|T|G|T|C|C|C|A|C|A|C|T|T|C 2326
Db      720  I|l|e|i|l|h|i|s|g|i|u|g|i|p|h|e|h|i|s|y|s|e|r|a|r|g|i|y|V|a|l|l|e|V|a|l|V|a|l|s|e|r|g|i|h|i|s|h|p|h 739
Oy      2327  A|T|C|A|G|A|G|C|G|G|G|G|T|A|T|C|T|T|G|A|T|A|G|A|G|A|T|T|G|C|T|C|A|G|C|T|G|C|G|C|T|T|G|A|G|C 2386
Db      740  I|l|e|i|n|s|e|r|a|r|g|t|r|p|C|y|s|i|l|e|h|e|g|i|u|r|g|i|u|l|e|a|l|n|h|r|t|r|p|g|i|h|p|h|e|l|e|s|e|r 759
Oy      2387  A|G|T|G|T|G|G|T|A|T|C|A|T|T|G|C|T|G|C|A|G|A|G|G|T|G|A|G|A|G|C|C|T|G|C|A|G|G|C|A|G 2446
Db      760  S|e|r|a|r|g|a|l|a|g|i|l|e|i|l|e|h|e|i|l|e|V|a|l|l|e|u|g|i|n|y|s|V|a|l|g|i|u|y|s|h|r|h|e|u|l|e|u|a|r|g|i|n 779
Oy      2447  C|A|G|G|T|G|A|G|C|T|G|T|C|C|G|C|T|T|C|A|G|C|A|G|A|C|A|C|T|T|A|C|T|G|A|G|T|G|A|G|A|G|A|G|A|G|A|G|T|G|C 2506

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Db      780  G|n|V|a|l|G|i|u|e|r|y|r|a|r|g|l|e|u|s|e|r|a|r|g|a|n|h|r|h|y|r|l|e|u|g|i|u|r|p|i|u|a|s|p|S|e|r|V|a|l 799
Oy      2507  C|T|G|G|G|G|G|G|C|A|C|A|T|T|T|G|G|A|G|A|C|T|C|A|G|A|A|A|G|C|C|T|G|G|A|T|G|G|T|A|A|T|C|A|T|G 2566
Db      800  L|e|u|G|i|y|r|g|h|i|s|h|e|h|r|h|p|r|a|r|g|l|e|u|a|r|g|y|a|h|a|l|e|u|e|u|a|s|p|i|y|s|e|r|t|r|p 819
Oy      2567  A|A|T|C|A|G|A|A|G|A|C|A|G|T|G|G|T|A|C|A|G|A|T|G|C|A|T|T|G|C|A|G|A|G|C|A|C|A|T|C|A|T|C 2620
Db      820  A|a|n|P|r|o|G|i|u|c|i|y|h|r|V|a|l|g|i|y|h|r|g|i|y|C|y|a|n|h|r|p|i|n|d|i|u|h|a|h|r|s|e|r|i|l|e 837

RESULT 7
AAE16102 standard; protein; 837 AA.
ID   AAE16102
AC   AAE16102;
DT   26-MAR-2002 (first entry)
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
OS   Homo sapiens.
OX   NC_000190151-A2.
PD   29-NOV-2001.
PF   23-MAY-2001; 2001MO-US016766.
PR   25-MAY-2000; 2000US-0207558P.
SCHE ) SCHERING CORP.
PT   Hardiman GT, Rock FL, Bazan JF, Kastlein RA, Ho SWK, Liu Y;
DR   WPI; 2002-083085/11.
DR   N-PDB; AAD26292.
XX   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
PS   Claim 3; Page 41; 297bp; English.
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified fragments can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC   Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC   sequence shown in page 240-243 (AAE16116). However these sequences differ
CC   at several locations
XX
SQ   Sequence 837 AA:
Alignment Scores: 0
Pred. No.: 4335.50
Score: 99.884
Length: 837
Matches: 837
Conservative: 0

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Best Local Similarity: 99.88% Mismatches: 0
Query Match: 50.54% Indels: 1
DB: 5 Gaps: 1
US-09-396-985b-1 (1-4868) x AAE16102 (1-837)

QY 107 ATGTGCGCTCGCGCTGGGAGACTGTATCCAGCCATGGCCTTCTCTCGCGTG 166
Db 1 MetSerLaserArgLeuAlaGlyThrLeuIleProLametaLapheLeuSerCysVal 20
QY 167 AGACGGAAGCGGAGACCCCTCGGAGAGTGTTCTTAATTAATTCAATGATG 226
Db 21 ArgProGlnSerThrGluProCysValGlu--ValProasnIleThrTyGlnCysMet 39
QY 227 GAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACAAGACTGACCTG 286
Db 40 GluLeuAsnPhenTyrrylsIleProAspAsnLeuProPheSerThrTyrsanLeuAspLeu 59
QY 287 AGCTTAATCCCGTAGGCAATTTAGGCAAGCTATAGCTTTCAGTTTCCGAGAACTGAC 346
Db 60 SerPheAsnProLeuArgHisLeuGlySerTySerPheSerPheProGlnLeuGln 79
QY 347 GTGCTGATTTATCCAGGTGTGAATTCAGAACTTGAAGATGGGGATTCAGAGCTTA 406
Db 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGlnAspGlyAlaTyrglnSerLeu 99
QY 407 AGCACCTCTCTCACTTAATATTGACAGAAACCCCATCCAGAGTTTAGCCCTGGAGCC 466
Db 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 467 TTTTTCGACTATCAAGTTTACAGAAAGCTGTGGCTGTGAGACAAATCTGACATCTTA 526
Db 120 PheSerClyLeuSerSerLeuGlnTyLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
QY 527 GAAACATTCGCCCATTTGGACATCTCAAAACTTTGAAAGACTTAATGTGGCTCAATCTT 586
Db 140 GluAsnPhenProIleGlyHisLeuTystrLeuIleGluLeuAsnValAlaHisAsnLeu 159
QY 587 ATCCAAATCTTCAAAATTACCTGAGTATTTTCTATCTGACCAATCTAGAGCACTTGAC 646
Db 160 IleGlnSerPheTystrLeuProGlnTyPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
QY 647 CTTTCCAGCAACAGATTCAAGATTTTATTTGACACAGACTGGGGGTTTCAATCAATG 706
Db 180 LeuSerSerAsnTystrIleGlnSerIleTystrCysThrAspLeuArgValHisGlnMet 199
QY 707 CCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAATCTTAATGAACTTTATCCACCGGT 766
Db 200 ProLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPhenIleGlnProGly 219
QY 767 GCATTTAAAGAAATTAGGCTTCAATAGCTGACTTAAGAATAATTTGATAGTTTAAT 826
Db 220 AlaPheIleGlnIleArgLeuHisTystrLeuThrLeuArgAsnAsnPhenAspSerLeuAsn 239
QY 827 GTAATGAAAACCTTGATTTCAAGGCTTGCGCTGTTTGAAGTCCATCGTTTGTTCTGGA 886
Db 240 ValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
QY 887 GAATTTAGAAATGAGAAACTTTGAAAAGTTTGACAAATCTGCTTCAAGGGCTGTGC 946
Db 260 GluPheArgAsnGlnGlyAsnLeuGlnTystrPheAspTystrAlaLeuGlnGlyLeuCys 279
QY 947 AATTGACATTTGAAGAAATCCGATTTAGCATCTTACTACTACCTCGATGATTAAT 1006
Db 280 AsnLeuThrIleGlnGlnPheArgLeuAlaTystrLeuAspTyrrylsLeuAspAspIleLe 299
QY 1007 GACTTATTTAATGTTTGAACAAATGTTCTTCAATTTCCCTGTGAGTGTGACTATGAA 1066
Db 300 AspLeuPheAsnTystrLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
QY 1067 AGGGTAAAGACCTTTTCTTAATTTGATGCGACATTTAGATTTAGATTTAACTGTAA 1126
Db 320 ArgValTystrAspPheSerTystrAsnPhenGlyTyrrylGlnHisLeuGlnLeuValAsnTystr 339

QY 1127 TTGACAGTTTCCCATTTGAAACTCAATCTTCAAAAGGCTTACCTTTCACCTTCCAC 1186
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QY 1187 AAAAGTGGAAATGCTTTTCCAGAACTTATCTTCAAGCTTGAATTTCTAGTCTCAGT 1246
Db 360 TystrGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
QY 1247 AGAAATGGCTGAGTTTCAAGGCTGTCTTCCAAAGTATTTTGAGCAACACGACCTTA 1306
Db 380 ArgAsnGlyLeuSerPheTystrGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1307 AAGTATTTAGATCTGAGCTTCAATGAGTGTATTAATCCATGATGTAACATTTCTGGGCTTA 1366
Db 400 TystrTystrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhenLeuGlyLeu 419
QY 1367 GAACAACTGACATCTTGAATTTCCAGCAATTTCAATTTGAAACAAATGATGATTTTCA 1426
Db 420 GluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuTystrGlnMetSerGlnPheSer 439
QY 1427 GTATTCTATCACTGAGAAACCTCATTTACTTTCATTTCTGATCTCACACAGAGTT 1486
Db 440 ValPheLeuSerLeuArgAsnLeuIleTystrLeuAspIleSerHisThrArgVal 459
QY 1487 GCTTTCAAATGGCATCTTCAATGGCTTGTCCAGTCTGAAATCTTGAATAATGGCTGGCAAT 1546
Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuTystrMetAlaGlyAsn 479
QY 1547 TCTTTCAGAGAAAACCTTCTCCAGATATCTTCAACAGCTGAGAAAACCTTACCTCTG 1606
Db 480 SerPheGlnGlnAsnPhenLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeu 499
QY 1607 GACCTCTCAAGTGTCACTGAGAGCTTGTCTCAACAGCAATTTAACTCACTCTCAGT 1666
Db 500 AspLeuSerGlnTystrGlnLeuGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 519
QY 1667 CTTCAAGTACTAAATGTGACCAACAACAATCTTTTCAATGGATAGCTTCCCTTAATG 1726
Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhenPheSerLeuAspThrPheProTystr 539
QY 1727 TGTCTGAACCTCCCTCCAGGTTCTTGAATCAAGTCTCAATCAATATGACTTCCAAAAA 1786
Db 540 CysLeuAsnSerLeuGlnValLeuAspTystrSerLeuAsnHisGlyMetThrSerTystr 559
QY 1787 CAGGAACACAGATTTTCCAAAGTACTAGCTTGTAAATCTTCAAGATGACTT 1846
Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY 1847 GCTTGTACTTGTGAACACAGAGTTTCTGCAATGATGATCAAGACCAAGGACGACTTGG 1906
Db 580 AlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleTystrAspGlnArgGlnLeuLeu 599
QY 1907 GTGAAAGTTGAACGAATGGAATGTGCAACACTTCAATATGACAGGACATGCTGTGCTG 1966
Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspTystrGlnGlyMetProValLeu 619
QY 1967 AGTTGAATATCACTGCAAGTGAATGAATGACATGATGCTGTGCGGCTCAAGTGTG 2026
Db 620 SerLeuAsnIleThrCysGlnMetAsnTystrHisIleGlyValSerValLeuSerVal 639
QY 2027 CTTGTAGTATCTGTTTGAACGATTTGCTATATGATCTTATTTTCAACGATGATCTTCT 2086
Db 640 LeuValValSerValValAlaValLeuValTystrPheTystrPheHisLeuMetLeuLeu 659
QY 2087 GCTGGCTGCAATAAGATGATGAGGTGAGAAACATGATGATGCTTGTGTTATCTACTCA 2146
Db 660 AlaGlyCysIleTystrTystrGlyArgGlyGlnAsnIleTystrAspAlaPheValIleTystr 679
QY 2147 AGCCAGATGAGGACTGGGTTAGGATGAGCTATGATTAAGAAATTTAAGAAAGGGGTGCT 2206
Db 680 SerGlnAspGlnAspThrValArgAsnGlnLeuValTystrAsnLeuGlnGlnValPro 699

QY 2207 CCATTTCAGCTCTGCTTCACTACAGAGACTTATTCCTCCGGTGGCCATTGCTGCCAC 2266
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 Db 700 ProPheGlnLeuCySleuHtstYrArgAspPheIleProGlyValAlaIleAlaIleAsn 719
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 QY 2267 ATCATCATTAAGGTTTCCATTAAGCCGAAAGGTGATTGTGTGTCTCCAGCACTTC 2326
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 Db 720 IleIleIleGlnGlyPheHtstYsSerArgIleValIleValValSerGlnHtstPhe 739
 |||||
 QY 2327 ATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGGAGGTTTCTGAGC 2386
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 Db 740 IleGlnSerArgTyrPheIlePheGlnIleValIleAlaIleHtstPheIlePheSer 759
 |||||
 QY 2387 AGTCGTCTGTATCATCTTCTTCTGCTCAGAGGTGAGAGACCTCTCAGGAG 2446
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 Db 760 SerArgAlaGlyIleIlePheIleValIleGlnIleValIleGlnIleuArgGln 779
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 QY 2447 CAGGTGAGCTGTACCGCTTCTCAGAGAGAACCTTACCTGGAGTGGAGACAGTGT 2506
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 QY 2507 CTGGGGGGGACATCTTCTGAGAGCAGTCAAGAAAGCCCTGCTGATGTTAATCATG 2566
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 Db 800 LeuGlyArgHtstIlePheHtstPArgIleuArgIleuArgIleuSerGlyIysSerItr 819
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 QY 2567 AATCCAGAAAGAACAGTGGGTACAGATGCAATTGGCAGAGAACATCTATC 2620
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 Db 820 AsnProGlnGlyHtstValGlyHtstGlyCysAsnHtstPheIleHtstIleHtstSerIle 837
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RESULT 8
 AB004776 ID AB004776 standard; protein; 837 AA.
 XX AC AB004776;
 XX DT 29-JAN-2003 (first entry)
 XX DE Human expressed protein tag (EPT) #1442.
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX OS Homo sapiens.
 XX PN WO200278524-A2.
 XX PD 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US009671.
 XX PR 28-MAR-2001; 2001US-0279495P.
 XX PR 21-MAY-2001; 2001US-0292544P.
 XX PR 08-AUG-2001; 2001US-0310801P.
 XX PR 01-OCT-2001; 2001US-0326370P.
 XX PR 04-DEC-2001; 2001US-0336780P.
 XX PR 20-FEB-2002; 2002US-0358985P.
 XX PA (ZYCO-) ZYCOS INC.
 XX PI Chicx RM, Tomlinson AJ, Urban RG;
 XX DR WPI; 2003-040607/03.
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukaemia.
 XX Example 2; SEQ ID NO 1442; 134p; English.
 XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 837 AA;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score:	0	837	837
Percent Similarity:	4335.50		
Best Local Similarity:	99.88%	0	0
Query Match:	50.54%	1	1
DB:	6	Gaps:	1

US-09-396-985B-1 (1-4868) x AB004776 (1-837)

QY 107 ATGTCGTCTGCGCTGTGGAGCTGTGATCCAGACATGACCTTCTCTGCGTG 166
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 Db 1 MetSerIleSerArgIleuAlaGlyHtstIleProAlaMetAlaPheIleuSerCysVal 20
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 QY 167 AGACCGAAAGCTGGAGCCCTGCGAGAGTGTCTTAATTTACTTATCATGATG 226
 |||||
 Db 21 ArgProGlnSerItrPheIleProCysValGlu---ValProAsnIleHtstYrGlnCysMet 39
 |||||
 QY 227 GAGCTGAATTTTCAGAAATCCCGCAACCTCCCTTCGACAGAAAGCTGAGCCTG 286
 |||||
 Db 40 GlnIleuAsnPheHtstYrIlePheProAsnIleuPhePheSerHtstYrAsnIleuAsn 59
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 QY 287 AGCTTAAATCCCTGAGGAGATTTAGCAGCTATAGCTTCTTCAGTTCCAGAACTG 346
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 Db 60 SerPheAsnProIleuArgHtstIleuGlySerItrPhePheSerPheProGlnIleuGln 79
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 QY 347 GTCTGTGATTTATCCAGGTGTGAATCCAGCAATGAGATGGGCTATGAGCCTA 406
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 Db 80 ValIleuAspIleuSerArgCysGlnIleGlnHtstIleGlnAspIleValItrGlnSerIleu 99
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 QY 407 AGCCACCTCTACCTTAATATTTGACAGAAAGCCATCCAGAGTTTGAAGCCCTGGAGCC 466
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 Db 100 SerHtstIleuSerHtstIleuHtstIleuHtstIleuHtstIleuHtstIleuHtstIleu 119
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 QY 467 TTTTCTGACTATCAAGTTTACAGAGCTGTGGTGTGGAGCAATTCAGATCTCTA 526
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 Db 120 PheSerGlyIleuSerIleuGlnIleuValAlaValGlnHtstIleuAlaSerIleu 139
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 QY 527 GAGAACTTCCCATTTGAGACTTCAAACTTTGAAGAACTTATATGTGCTCAATCTT 586
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 Db 140 GlnAsnPheProIleGlyHtstIleuHtstIleuHtstIleuHtstIleuHtstIleu 159
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 QY 587 ATCCATCTTTCAATTTACAGATTTTTCATCAATTCAGCAATTCAGAGCACTTGAGC 646
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 QY 647 CTTTCAGAACAAAGATTCAAGTATTTATGACAGACTTGGGGTTCTACATCAATG 706
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 Db 180 IeuserSerAsnHtstIleGlnSerIleYrCysHtstAspIleuArgIleuHtstIleuMet 199
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 QY 707 CCCCTACTCAATCTCTCTTTTAACTGTGCTGATCTTATGAACTTTATCCAAAGGT 766
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QY 767 GCATTTAAAGAAATTAAGCTTCAATAGCTGACTTAAAGAAATATTGTAAGTATTAAAT 826
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 QY 827 GTAATGAAAATTGATTTCAAGGCTGGCTGTTTGAAGCTCCATGGTTGGTTGGGA 886
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 Db 240 ValMeLythrCysIleGIngluIleuAlaGlyLeuGluIvalHtIsrGleuValleuGly 259
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 QY 887 GAATTTAGAAATGAAGAAATCTGGAAGAGTTGACAAATGCTCTAGAGGGCCGTGC 946
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 Db 260 GluPheArgasnIuGluYasnleuGluYbPheaspYsSerAlaleuGluGlyleuCys 279
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 QY 947 AATTGACCATTAAGAAATCCGATTAGCATTAAGTACTACTACTCGATGATATTAT 1006
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 Db 280 AsnleuThrlleIuGluPheArgleuAlaTyIleuhsprYrTyIleuhsprAllelle 299
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 Db 300 AspLeuPheasnCysleuThraenValSerSerPheSerleuValSerValThrIleGlu 319
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 QY 1307 AAGTATTTAGATCTGAGCTTCAATGATGTTATTAACATGAGTTCMAACTTCTTGAGCTTA 1366
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 Db 420 GluGlnleuGlnIuhIseuAspPheGlnHsIerAsnleuYsgImetSerGluPheSer 439
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 Db 500 AspLeuSerGlnCysGlnleuGluGlnleuSerProthraIaPheasnSerleuSerSer 519
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Db 580 AlaCysThrCysGluHsIleGlnSerPheleuGlnTrpIleYAspGlnArgGlnleuLeu 599
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 QY 1907 GTGGAAGTTGAACGAATGGAATGTGCACACCTTCAGAAACAGAGGCAATGCTGAGCTG 1966
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 Db 600 ValGluValGluArgMetGluCysAlaThrProSerAspIlysgIlnIleMetProValleu 619
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 QY 1967 AGTTGAATATCACTCGTGCAGATGAATAGAACCATCATCATGATGGTGGCTCTCAGTGTG 2026
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 Db 620 SerleuAsnIleThrCysGlnMetCasnlystrHrIleIleGlyValSerAlleuSerVal 639
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 QY 2087 GCTGGCTGATTAAGTAAGTGTAGAGTGAACCACTATAGAGCCCTTGTATCTATCTCA 2146
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 QY 2207 CCATTTCACTCTGCTTCACTACAGAGACTTATTTCCCGGTGGCCATTCCTGCCAAC 2266
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 QY 2447 CAGGTGAGCTGTACCGCTTCCAGACAGAAACACTTACCTGAGTGGAGGAGCACTGTGC 2506
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 |||||
 QY 2507 CTGGGCGGCAACATCTTCTGAGACGACTCAGAAAGCCCTGCTGATGATGAATCATGAG 2566
 |||||
 Db 800 leuGlyArgHsIlePheThrPargleuArgIyAlaIleuAsnAspGlyYsSerTrp 819
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 QY 2567 AATCCAGAAAGAACAGTGGGTACAGGATGCATTTGGCAGAGCAACATCTATC 2620
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 Db 820 AsnProGluGlyThrValaGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 837
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 RESULT 9
 AAEI6116
 ID AAEI6116 standard; protein; 837 AA.
 XX
 AC AAEI6116;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 XX Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
 DE
 XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH
 FT MISC-difference 211
 FT /label= Unknown
 FT /note= "Encoded by AAY"
 XX
 XX W0200190151-A2.

PD 29-NOV-2001.
 XX 23-MAY-2001; 2001MO-US016766.
 PF 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI; 2002-083086/11.
 DR N-PSDB; AAD26306.
 XX New DMAX Toll like receptor (DTRL) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS Claim 3; Page 240-243; 297pp; English.
 XX The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DMAX Toll like receptor (DTRL) protein and their corresponding
 CC nucleic acids. The DTRL is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTRL is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTRL is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTRL or its various fragments. The
 CC purified DTRL can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTRL or cells that express it. The present sequence is
 CC human DTRL4 protein, alternative version. The DTRL4 gene is located on
 CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
 CC be similar to the sequence shown in page 41 (AAE16102). However these
 CC sequences differ at several locations
 XX
 XX Sequence 837 AA:
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4328.50 Matches: 836
 Percent Similarity: 99.76% Conservative: 0
 Best Local Similarity: 99.76% Mismatches: 1
 Query Match: 50.45% Indels: 1
 DB: 5 Gaps: 1
 US-09-396-985b-1 (1-4868) x AAE16116 (1-837)
 QY 107 ATGTCTGCTCGGCGCTGGAGACTGTGATCCAGCCATGCGCTCTCTCGGCG 166
 DB 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
 QY 167 AGACGAGAAGCGGGAGCCCTGCGTGGAGGTGCTTCTATATCTTCAATGAGANG 226
 DB 21 ArgProGlnSerThrGlnProCysValGln--ValProAsnIleThrTyrglnCysMet 39
 QY 227 GAGCTGAATTTCTCAAAATCCCGACAACCTCCCTTCTCAACAAGAGCTGACCTG 286
 DB 40 GluLeuAsnPheTyrlsileProAspAsnLeuProPheSerThrTyrsanLeuAspLeu 59
 QY 287 AGCTTTAATCCCTGAGGCACTTTAGGAGCTATAGCTTCTTCAGTTTCCAGAACTGACG 346
 DB 60 SerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGlnLeuGln 79
 QY 347 GTCTGATTTATCCAGGTGTAATCCAGCAATGAATGAGGAGATTCAGAGCTTA 406
 DB 80 ValLeuAspLeuSerThrGlyGlnIleGlnThrIleGlnAspGlyAlaTyrglnSerLeu 99
 QY 407 AGCACCTCTCTAATTATATTGACAGAAACCCATCCAGATTAGCCCTGGAGGCC 466

DB 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 QY 467 TTTCTGAGCTATACAGATTATGAGAGCTGGTGGCTGGAGCAATCTAGATCTCTA 526
 DB 120 PheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSerLeu 139
 QY 527 GAGAACTTCCCATTTGAGACATCTCAAAACTTTGAAAGAACTTATGAGTGCACAACTT 586
 DB 140 GluAsnPheProIleGlyHisLeuTyThrLeuLysGluLeuAsnValAlaHisAsnLeu 159
 QY 587 ATCCAACTTTTCAATTAATTAATCTGAGATTTTCTTAATCTGACCAATCTAGACACTTGAC 646
 DB 160 IleGlnSerPheLeuSerLeuProGlyTyPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
 QY 647 CTTTCAGACAAACAAGTATCAAGTATTTATGACAGACTGGGGGTTCTACATCAANG 706
 DB 180 LeuSerSerAsnLysIleGlnSerIleTyCysThrAspLeuArgValLeuHisGlnMet 199
 QY 707 CCCCTACTCAATCTCTCTTAGACTGTGCTGCTGAATCTTATGAACTTTATCCAGCAGGT 766
 DB 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeu***PrometAsnPheIleGlnProGly 219
 QY 767 GCATTTAAAGAAATTAGGCTTCTAATAGCTGACTTTAAGAATAATTTGATTAAT 826
 DB 220 AlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 QY 827 GTAATGAAAACTTGATTTCAAGGTCTGGCTGTTTGAAGTCCATGCTTTGCTTCGGGA 886
 DB 240 ValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
 QY 887 GAATTTAGAAATGAAGAACTTGAAAGTTTGAACAAATCTGCTCTAGAGGCTGTGC 946
 DB 260 GluPheArgAsnGlnLysLeuGlnLysPheAspLysSerAlaLeuGlnLysCys 279
 QY 947 AATTGACCATTTGAGAAATTCGATTAGCAATCTTACACTTACCTGATGATATTATT 1006
 DB 280 AsnLeuThrIleGlnGlnPheArgLeuAlaTyLeuAspTyTyLeuAspAspIleIle 299
 QY 1007 GACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGGAGTGCATATTGAA 1066
 DB 300 AspLeuPheAsnLysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
 QY 1067 AGGCTAAAGAACTTTCTTATATATTCCGATGGAGCAATTTAGATTAGTAACTGTA 1126
 DB 320 ArgValLysAspPheSerTyrsanPheGlyTyrglnHisLeuGlnLeuValAsnCysLys 339
 QY 1127 TTGGACAGTTTCCCATTTGAAACTCAATCTCTCAAAAGGCTTCTTCACTTCCAC 1186
 DB 340 PheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsn 359
 QY 1187 AAGGTGGGAATGCTTTTTCAGAGTTGATCTACAGAGCTTGAGTTTCTAGATCTCAGT 1246
 DB 360 LysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
 QY 1247 AGAAATGGCTGAGTTTCAAGGTGCTGTTTCAAGAGTATTTGGGCAACACAGCTTA 1306
 DB 380 ArgAsnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
 QY 1307 AAGTATTTAGATCTGAGCTTCAATGAGTGTATATTAATCCATGATGATCAACTTCTGGCTTA 1366
 DB 400 LysTyrlsLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
 QY 1367 GAACAACATGAAACATTTGAGATTTCCAGCATTTCAATTTGAAACAAATGAGTGGTTTCA 1426
 DB 420 GluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPheSer 439
 QY 1427 GTATTCCTTCACTGAGAAACCTCAATTTACTTGAATTTTCAATCTGACACCAAGATT 1486
 DB 440 ValPheLeuSerLeuArgAsnLeuIleTyrlsLeuAspIleSerHisThrHisArgVal 459
 QY 1487 GCTTTCAATGGGATCTTCAATGGCTTGTCCAGTCTGAACTTTGAAATGGCTGGCAAT 1546


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Db      460 AlaPheAsnGlyllePheAsnGlyleuSerSerleuGlnValleuIysMeAlaGlyAsn 479
QY      1547 TCCTTCCAGGAAACCTTCCTCCAGATATCTTCAGAGAGGTTGAGAACTTGACCTCCG 1606
Db      480 SerPheGlnIleuAsnPheleuProAspIlePheThrGlnleuArgAsnleuThrPheleu 499
QY      1607 GACCTCTCTCAGATGTCACATGAGAGAGATTGTCTCCACAGACATTTAACTCAGCTCCAGT 1666
Db      500 AspIeuSerGlnCysGlnleuGlnleuSerProThrIlePheAsnSerleuSerSer 519
QY      1667 CTTCAGGTAATAATATGAGCCACACACTTCTTTCAATGGATACGTTCTTATAG 1726
Db      520 leuGlnValleuAsnMetSerIleAsAsnAspPheSerleuAspThrPheProIlyAs 539
QY      1727 TGTGTGAACCTCCCTCAGGTTCTTGAATACAGTCACTCACTCAATATGACTTCCAAA 1786
Db      540 CysleuAsnSerleuGlnValleuAspIlySerleuAsnIlelleCtnrSerIySAs 559
QY      1787 CAGGAACTACAGCATTTTCCAGATAGTCTAGCTTTCTTAATCTTACTCAGAAATGACTT 1846
Db      560 GlnGlnleuGlnIlePheProSerSerleuAlaPheleuAsnleuThrGlnAsnAspPhe 579
QY      1847 GCTTTGATCTTTGAAACACAGAGATTCTTCGCAATGATCAGACACAGAGAGCTCTTG 1906
Db      580 AlaCysThrCysGlnIleAsnSerPheleuGlnIleThrIleIyAspGlnArgGlnleu 599
QY      1907 GTGGAAGTTGAAGAAATGGAATGGAACCTTCATATATGAGAGGAGGAGGAGGCTGCTG 1966
Db      600 ValGlnValGlnIleArgMetGlnCysAlaThrProSerAspIySglnIyMetProValleu 619
QY      1967 AGTTGAAATATCACTGTCCAGATGAAATAGACATCATTTGGTGTGCTCAGATGTC 2026
Db      620 SerleuAsnIleThrCysGlnMetAsnIyThrIleleGlyValSerValleuSerVal 639
QY      2027 CTGTGATATCTGTGTGAGACAGTTCTGCTCATATGATTTCACTTATTTCACTGATGCTTCT 2086
Db      640 leuValValSerValValAlaValleuValIlyrIySerPheIleProGlyValAlaIleAlaAsn 659
QY      2087 GCTGGCGTCATTAAGTATGATGATGAGGAGAAACATCTATATGCTTGTATCTACTCA 2146
Db      660 AlaGlyValIleIySglnIyArgGlyGlnAsnIleIyAspAlaPheValIleIySer 679
QY      2147 AGCCAGAGATGAGAGCTGGTAAAGAAATGAGCTAGTAAAGATTTAAAGAAAGAGGAGTCT 2206
Db      680 SerGlnAspGlnAspIlyrValArgAsnGlnleuValIySAsnleuGlnIyGlyValPro 699
QY      2207 CCATTTCACTCTGCTTCACTACAGACTTATATCCCGGTGTGGCCATTTGCTGCCAAC 2266
Db      700 ProPheGlnleuCysleuIleIyArgAspPheIleProGlyValAlaIleAlaAsn 719
QY      2267 ATCATCATGAAGGTTCCATTAAGCGCAAGGATGTTGTGTGTCGTCGCGACATTC 2326
Db      720 IleIleIleSglnIyPheAsnIySAspIyValIleValValIleValIleValIleValIle 739
QY      2327 ATCCAGAGCCGCTGCTGATCTTGAATATGAGATTTCTGACACTGCGACATTTCTGAGC 2386
Db      740 IleGlnSerArgIlyrCysIlePheGlnIyIleIleIleGlnIleIleIleIleIleIle 759
QY      2387 AGTCGTGCTGATCATTTCTTCAATGTCCTGAGAGGATGAGAAAGACTTGTCTCAGGAG 2446
Db      760 SerArgIleGlyIleIlePheIleValleuGlnIySglnIySglnIleuValArgGln 779
QY      2447 CAGGTGAGGCTGATCCGCTTCACAGAGAAACCTTACCTGAGTGGAGAGACAGTCTC 2506
Db      780 GlnAlaGlnleuIyArgleuSerArgAsnThrIyIleuGlnIyIleuAspSerVal 799
QY      2507 CTGGGAGGAGCATCTTCTGAGAGAGACTCAGAAAGCCCTGCTGAGTGGATTAATCAGG 2566
Db      800 leuGlnIyArgIleIlePheIleIlePheIleIleIleIleIleIleIleIleIleIleIle 819
QY      2567 AATCCAGAGAAACAGTGGGTACAGATGCATTTGGCAGAGAGAGCAACATCTATC 2620
Db      820 AsnProGlnIyThrValIleGlyThrGlyCysAsnIlyrGlnIleAlaIleThrSerIle 837

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RESULT 10
AD057782
ID AD057782 standard; protein; 808 AA.
XX
AC AD057782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN W02004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003MO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
XX
DR N-PSDB; AD057780, AD057781.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 3; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 808
Score: 4178.00 Matches: 805
Percent Similarity: 99.88% Conservative: 2
Best Local Similarity: 99.63% Mismatches: 1
Query Match: 48.70% Indels: 0
DB: 8 Gaps: 0
US-09-396-985b-1 (1-4868) x AD057782 (1-808)
QY      197 GTGGTTCCTTAATTTTCTTATATGATGAGAGCTGAATTTCTACAAATCCCGACAC 256
Db      1 ValValProAsnIleThrIyGlnCysMetGlnleuAsnIleIySglnIleProAsn 20
QY      257 CTCCCTTTCACACCAAGAACTGAGCTTGAATTCCTCGAGGACATTTAGGAGC 316
Db      21 leuProPheSerIlyrIySAsnleuAspIleuSerPheAsnProIleuArgIleuGlySer 40
QY      317 TATAGCTTCTTCAATTTCCAGAACTGACAGTGTGATTTATCCAGTGTGAATCAG 376
Db      41 TySerPhePheSerPheProGlnleuGlnValleuAspIeuSerArgGlnIleGln 60

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QY 377 ACAATTGAAGATGGGGCATATCAGAGCCTAAGCCACCTCTCTACCTTAATATTGACAGGA 436
Db 61 ThrileglunapglYalatyrglnSerleuSerHisleuSerThrleuileleThrGly 80
QY 437 AACCCCATCCAGAGTTTAAAGCCCTGGAGACCTTTCTGACATATCAAGTTTACAGAACCTG 496
Db 81 AsnProIleGlnSerleuAlaleuGlyAlaphSerGlyleuSerSerleuGlnlyleu 100
QY 497 GTGGCTGTGGAGCAAAATCTAGCATCTCTAGAGAACTTCCCAATTTGACATCTCAAACT 556
Db 101 ValAlaValGlnThrAsnleuAlaSerleuGlnAsnheProIleGlyHisleuLysThr 120
QY 557 TTGAAAGACCTTAATGTGGCTCACAACTTATCCAACTTTCAAAATACAGATATTTT 616
Db 121 LeuLysleuLeuAsnValAlaHisAsnleuileGlnSerPheLysleuProGlnLysPhe 140
QY 617 TCTAATCTGACCAATCTTAGAGCACTTGACCTTTCCAGCAACAAGATTCAAAATATTAT 676
Db 141 SerAsnleuThrAsnleuGlnHisleuAspLeuSerSerAsnLysileGlnSerIleTyr 160
QY 677 TGGACAGACTTGGGGGTTCTACATCAAAATGCCCTACTCAATCTCTCTTAGACCTGCTC 736
Db 161 CysThrAspLeuArgValleuHisGlnMetProleuLeuAsnleuSerleuAspLeuSer 180
QY 737 CTGAATCCTATGAACCTTATCCAAACAGGTGATTTAAAGAAATTTAGGCTTCAATAGCTG 796
Db 181 LeuAsnProMetAsnPheileGlnProGlyAlaphLysGlnLysleuGlnHisLysleu 200
QY 797 ACTTAAAGAAATATTTTGAATAGTTTAAATGTAAATGAACCTTGATTTCAAGCTGCTGCT 856
Db 201 ThrleuArgAsnAsnPheAspSerleuAsnValMetLysThrCysileGlnGlnlyleuAla 220
QY 857 GGTTTAGAAGTCCATCGTTGGTTCTGGAGAAATTTGAAATGAGAAACCTTGAAGAG 916
Db 221 GlyleuGlnlyValHisArgleuValleuGlnPheArgAsnGlnGlnlyAsnleuGlnLys 240
QY 917 TTTGACAAATCTGCTAGAGAGGCTGTCGCAATTTGACCATTTGAGAAATTCGATTAGCA 976
Db 241 PheAspLysSerAlaleuGlnGlnlyleuCysAsnleuThrileGlnGlnPheArgleuAla 260
QY 977 TACTTAGACTACTACCTCGATGATATTATTGACTTATTATTGTTGACAAATGTTTCT 1036
Db 261 TyrlleuAspTyrTyrleuAspAspIleileAspPheAsnCyseuThrAsnValSer 280
QY 1037 TCAATTTCCCTGGGTGAGTGTGACTATTTGAAAGGTTAAAGACTTTTCTTAATTTGGA 1096
Db 281 SerPheSerleuValSerValThrileLysSerValLysAspPheSerTyrAsnPheGly 300
QY 1097 TGGCAACATTTAGTAATAGTTAACTGTAAATTTTGACAGTTTCCCACTTGAAGAACTCAA 1156
Db 301 TrpGlnHisleuGlnleuValAsnCyLysPheGlnGlnPheProThrleuLysPheLys 320
QY 1157 TCTCTCAAAAAGGCTTACTTCACTTCCAAAGAGTGGAAATGCTTTTTCAGAAAGTTGAT 1216
Db 321 SerleuLysArgleuThrPheThrSerAsnLysGlnGlnAsnAlaphSerGlnValAsp 340
QY 1217 CTACCAAGCCTTGAAGTTTCTAGATCTCAGTAAGAAATGGCTTGAAGTTTCAAGTTGCTG 1276
Db 341 LeuProSerleuGlnPheleuAspLeuSerArgAsnGlnLysSerPheLysGlyCysCys 360
QY 1277 TCTCAAGTGATTTTGGGACCAACAGCCTTAAAGATTATTAGTTGAGCTTCAATGGCTGT 1336
Db 361 SerGlnSerAspPheGlnTyrTrpLysSerleuLysTyrleuAspLeuSerPheAsnGlyVal 380
QY 1337 ATTACATGAGTTCAAACTTCTTGGGCTTAGAAACAATAGACATCTGATTTCCAGCAT 1396
Db 381 IleThrSerSerSerAsnPheleuGlnGlnGlnleuGlnHisleuAspPheGlnHis 400
QY 1397 TCCAAATTTGAAACAATGAGTGAAGTTTTCAGTATCTCTATCACTCAGAAACCTCATTTAC 1456
Db 401 SerAsnleuLysGlnMetSerGlnPheSerValPheleuSerleuArgAsnleuLysTyr 420

QY 1457 CTGACATTTCTCATATCTACACAGAGTTGCTTTCAATGGCATCTTCAATGGCTTGCC 1516
Db 421 LeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY 1517 AGTCTGAGAGTCTTGAAGATGGCTGGCAATCTTTTCCAGGAAACCTTCTTCCAGATATC 1576
Db 441 SerleuGlnValleuLysMetAlaGlyAsnSerPheGlnGlnAsnPheleuProAspIle 460
QY 1577 TTCAAGAGCTGAGAACTTGACCTTCCGTGAGCTCTCAGGTGCAACTGAGGACATTTG 1636
Db 461 PheThrGlnleuLysAsnleuThrPheLeuAspLeuSerGlnCyseGlnleuGlnleu 480
QY 1637 TCTCAACAGCACTTAACTCACTCTCCAGTCTTCAAGTACTTAATATGAGCCACAACAC 1696
Db 481 SerProThrAlaphAsnSerleuSerSerleuGlnValleuAsnMetSerHisAsnAsn 500
QY 1697 TCTTTTCAATGATACGTTTCTTATTAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAAC 1756
Db 501 PhePheSerleuAspThrPheProTyrLysCysleuAsnSerleuGlnValleuAspTyr 520
QY 1757 AGCTCAATCAATATGACTTCCAAACCAAGAACTAAGACATTTCCAAAGTCTA 1816
Db 521 SerleuAsnHisIleMetThrSerLysGlnGlnleuGlnHisPheProSerSerleu 540
QY 1817 GCTTCTTAAATCTTACTCAGATGACTTGTGCTTGTACTTGTGAACACAGAGTTTCTG 1876
Db 541 AlaphleuAsnleuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheleu 560
QY 1877 CAATGATCAAGAGCAGAGGACAGCTCTTGGTGGAAGTTGAACGAATGAATGTGACACA 1936
Db 561 GlnTrpIleLysAspGlnArgGlnleuLeuValGlnValGlnArgMetGlnCysAlaThr 580
QY 1937 CTTTCAGATPACAGAGGCGCATGCTGCTGCTGAGATTTGAATATCACCTTCAAGATTAAG 1996
Db 581 ProSerAspLysGlnGlnLysMetProValleuSerleuAsnIleThrCysGlnMetAsnLys 600
QY 1997 ACCATCAATGGTGTGTCGCTCAGGTGCTGCTGATCTGTTGAGAGATTCGTGCTC 2056
Db 601 ThrIleIleGlnlyAlaSerValleuSerValleuValAlaSerValAlaAlaValleuVal 620
QY 2057 TATAGTTCTATTTTCACTGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2116
Db 621 TyrlLysPheTyrPheHisleuMetleuLeuAlaGlyCysIleLysTyrGlnArgGln 640
QY 2117 AACATCTAGATGCCCTTTGTATCTACTCAAGCAGATGAGAGACCTGGGTAAGAAATGAG 2176
Db 641 AsnIleTyrAspAlaphValIleTyrSerSerGlnAspGlnAspTyrValArgAsnGln 660
QY 2177 CTAGTAAAGAAATTTAGAAAGAGGGGCTCCATTTCAAGTCTGCTTCACTACAGAGAC 2236
Db 661 leuValLysAsnleuGlnGlnGlnlyValProProPheGlnleuCyseuHisTyrArgAsp 680
QY 2237 TTTATTTCCCGTGTGACATTTGCTGCAACATATCATCATGAAGTTTCCATAAAGCCGA 2296
Db 681 PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnLysPheHisLysSerArg 700
QY 2297 AAGGTATTTGTTGGTGTGCCAGCACTTCATCAGAGCCGCTGGTGATCTTTGAATAT 2356
Db 701 LysValIleValValAlaSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnLys 720
QY 2357 GAGATTGCTCAGACCTGGGCACTTCTGAGAGCGAGCTGATCACTCACTTCAATGTCCTG 2416
Db 721 GlnIleAlaGlnThrTrpGlnPheleuSerSerArgAlaGlyIleIlePheIleValleu 740
QY 2417 CAGAAAGTGAAGAGACCTGTCTCAGCAGCAGGTGAGCTGACCGCTTCCACAGAG 2476
Db 741 GlnLysValGlnLysThrleuLysArgGlnValGlnleuLysArgleuLysSerArg 760
QY 2477 AACACTTACCTGAGAGTGGAGAGCAGGTGCTGGGGCGGCAACTTTCTGAGAGCACTC 2536
Db 761 AsnThrTyrleuGlnLysTrpGlnAspSerValleuGlnYArgHisIlePheThrPargArgleu 780
QY 2537 AGAAAGCCCTGTGATGATGTAATCATGGAATCCAGAGGAACAAGTGGGTACAGATGC 2596

DB 781 ArglyAlaIleuLeuaspGlyysSerTPAsnProGluGlyThrValGlyThrGlyCys 800
QY 2597 AATTGGCAGGAGCAACATCTATC 2620
DB 801 AsnTrpGlnGluAlaThrSerIle 808
RESULT 11
AD057785
ID AD057785 standard; protein; 808 AA.
XX
AC AD057785;
XX
DT 12-AUG-2004 (first entry)
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003MO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
XX MPI; 2004-400726/37.
DR N-PSDB; AD057783, AD057784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
in treating sepsis and asthma, by comparing the TLR4 polynucleotide
sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
change in a TLR4 polynucleotide sequence of an old world monkey
comprising comparing the TLR4 polynucleotide sequence of the Old World
monkey with corresponding TLR4 polynucleotide sequence of a human. The
method of the invention has antibacterial, immunosuppressive, and
antiasthmatic activity. The method is useful in identifying a nucleotide
change in a TLR4 polynucleotide sequence of an old world monkey where the
change may be associated with reduced sensitivity to Gram-negative
bacterial infection. The methods, agents and composition are useful in
treating sepsis, severe sepsis or septic shock and asthma. The present
sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA.
Alignment Scores:
Pred. No.: 0 Length: 808
Score: 4167.00 Matches: 803
Percent Similarity: 99.75% Conservative: 3
Best Local Similarity: 99.38% Mismatches: 2
Query Match: 48.57% Indels: 0
DB: 8 Gaps: 0
US-09-396-985b-1 (1-4868) x AD057785 (1-808)
QY 197 GTGGTCTCAATATTAATTCATGATGAGTGAAATTTTCACAAAATCCCGAGAAC 256
DB 1 ValValProAsnIleTrpGlnCysMetGluLeuAsnPheTrpIleProAspAsn 20
QY 257 CTCGCCCTTCAACCAAGACCTGACCTGAGCTTTATCCCTGAGGCAATTTAGGAGC 316

DB 21 LeuProPheSerThrIlyAsnLeuAspLeuSerPheAsnProLeuArgIleuGlySer 40
QY 317 TATAGCTTTTCAAGTTTCCCAAGACTGCAGGCTGTGATTTTCCAGGCTGTAATCCAG 376
DB 41 TyrSerPhePheSerPheProGluLeuGlnValIleuAspLeuSerArgCysGluIleGln 60
QY 377 ACAATTTGAAGATGGGGCATATCAGAGCCCTAACCCACTCTCTCACTTAATATTGACAGA 436
DB 61 ThrIleGluAspGlyAlaIleTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
QY 437 AACCCATCAGAGTTTAACTCCCTGGAGCCCTTTTGTGACTATCAAGTTTACAGAACTG 496
DB 81 AsnProIleGlnSerLeuIleuGlyAlaPheSerGlyLeuSerSerLeuGlnIlySleu 100
QY 497 GTGGCTGTGAGACAAATTTAGCATCTCTAGAGAACTTCCCATTTGGAATCTCAAAACT 556
DB 101 ValAlaValAlaGluThrAsnLeuAlaSerLeuGluAsnPheProIleGlyIleuIlyTrp 120
QY 557 TTGAAGAAGACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTACCTGAGTATTT 616
DB 121 LeuIlySGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIlySleuProGluIlyrPhe 140
QY 617 TCTAATCTGACCAATCTAGAGCACTTGACCTTTCAGGACAGAAATTCAAAGTATTAT 676
DB 141 SerAsnLeuThrAsnLeuGluIlyrIleuAspLeuSerSerAsnIlyIleGlnSerIleTrp 160
QY 677 TGACAGAGACTTGGGGTTTACATCAAAATGCCCTTACTCAATCTCTTACCACTGCTGC 736
DB 161 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
QY 737 CTGAATCTATGAACTTTATCCAACTGAGTGAATTTAAAGAAATTTAGGCTTCAATAGCTG 796
DB 181 LeuAsnProMetThrPheIleGlnProGlyAlaPheIlyGluIleArgLeuHisIlySleu 200
QY 797 ACTTTAAGAAATTAATTTTGAATAGTTTAAATGTAATGAAATCTTGATTCAGGCTGTGCT 856
DB 201 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetIlyThrCysIleGlnIlyLeuAla 220
QY 857 GGTTTAGAGTCCATGCTTTGGTTCCTGGAGAAATTTAGAAAGAACTTGGAAGAAG 916
DB 221 GlyLeuGluValAlaArgIleuValLeuGlyGluPheArgAsnGluIlyAsnLeuGluIly 240
QY 917 TTTGACAAATTCGCTTAGAGGGCTGTGCAATTTGACCATTTGAAGATTCGATTAGCA 976
DB 241 PheAspIlySerAlaLeuGluIlyLeuCysAsnLeuThrIleGluIleuPheArgLeuAla 260
QY 977 TACTTACTACTACTCTCGATGATATTAATTTGACTTTAATTTGTCAAATGTTTCT 1036
DB 261 TyrLeuAspTyrTyrIleuAspPheIleIleAspLeuPheAsnIlySerThrAsnValSer 280
QY 1037 TCAATTTCCCTGGTGTGAGTGTGACTATTTGAAAGGTTAAAGACTTTCTTATAATTCGGA 1096
DB 281 SerPheSerLeuValSerValThrIleGluValIlyAspPheSerTrpAsnPheGly 300
QY 1097 TGGCAACATTTAGAAATTAAGTAACTGTAAATTTGACAGTTTCCCATTTGAATCTCAAA 1156
DB 301 TrpGlnHisLeuGluLeuValAlaCysIlyAspPheGlyGlnPheProThrLeuIlySleuIly 320
QY 1157 TCTCTCAAAAGCTTTACTTTCACTTCCAACTGAGGAAATGCTTTTTCAGAAAGTTGAT 1216
DB 321 SerLeuIlyArgLeuThrPheThrSerAsnIlyGlyIlyAsnAlaPheSerGluValAsp 340
QY 1217 CTACCAAGCTTGAGTTTCTAGATCTCAGTAAAGAGGCTTGAGTTTCAAAAGTTTCTGT 1276
DB 341 LeuProSerLeuGluIleuPheuAspLeuSerArgAsnGlyLeuSerPheIlySGlyCys 360
QY 1277 TCTCAAGGATTTTGGGACCAACAGCCTTAAGTATTTGATGTGAGCTTCAATGGTGT 1336
DB 361 SerGlnSerAspPheGlyThrThrSerLeuIlyTrpIleuAspLeuSerPheAsnGlyVal 380
QY 1337 ATTACCATGATTTCAAACTTCTTGAGCTTGAACCACTGAATCTGATTTTCCAGCAT 1396

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Db      381  ILethrMetSerSerAenPheLeuGlyLeuGluGluLeuGluHISleuAaspPheGlnHIS 400
QY      1397  TCCAAATTTGAAACAAATAGAGTATTTTCAGTATTTCTCATCTCAGAAACCTCATTTAC 1456
Db      401  SerenleuysgInMetSerGluPheSerValPheleuSerleuAysAenleuIleTyr 420
QY      1457  CTTGACATTTCTCATPACTCACAACAGAGTTGCTTTCAATGGCATCTTCAATGGCTTGTCC 1516
Db      421  LeuApsIleSerHISThrHISThrArgValAlaPheAenGlyIlePheAenGlyLeuSer 440
QY      1517  AGTCTCAGAGCTTGAAAAATGCTGGCAATTTCTTCCAGAAACCTTCTTCCAGATATC 1576
Db      441  SerleuGluValleuAysMeCAlaGlyAasnSerPheGlnGluAenPheleuProAaspIle 460
QY      1577  TTCACAGAGCTGAGAAACTTGACCTTCTGGACCTCTCTGATGTCACATGAGCAGATG 1636
Db      461  PheThrGluLeuAysAenleuThrPheleuAaspSerGlnGlnleuGluGlnleu 480
QY      1637  TCTTCAAACAGATTAACTCATCTTCCAGTCTTCAAGTACTAAATATGAGCCACAACAC 1696
Db      481  SerProThrAlaPheAasnSerleuSerleuGlnValleuAasnMetSerHISAsn 500
QY      1697  TTCTTTTCATTTGATAGTTCCTTATTAAGTGTCTGAACCTCCCTCCAGGTTCTGATTA 1756
Db      501  PheheserleuAapThrPheProTyrLysCysleuAasnSerleuAysValleuAaspTyr 520
QY      1757  AGTCTCAATCATCATATGACTTCCAAAACAGAACTCAAGCATTTTCCAAAGTACTA 1816
Db      521  SerleuAasnHISleuThrSerleuAysGlnleuGlnleuGlnHISpheProSerleu 540
QY      1817  GCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTATCTTGTGAACAACAGATTTCTG 1876
Db      541  AlaPheleuAenleuThrGlnAasnAaspPheAlaCysThrCysGlnHISGlnSerPheleu 560
QY      1877  CAATGATTCAGAGACCGAGAGCAGCTTGTGTGAAGTTGAACAAATGAATGTTCACAA 1936
Db      561  GlnThrPheLysAaspGlnAysGlnleuLeuValGlnValGlnAysMetGlnCysAlaThr 580
QY      1937  CCTTCAGATAGACGAGGAGCATGCTGTGTGAGTTGAATPACCTCTCATGATGAATAG 1996
Db      581  ProSerAaspLysGlnGlnLysMetProValleuSerleuAasnHISThrCysGlnMetAaspLys 600
QY      1997  ACCATCATTTGATGTGTGCTCTCATAGTGTGCTTGTATCTTGTGTGAAGATTTCTGATC 2056
Db      601  ThrIleIleGlyAlaSerValleuSerValleuValSerValAlaAlaValleuVal 620
QY      2057  TATTAAGTTCTAATTTTCACTGATGCTTCTGTGCTGTGCATTAAGATGTTAGAGGTGA 2116
Db      621  TyrLysPheTyrPheHISleuMetleuAlaGlyCysIleLysTyrGlnAysGln 640
QY      2117  AACATCTAATGATGCTTTGTATTAATCTCAAGCCAGAGATGAGACCTGGGTAAAGATGAG 2176
Db      641  AsnValLysAaspAlaPheValIleTyrSerSerGlnAaspGlnAaspTyrValAysAsgln 660
QY      2177  CTAGTAAAGATTTAGAGAAAGGGGTCTCTCATTTGAGCTTGTCTTCACTACAGAGAC 2236
Db      661  leuValLysAasnleuGlnGlnGlyValProProPheHISleuAysleuHISLysTyrAasp 680
QY      2237  TTTATTTCCGGTGTGSCCATGTGCTGCCAACATCATCAATGAAGTTTCCATTAAGCCGA 2296
Db      681  PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHISGlnGlyPheHISLysSerArg 700
QY      2297  AAGGTGATTTGTGTGTGCTCCAGCACTTCATCCAGACCGGTGTATCTTGAATAT 2356
Db      701  LysValIleValValValSerGlnHISpheIleHISThrArgTyrCysIlePheGlnTyr 720
QY      2357  GAGATTGCTGAGACTGCGAGTTTCTGAGAGTGTGCTGTATCATTTCAATGTCTGTG 2416
Db      721  GlnIleHISGlnHISThrPheHISleuSerSerThrArgAlaGlyIleIlePheIleValleu 740
QY      2417  CAGAGGTGAGAAAGACCTGTCTCAGGACAGGTGAGGTGATGACGCTTCTCAGAGG 2476
Db      741  GlnLysValGlnLysThrleuLeuAysGlnGlnValGlnleuTyrArgleuLeuSerArg 760

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QY      2477  AACACTTACCTGAGAGTGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGACGACTC 2536
Db      761  AsnThrTyrleuGlnTyrPheLysAaspSerValleuGlyThrHISlePheThrPArgArgleu 780
QY      2537  AGAAAGCCCTCTGATGTGTAATCATGGAATCCAGAGGACAGTGGGTACAGATGC 2596
Db      781  ArgLysAlaLeuLeuAaspGlyLysSerTrpAasnProGlnGlyThrValGlyThrGlyCys 800
QY      2597  AATTGGAGGAGAGCAACATCTATC 2620
Db      801  AsnTrpGlnGlnAlaThrSerIle 808

RESULT 12
ID      AD057803
AC      AD057803;
DT      12-AUG-2004 (first entry)
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX      XX
XX      toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
OS      Pan troglodytes.
XX      XX
XX      WO2004042365-A2.
XX      XX
XX      21-MAY-2004.
XX      XX
XX      03-NOV-2003; 2003WO-US036247.
XX      XX
XX      01-NOV-2002; 2002US-0423113P.
XX      XX
XX      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX      XX
XX      Measles W;
XX      XX
XX      WPI; 2004-400726/37.
XX      XX
XX      N-PSDB; AD057801, AD057802.
XX      XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX      XX
PS      Disclosure; SEQ ID NO 24; 11pp; English.
XX      XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX      XX
SQ      Sequence 808 AA.

Alignment Scores:
Pred. No.: 0
Score: 4164.00
Percent Similarity: 99.63%
Best Local Similarity: 99.38%
Query Match: 48.54%
DB: 8
Gaps: 0
Length: 808
Matches: 803
Conservative: 2
Mismatch: 3
Indels: 0
Gaps: 0

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US-09-396-985b-1 (1-4868) x AD057803 (1-808)

QY 197 GTGGTTCCTAATATTACTTATCAATGCATGAGCTGAATTTCTACAAATCCCGACAAAC 256
Db 1 ValValProksnilethrlYrGlncYsmetGlueuamphetrYlYsIleProAspAsn 20
QY 257 CTCCCTCTCTCAACCAAGAACTTGAGACTTGATTAATCCCTGAGGCACTTTAGGACG 316
Db 21 LeuProPheSerThrYrAsnLeuAspLeuSerPheAsnProLeuAlghIleuGlySer 40
QY 317 TATAGCTTCTTCAAGTTCCCGAAGCTGAGGTGTGATTTATCCAGGTGTGAATCTCAG 376
Db 41 TyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgGlyIleGln 60
QY 377 ACAATTGAAGATGGGGCATATCAGAGCTTGAAGCCACTCTCTACCTTAATATTGACAGCA 436
Db 61 ThrIleGluAspGlyAlaYrGlnSerLeuSerHileuSerThrLeuIleLeuThrGly 80
QY 437 AACCCCATCCAGAGTTTAGCCCTGGAGCCTTTTCTGACTATTCAGATTACAGAACCTG 436
Db 81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnYsLeu 100
QY 497 GTGGCTGTGGAGCAAACTTAGCATCTCTAGAGAACTCCCACTTGGACATCTCAAAACT 556
Db 101 ValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHileuYsThr 120
QY 557 TTGAAGAAGCTTAATGTGCTCACAATCTTATCCAACTTTCAAAATTACCTGATATTTT 616
Db 121 LeuYsGluLeuAsnValAlaHileuAsnLeuIleGlnSerPheYsLeuProGluYrPhe 140
QY 617 TCTAATCTGACCAATCTTAGAGCACTTGAGCCTTTCCAGCAACAGATTCAAGATTATAT 676
Db 141 SerAsnLeuThrAsnLeuGlnHileuAspLeuSerSerAsnYsIleGlnSerIleYr 160
QY 677 TGCACAGACTTGGGGGTCTTACATCAAAATGCCCTATCATCTCTTTAGACTGCTGC 736
Db 161 CysThrAspLeuArgValLeuHileuHileuMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
QY 737 CTGAATCTCTATGAACCTTATCCAAACAGGTGCAATTTAAGAAATTAGCTTCAATAGCTG 796
Db 181 LeuAsnProMetAsnPhelIleGlnProGlyAlaPheYsGluIleArgLeuHileuYsLeu 200
QY 797 ACTTTAAGAAATTAATTTGATAGTTTAATGTAATGAAACTGTATTCAGAGCTGCGCT 856
Db 201 ThrLeuAspGlnAsnPhelAspSerSerLeuAsnValMetYsThrCysIleGlnGlyLeuAla 220
QY 857 GGTTAGAAGTCCATGCTTGGTCTGAGGAAATTTGAATGAGGAAACTTGGAAG 916
Db 221 GlyLeuGluValHileuArgLeuValLeuGlyGluProPheArgAsnGluGluAsnLeuGluYs 240
QY 917 TTTCACAAATCTGCTTAGAGGGCTGTGCAATTTGACATTTGAAGAAATTCGATTAGCA 976
Db 241 PheAspYsSerAlaLeuGlnGluGlyLeuCysAsnLeuThrIleGlnGluProPheArgLeuAla 260
QY 977 TACTTAGACTACTACCTCGATGATATTTAGACTTATTAATGTTTGAACAAATGTTTCT 1036
Db 261 TyrLeuAspYrYrYrLeuAspAspIleIleAspLeuPheAsnYsLeuThrAsnValSer 280
QY 1037 TCAATTTCCCTGGAGGTGAGCATTTGAAGGTAAGAACTTTTCTTAATTTCCGA 1096
Db 281 SerPheSerLeuValSerValThrIleYsSerValIlyAspPheSerYrAsnPhelGly 300
QY 1097 TTGCACATTTAGAAATTAGTTAACTGTAAATTTTGAACAGTTTCCACATTTGAACCTCAA 1156
Db 301 TrpGlnHileuGlnLeuValYsCysAlaYsPheGlyGlnPheProThrLeuYsLeuYs 320
QY 1157 TCTCTCAAAAAGGCTTACTTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAAATGAT 1216
Db 321 SerLeuYsArgLeuThrPheThrSerAsnYsGlyGlyAsnAlaPheSerGluValAsp 340
QY 1217 CTACCAAGCTTAGAGTTTCTAGATCTCAGTAGAAATGGCTTGAATTTCAAGGTTGCTGT 1276
Db 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheYsGlyCysCys 360

QY 1277 TCTCAAGATGATTTTGGGACAAACAGCTTAAAGTATTTAGATCTGAGCTTCAATGGTGT 1336
Db 361 SerGlnSerAspPheGlyThrThrSerLeuYsYrLeuAspLeuSerPheAsnGlyVal 380
QY 1337 ATTACCATGAGTTCAAACTTCTTGGGCTTAGAAACATCTAGAACATCTGGATTTCCAGCAT 1396
Db 381 IleThrMetSerSerAsnPhelLeuGlyLeuGlnGlnLeuGlnHileuAspPheGlnHileu 400
QY 1397 TCCAAATTTGAACAAATGAGTAGTTTTCAGTATCTCTCACTCAGAAACCTCAATTTAC 1456
Db 401 SerAsnLeuYsGlnMetSerGluPheSerValPheLeuSerLeuAspGlnLeuIleYr 420
QY 1457 CTTCACATTTCTCAATCTCACACAGAGTGTCTTCAATGGCATCTTCAATGGCTTGTCC 1516
Db 421 LeuAspIleSerHileuThrHileuThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY 1517 AGCTCGAAGTCTTGAAAATGGGTGGCAATTTCTTCCAGAAAACCTTCTTCCAGATATTC 1576
Db 441 SerLeuGluValLeuYsMetAlaGlyAsnSerPheGlnGluAsnPhelLeuProAspIle 460
QY 1577 TTCAAGAGCTGAGAAACTTGACCTTCTGAGCCTCTCAAGTGTCAACTGAGCAGTTG 1636
Db 461 PheThrGluLeuAspGlnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeu 480
QY 1637 TCTCAACAGCACTTAACTCACTCTCCAGTCTTCAGGTACTAATATGAGCCAACAAC 1696
Db 481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHileuAsnAsn 500
QY 1697 TTTCTTTTCATGGATACGTTTCTTATTAAGTGTCTGAATCTCCCTCCAGGTTCTTGATATC 1756
Db 501 PhePheSerLeuAspThrPheProYrYsCysLeuAsnSerLeuGlnValLeuAspYr 520
QY 1757 AGCTCAATCACTAATATGACTTCCAAAAACAGAACTACAGACTTTTCCAACTAGACTCA 1816
Db 521 SerLeuAsnHileuMetThrSerYsYsGlnGlnLeuGlnHileuPheProSerSerLeu 540
QY 1817 GCTTTCTTAAATCTTACCTGAAATGACTTGTCTTGTAGTGTGAACACAGAGTTTCTGT 1876
Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHileuGlnSerPheLeu 560
QY 1877 CAATGATCAAGGACCAAGAGGCAAGCTTGTGGTGAAGTTGAACGAATGGAAATGTGCACA 1936
Db 561 GlnTrpIleYsAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAlaThr 580
QY 1937 CTTTCAATAGAGGAGGCAATGCTGTGCTGAGTTTGAATATCACTGTCAGATGAATAG 1996
Db 581 ProSerAspYsGlnGlyMetProValLeuSerLeuAsnHileuThrCysGlnMetAsnYs 600
QY 1997 ACCATCATTTGGTGTGTGCTGCTCAAGTGTCTTGAATCTGTGTAGCAATGCTGTGTC 2056
Db 601 ThrIleIleGlyValSerValLeuSerValLeuValSerValAlaValLeuVal 620
QY 2057 TATAAGTCTATTTTCACTGATGCTTCTTGTGCTGCTGCATTAAGATAGTAGAGTGAA 2116
Db 621 TyrYsPheThrPheHileuMetLeuLeuAlaGlyCysAlleuYsYrGlyArgGlyGln 640
QY 2117 AACATCTATGATGCTTGTATCTACTCAAGGCAAGAGGAGTGGGTAAGAAATGAG 2176
Db 641 AsnIleYrAspAlaPheValIleYrYsSerGlnAspGluAspTrpValAlaGlnGln 660
QY 2177 CTAGTAAAGAAATTTAGAAAGGGGTGCTCCATTTCAAGTGTGCTTCACTACAGAGAC 2236
Db 661 LeuValIlyAsnLeuGlnGluGlyValProProPheGlnLeuCysLeuHileuYrArgAsp 680
QY 2237 TTTATTTCCGGGTGTGGCCATGTGTGCCAAACATCATCATGAAAGTTTCCATTAAGCCGA 2296
Db 681 PheIleProGlyValAlaIleAlaIleAsnIleIleHileuGlnGlyPheHileuYsSerArg 700
QY 2297 AAGGATATGTTGTGTGTGCCAGCACTTCATCCAGAGCGGTGTATCTTGAATAT 2356
Db 701 LysValIleValAlaValSerGlnHileuPheIleGlnSerArgTrpCysIlePheGluYr 720
QY 2357 GAGATTTGCTCAGACTTGAGCAATTTCTGACAGCTGTGTGATCATCTTCAATTTGTCTGT 2416

Db 721 GIIIEALAGIINHRTPIGSPINPHELEUSERSERARGALACIYLEILEPHELEVALLEU 740
 QY 2417 CAGAGGTGGAGAAAGACCTGCTCAGCAGCAGGTGAGCTGTACCGCTTCTCAGCAGG 2476
 Db 741 GIIIVaIaGIuIySThIRLeuLeuARGGIaIaGIuIeUyIRaRgLeuLeuSERaRg 760
 QY 2477 AACACTTACCTGGAGTGGAGGAGCAGTGTCTGGGGGGGCAACATCTTGAGACGACTC 2536
 Db 761 ASnIRhIRyIeUgIuIRgIuIaSPeRValLeUgIaRgHISIIePHeIRPaRgARgLeU 780
 QY 2537 AGAAAGCCCTGCTGTGATGTGTAATCATGTGATCCAGAGAAACAGTGGGTACAGATGC 2596
 Db 781 ARGlyeAlaIeUeUaSPgIyIySeRTRPaSnPRoGluIyThRValGIyThnGIyCyS 800
 QY 2597 AATTGGCAGGAGCAACATCTATC 2620
 Db 801 ASnIRPglngIuIaIaThRSeRIle 808
 RESULT 13
 AAM86352 standard; protein; 799 AA.
 ID AAM86352
 XX AAM86352;
 AC AAM86352;
 XX 15-MAR-1999 (first entry)
 DT Human DNAX toll-1-like receptor DTLR4.
 DE Human DNAX toll-1-like receptor DTLR4.
 XX DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KM interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KM modulate inflammatory function; morphological effect;
 KM immunological disorder.
 XX Homo sapiens.
 OS
 XX WO9805047-A2.
 PN 12-NOV-1998.
 PD 07-MAY-1998; 98WO-US008979.
 XX PF 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX (SCHE) SCHERING CORP.
 PA
 XX Hardman GT, Rock FL, Bazan JF, Kastelein RA;
 PI WPI, 1999-059670/05.
 DR N-PSDB; AAV80666.
 XX Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 PT metabolism, modulate inflammatory function or innate immunity responses.
 XX Example; Page 115-117, 171pp; English.
 XX The present invention specifically describes human DNAX toll-1-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 XX

SQ Sequence 799 AA;
 Alignment Scores:
 Pred. No.: 0
 Score: 4141.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 48.27%
 DB: 2
 Gaps: 0
 US-09-396-985b-1 (1-4868) x AAM86352 (1-799)
 QY 224 ATGAGCTGATATTCTACAAATCCCGCAACACCTCCCTTCTCAACCAAGAACTGGAC 283
 Db 1 MetGIuLeuAsnPhEyrIRyISIIePRoAsPAsnLeuPRoPheSerhIRyASnLeuAsp 20
 QY 284 CTGAGCTTAAATCCCTGAGGCAATTAGGCACTATAGCTTTCAGTTTCCAGAACTG 343
 Db 21 LeuSerPheAsnPRoLeuARgHISleUGIySeRTRSeRPhESeRPRoGluLeu 40
 QY 344 CAGGTGCTGATTTATCCAGGTGTGAATCCAGAACTGAAGATGGGGCATTCAGAGC 403
 Db 41 GIaIaIeUaSPeRValLeUgIaRgHISIIePHeIRPaRgARgLeU 60
 QY 404 CTAGCCACCTCTCTACTTAATATTGACAGAAACCCCATCCAGAGTTTAGCCCTGGGA 463
 Db 61 LeuSerHISleuSerhIRleuIIeUeThnRgIyAsnPRoIleGInSeRIleuAlaIeUGIy 80
 QY 464 GCCTTTTCTGACTATCAAGTTTACAGAACTGTGGCTGTGAGACAAATCTAGCATCT 523
 Db 81 AlaPheSerCIyEUSerSeRIeUGIySeUaIaIaValGIuThRAsnLeuAlaSeR 100
 QY 524 CTGAGAACTTCCCATTTGGACATCTCAAACTTGAAGAACTTAATGTGGCTCCCAAT 583
 Db 101 LeuGIaAsnPhEPRoIleGIyHISleUySThLeuISleUeUaSnValaIaAsn 120
 QY 584 CTTATCCAACTTTCAATTAATTAACCTGAGTATTTTCTATCTGACCAATCTAGAGCACTTG 643
 Db 121 LeuIIeGInSeRPhEYSeUePRoGluIyRPhSeRAsnLeuThRAsnPhEAspSeRIeU 140
 QY 644 GACCTTTCAGCAACAAGATTCAAAGTATTTATTTGACAGACTTGGGGTTTACATCAA 703
 Db 141 AsPLeuSeRSeRAsnIySIIeGInSeRIleTyCySThRAsPLeuARgValaIeUaHISGIn 160
 QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAATCCATTAAGACTTTATCCAAACA 763
 Db 161 MeCPRoLeuLeuAsnLeuSeRIeUaSPeRSeRIeUaSPRoMeCAsnPhEIIeGInPRo 180
 QY 764 GTGCATTTAAAGAAATTAAGGCTTCATTAAGCTGACTTAAGAATAATTTGATAGTTTA 823
 Db 181 GIyAlaPheUySIIeUleRgIeUaHISySeUeThRleuRgAsnAsnPhEAspSeRIeU 200
 QY 824 AATGTAATGAAMAATTGTATTCAGGCTGTGGCTGTTTAGAAGTCCATCGTTTGGTCTG 883
 Db 201 ASnValMeIRySThRySIIeGInGIyLeUaHISGInGIyLeUaIuValHISARgLeUaIleU 220
 QY 884 GGAATTTGAATGAATGAAGAACTTGAAGAAAGTTTGACAATCTGCTCTAGAGGGCTG 943
 Db 221 GIyGIuPheARgAsnGIuGIyAsnLeUGIyPheAsPlySSeRAlaLeuGIuGIyLeU 240
 QY 944 TGAATTTGACATTTGAGAAATCCGATTGACATTAAGTACTTACATCACTCCATGATAT 1003
 Db 241 CyAsnLeuThRIleGIuGIuPheARgLeUaIaRyLeuAsPlyTyRLeuAsPAspIle 260
 QY 1004 ATGACTTATTAATTTGACAAATGTTTCTTCATTTTCCCTGGTGAAGTGTGACTATT 1063
 Db 261 IISleAsPLeuPhAsnCySleuThRAsnValSeRSeRSeRSeRSeRSeRSeRSeRSeR 280
 QY 1064 GAAAGGTTAAAGACTTTTCTTAATTTGATGGCAACTTTAGAAATTAAGTTAGTTACTGT 1123
 Db 281 GIuARgValIyAsPPhESeRTRAsnPhEGLTyRGIaHISleUGIuIeUaIaSnCyS 300
 QY 1124 AATTTTGACAGTTCCTCCACATTTGAAGAACTCAAAATCTCTCAAAAGGCTTACTTCAC 1183

```

Db      |||
301  LysPheGlyGlnPheProThrLeuLysLeuYSerLeuLysArgLeuThrPheThrSer 320
Qy      |||
1184  AACAAAGTGGGAATGCTTTTTCAGAAATGATATCAACAGCTTGAGTTTCAAGATCTC 1243
Db      |||
321  AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
Qy      |||
1244  AGTAGAAATGGGCTTGAGTTTCAAGGTTGCTTCAAGATGATTTTGGGACACAGC 1303
Db      |||
341  SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Qy      |||
1304  CTAAAGTATTTAGATGTCAGCTTCAATGCTGTTATTAACATGAGTTCAAACTTTGGGC 1363
Db      |||
361  LeuLysTyrlLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
Qy      |||
1364  TTAGAACAACTAGAACATCTGGAATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGT 1423
Db      |||
381  LeuGluGlnLeuGlnIleLeuAspPheGlnIleSerAsnLeuLysGlnMetSerGluPhe 400
Qy      |||
1424  TCAGTATTCCTATCACTCAGAAACCTTATTACTTGACATTTCTGATTACTCAACACAG 1483
Db      |||
401  SerValPheLeuSerLeuAspGlnLeuIleTyrlLeuAspIleSerThrIleuArgIle 420
Qy      |||
1484  GTTGCTTTCAATGGCATCTTCAATGGCTGTCGAGTCTCGAAGTCTTGAATGGCTGGC 1543
Db      |||
421  ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
Qy      |||
1544  AATCTTTTCCAGGAAAATCTCTCCAGATATCTTCCAGACAGCTGAGAAAATGACCTTC 1603
Db      |||
441  AsnSerPheGlnGlnIleuAsnPheLeuProAspIlePheThrIleuArgAsnLeuThrPhe 460
Qy      |||
1604  CTGGAACCTCTCAGAGTCAACTGGAGCAGTGTGCTCCAAAGCATTTAACTCACTCTCC 1663
Db      |||
461  LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
Qy      |||
1664  AGTCTTCAGGTAATTAATATAGACACACAACTCTTCTTCAATGGATACGTTTCCTTAT 1723
Db      |||
481  SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 500
Qy      |||
1724  AAGTGTCTGAACCTCCTCCAGGTTCTTGATTACAGTCTCAATCACTAATAGACTTCCAA 1783
Db      |||
501  LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
Qy      |||
1784  AAACAGGAATCTACAGCATTTTCCAGATGCTGAGCTTCTTAATCTTAATCTCAAGAAATG 1843
Db      |||
521  LysGlnGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsp 540
Qy      |||
1844  TTGCTTTGTATCTTGTAACACACAGAGTTTCTGCAATGATCAAGACAGGACAGCTC 1903
Db      |||
541  PheAlaCysThrCysGlyHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
Qy      |||
1904  TTGGTGAAGTGAAGCAATGGAATGTGCAACACTTCAGATTAAGCAGGGCATGCTGTG 1963
Db      |||
561  LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
Qy      |||
1964  CTGAGTTTGAATATCACTGTCAGATGAATGAATGAATCACTTGGTGTGGTCTCAGT 2023
Db      |||
581  LeuSerLeuAsnIleThrCysGlnMetCAsnLysThrIleIleGlyValSerValLeuSer 600
Qy      |||
2024  GTGCTGTAGTATCTGTGTGAGCAGTTCTGCTATTAAGTCTAATTTTCACTGATGCTT 2083
Db      |||
601  ValLeuValValSerValValAlaValLeuValTyrlTyrlSerPheHisIleMetLeu 620
Qy      |||
2084  CTTGCTGGCTGCATAAAGTATGTGAGAGGTGAAAACATCTATGATGCTTGTATATCAC 2143
Db      |||
621  LeuAlaGlyCysIleLysTyrlGlyArgGlyGluAsnIleTyrlPheAlaPheValIleTy 640
Qy      |||
2144  TCAAGCCAGATGAGAGCTGGGTAAAGAAATGAGCTATTAAGATTTTGAAGAAAGGGGTG 2203
Db      |||
641  SerSerIleAspGlnAspTyrValArgAsnGluLeuValLysAsnLeuGluGluGlyVal 660
Qy      |||
2204  CTTCCATTTGAGCTGCTGCTTCACTACAGAGACTTTATTCCTCCGGTGTGGCATTTGCC 2263

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Db      |||
661  ProProPheGlnLeuCysLeuHisIleTyrlArgAspPheIleProGlyValAlaIleAla 680
Qy      |||
2264  AACATCATTCAGTAAGTTCATTAAGCCGAAAGGTGATTTGTTGGTGTCCGACAC 2323
Db      |||
681  AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHis 700
Qy      |||
2324  TTCATCCAGAGCCGCTGTGTATCTTTGAATATGAGATTTGCTCAGACTGGCAGTTTCTG 2383
Db      |||
701  PheIleGlnSerArgIlePheGlyIlePheGlnIleValGlnIleThrIleThrPheLeu 720
Qy      |||
2384  AGCAGTGTGCTGTGATCATCTTCATTTCTCTGCAGAGGTGAGAGAACCTGCTCAGG 2443
Db      |||
721  SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuAsp 740
Qy      |||
2444  CAGCAGTGGAGCTGTAACGCCCTTCCAGCAGGAACACTTACCTGAGTGGAGCAGT 2503
Db      |||
741  GlnGlnValGlnLeuTyrlArgLeuSerArgAsnThrTyrlLeuGluThrGluAspSer 760
Qy      |||
2504  GTCTTGGGGCGGCACATCTTCTGAGACGACTCAGAAAAGCCCTGCTGATGGTAAATCA 2563
Db      |||
761  ValLeuGlyArgHisIleIlePheThrPargArgLeuArgValAlaLeuLeuAspGlyLys 780
Qy      |||
2564  TGGATTCAGAAAGAACAGTGGGTACAGATGCAATTTGGCAGAGCAACATTTATTC 2620
Db      |||
781  TrpAsnProGluGlyThrValGlyThrGlyCysAsnThrGlnGlnAlaThrSerIle 799

RESULT 14
AAEL6093
ID  AAEL6093 standard; protein; 799 AA.
XX
AC  AAEL6093;
XX
DT  26-MAR-2002 (first entry)
XX
DE  Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW  Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM  Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS  Homo sapiens.
PN  WO200190151-A2.
XX
PD  29-NOV-2001.
XX
PF  23-MAY-2001; 2001MO-US016766.
XX
PR  25-MAY-2000; 2000US-0207558P.
XX
PA  (SCHE ) SCHERING CORP.
PI  Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
XX  WPI; 2002-083085/11.
DR  N-PSDB; AAD26283.
XX
PT  New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT  conditions exhibiting abnormal expression of the receptors of their
PT  ligands, particularly abnormalities manifested by immunological
PT  disorders.
XX
XX  Claim 1; Page 35; 297pp; English.
XX
CC  The invention relates to mammalian receptor proteins, e.g., primate,
CC  human DNAX Toll like receptor (DTLR) protein and their corresponding
CC  nucleic acids. The DTLR is useful for treating conditions exhibiting
CC  abnormal expression of the receptors of their ligands. Such abnormality
CC  is manifested by immunological disorders. In particular, the DTLR is
CC  useful for treating various disease or disorders associated with abnormal
CC  expression or abnormal triggering of response to a ligand. The DTLR is
CC  also useful as an immunogen for the production of antibodies or antibodies
CC  specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC  receptor family members, for the DTLR or its various fragments. The

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CC purified DTR can be used to screen monoclonal antibodies or antigen-binding fragments. The antibodies are useful for screening expression libraries for particular expression products. These are useful for CC detecting or diagnosing various immunological conditions related to CC expression of DTR or cells that express it. The present sequence is human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33

XX Sequence 799 AA:

Alignment Scores:

Pred. No.:	0	Length:	799
Score:	4141.00	Matches:	799
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.27%	Indels:	0
DB:	5	Gaps:	0

US-09-396-985B-1 (1-4866) x AAE16093 (1-799)

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QY 224 ATGAGCTGAATTTCTACAAATCCCGACACCTCCCTTCTCAACCAAGAACTTGAC 283
DB 1 MetGluLeuasnphenylrlyslleProaspasnleuProheseThrllysaenleuasp 20
QY 284 CTGAGCTTTAATCCCTGAGGCAATTAGGCACTTAAGCTTTCTTCAAGTTTCCCAAGACTG 343
DB 21 LeuSerPheasnProleuAargHlsleuGlySerTyrSerPhePheSerPheProGluLeu 40
QY 344 CAGCTCTGATTTATTCAGAGTGTGAATTCAGACAACTTGAAGATGGGGCATTCAGAGC 403
DB 41 GlnValleuaspheuserAargCysGluIleGlnThrIleGluaspGlyAlaTyrGlnSer 60
QY 404 CTAAAGCACTCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTAGGCTTGGA 463
DB 61 LeuSerHisleuSerThrleuIleleuThrGlyAsnProIleGlnSerleuAlaleuGly 80
QY 464 GCCTTTTCGACTATCAAGATTACAGACGCTGCTGTGGAGCAAAATCTTACGACTCT 523
DB 81 AlaphSerGlyleuSerSerleuGlnLysleuValAlaValGlnThrAsnleuAlaSer 100
QY 524 CTAGAGAACTTCCCATTTGACATCTCCAAAATTGAAAAGACTTAAATGTGGCTCACAAT 583
DB 101 LeuGluAsnphenProIleGlyHlsleuLysThrleuLysGluLeuasnValAlaHlsasn 120
QY 584 CTATCCAACTCTTCAATATACCTGAGTATTTTCTATCTGACCAATCTTACAGACTTG 643
DB 121 LeuIleGlnSerPheLysleuProGluTyrPheSerAsnleuThrAsnleuGluHlsleu 140
QY 644 GACCTTTCAGAACAGATTCAAGATTATTTATTTGACAGACTTGCGGTTCTTACATCAA 703
DB 141 AspleuSerSerAsnLysIleGlnSerIleTyrCysThrAspleuAargValIleuHlsGln 160
QY 704 ATGCCCTTACTCAATCTCTTTTACAGCTGTCCCTGTAATCTTATGAACTTTATTCACCA 763
DB 161 MetProleuLeuasnleuSerleuAspleuSerleuAsnProMetAsnPhelIleGlnPro 180
QY 764 GGTGCACTTTAAAGAAATTAGGCTTCAAGCTGACCTTAAAGAAATATTTTGAATGTTA 823
DB 181 GlyAlaPheLysGluIleAargLeuHlsLysleuThrleuAargAsnPhenleuAspSerleu 200
QY 824 AATGTATGAAATCTGTATTCAGAGCTGCTGCTGTTTGAAGTCCATCTTTGGTCTTG 883
DB 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyleuGluValHlsAargLeuValLeu 220
QY 884 GGAAGATTTTGAATGAAGAACTTGAAAAGTTTGAACAATCTGCTTGAAGAGGCTG 943
DB 221 GlyGluPheAargAsnGluGlyAsnleuGluLysPheAspLysSerAlaleuGluGlyLeu 240
QY 944 TGAATTTGACCTTGAAGAACTTCGATTGACATCTTAACTTAACTTGAATCTGATAT 1003
DB 241 CysAsnleuThrIleGluGlnPheAargLeuAlaTyrleuAspTyrTyrleuAspAspIle 260
QY 1004 ATTGACTTATTTAATTTTGAACAATGTTTCTTCAATTTCCCTGGAGTGTGACTAT 1063

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DB 261 IleAspleuPheasnCysleuThrAsnValSerSerPheSerleuValSerValThrIle 280
QY 1064 GAAAGGGTAAAGAACTTTTCTTAATTTGAGATGGCAACTTGAATTAAGTAACTGT 1123
DB 281 GluAargValLysaspPheSerTyrAsnPhenGlyTyrGlnHlsleuGluLeuValAsnCys 300
QY 1124 AAATTTGACAGTTTCCCACTTGAACCTGAAATCTGAAATCTTCAAAAGCTTACTTCACTTC 1183
DB 301 LysPheGlyGlnPheProThrleuLysleuLysSerleuLysAargLeuThrPheThrSer 320
QY 1184 AACAAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTTCAGATCTC 1243
DB 321 AsnLysGlyGlyLysAsnAlaphSerGluValAspleuProSerleuGluPheLeuAspleu 340
QY 1244 AGTAAATAGCTTGAGTTTCAAGGCTGCTTCTCAAGTGAATTTTGGAGCAACAGC 1303
DB 341 SerAargAsnGlyleuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
QY 1304 CTAAATATTTAGATCTGAGCTTCAATGTGTATTAACAATGATTCAACTTCTTGAGC 1363
DB 361 LeuLysTyrleuAspPheuserPheAsnGlyValIleThrMetSerSerAsnPhenleuGly 380
QY 1364 TTGAAACAACATAGACATCTGATTTCCAGCATTTCCAAATTTGAAACAATGAGTACTT 1423
DB 381 LeuGluGlnleuGluHlsleuAaspPheGlnHlsSerAsnleuLysGlnMetSerGluPhe 400
QY 1424 TCAGTATTCCTATCACTGAGAAACCTCAATTAACCTTGACATTTCTCATCTCACACAGA 1483
DB 401 SerValPheleuSerleuAargAsnLysIleTyrleuAspIleSerHlsThrHlsThrAarg 420
QY 1484 GTTGCTTTCAATGAGCATCTTCAATGAGCTTGTCCAGTCCGAAATCTTGAATGAGCTGAGC 1543
DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGluValleuLysMetAlaGly 440
QY 1544 AATTTCTTCCAGGAAATCTTCTTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1603
DB 441 AsnSerPheGlnGluAsnPhenleuProAspIlePheThrGluLeuAargAsnleuThrPhe 460
QY 1604 CTGAGACTCTCAGGTCAACTGAGGAGCTTCTCCCAACACATTTAATCACTGCTCC 1663
DB 461 LeuAspleuSerGlnCysGlnleuGluGlnleuSerProThrAlaPheAsnSerleuSer 480
QY 1664 AGCTTCAGGTACTTAATATAGACCAACAACACTTCTTTCATTTGATGATGATGCTTAT 1723
DB 481 SerleuGlnValleuAsnMetSerHlsAsnAsnPhenPheSerleuAspThrPheProTyr 500
QY 1724 AAGTGTCTGAATCTCCCTCCAGGTTCTTGATTTACAGTCCATGACATATGACTTCCAA 1783
DB 501 LysCysleuAsnSerleuGlnValleuAspTyrSerleuAsnHlsIleMetThrSerLys 520
QY 1784 AACACGAATACAGCATTTTCCAGTATGCTTACTTCTTAATCTTACTCAGAAATGAC 1843
DB 521 LysGlnGluLeuGlnHlsPheProSerSerleuAlaPheleuAsnleuThrGlnAsnAsp 540
QY 1844 TTGCTTGTACTGTTGAACACAGAGTTTCTCAGATGATCAAGGACGAGGACGCTC 1903
DB 541 PheAlaCysThrCysGlnHlsGlnSerPheleuGlnThrIleLysAspGlnAargGlnleu 560
QY 1904 TTGGTGAAGTTGAAGAAATGGAATGTGCAACCTTCAGATTAAGCAGGCAATGCTGTG 1963
DB 561 LeuValGluValGluLysGlnMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
QY 1964 CTGAGTTTGAATATCACCTGTGAGATGATTAACACATCATTTGGTGTGTGGTCTCACT 2023
DB 581 LeuSerleuAsnHlsThrCysGlnMetAsnLysThrIleIleGlyAlaSerValleuSer 600
QY 2024 GTGCTGTGATCTGTTGAGCAGTTCTGCTATTAAGTTCTAATTTCACTGATGCTT 2083
DB 601 ValleuValLysSerValAlaAlaValleuValTyrLysPheThrPheHlsleuMetleu 620
QY 2084 CTGTGCTGCTGCAATAAGATGAGTGAAGGTAACAATCATATGATGCTTGTATATCAC 2143
DB 621 LeuAlaGlyCysIleLysTyrGlyAargGlyGluAsnIleTyrAspAlaPheValIleTyr 640

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QY 2144 TCAGCCAGGATGAGACTGGTAAAGAAATAGCTAAGTAATTAGAAAGAGGCTG 2203
| | | | |
Db 641 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 660
QY 2204 CCTCCATTTCAGCTTCGCTTCCTACAGACTTTATTCCTCCGCTGGCCATTGCTGCC 2263
| | | | |
Db 661 ProProPheGlnLeuLeuCysLeuHisArgAspPheLeuProGlyValAlaIleAla 680
QY 2264 AACATCATCCATAGAGTTTCCATAAAGCCGAAAGGTATGTGTGGTGTCCCGAC 2323
| | | | |
Db 681 AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValIleSerGlnHis 700
QY 2324 TTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTGACCTGGCAGTTTCTG 2383
| | | | |
Db 701 PheIleGlnSerArgTrpCysIlePheGlnIuTrGlnIleGlnIleHisTrpGlnPheLeu 720
QY 2384 AGCAGTCGTGCTGTATTCATCTTCATTTGCTTCGACAGAGGTGAGAAACCTGCTCAG 2443
| | | | |
Db 721 SerSerArgLysIleGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 740
QY 2444 CAGCAGGTGAGCTGTACCGCCTTCTCAGAGAGAACTTACCTGAGTGGAGAGCACT 2503
| | | | |
Db 741 GlnGlnValGlnLeuLeuTrpArgLeuLeuSerArgAsnThrTrpLeuGlnTrpGlnAspSer 760
QY 2504 GTCTCTGGGCGGACATCTTCTGGAAGCAGACTGAGAAAGCCCTGCTGATGGTAAATCA 2563
| | | | |
Db 761 ValLeuGlnArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
QY 2564 TGGAAATCCAGAGAAACAGTGGGTACAGATGCAATTTGGCAGAGAACACATCTTATC 2620
| | | | |
Db 781 TrpAsnProGlnGlnTrpValGlnTrpGlyCysAsnTrpGlnIuAlaThrSerIle 799

RESULT 15

ABB83162
ID ABB83162 standard; protein; 799 AA.
AC ABB83162;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human Toll-like receptor-4, Tlr4.
XX
KW Human; virulence; antibacterial; fungicide; parasiticide; receptor;
KM cytotoxic; immunostimulatory; scavenger receptor; Toll receptor;
XX respiratory tract infection; Toll-like receptor; Tlr4.
OS Homo sapiens.
XX
PN MO200235236-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001WO-FR003352.
XX
PR 27-OCT-2000; 2000FR-00013883.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Jeannin P, Magistrelli G, Herbault N, Bonnefoy J;
XX
DR MPI; 2002-383586/41.
XX
PT Toll receptor, useful as carrier or adjuvant in vaccine, promotes a
XX
PT cytotoxic T cell response.
XX
PS Disclosure; Page 58-60; 71pp; French.
XX
CC The present invention relates to a method for identifying new therapeutic
CC compounds (1) by selecting molecules that bind to scavenger receptors and
CC signal through a Toll receptor. The present sequence is the protein

CC sequence for human Toll-like receptor-4, Tlr4, which was used to
CC illustrate the method of the invention. (1) are useful as carriers and/or
CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC tumour cell, especially a pathogen that causes respiratory tract
CC infection, also more generally for inducing an immune response. (1) can
CC also be used for specific targeting of active agents (antigens etc.) to
CC antigen-presenting cells (especially immature dendritic cells), for
CC subsequent internalisation by these cells

SQ Sequence 799 AA;

Alignment Scores:

Pred. No.:	0	Length:	799
Score:	4141.00	Matches:	799
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.27%	Indels:	0
DB:	5	Gaps:	0

US-09-396-985B-1 (1-4868) x ABB83162 (1-799)

QY 224 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCTCCCTTCAACCAAGAACTGGAC 283
| | | | |
Db 1 MetGlnLeuAsnPheTrpLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
QY 284 CTGAGCTTAAATCCCTGAGGACATTTAGGACGATTAAGCTTCTTCAGTTTCCAGAACTG 343
| | | | |
Db 21 LeuSerPheAsnProLeuArgHisLysGlySerTrpSerPheSerPheProGlnLeu 40
QY 344 CAGGTCTGGAATTTATCCAGGTGTGAATCCAGACAAATTAAGATGGGCGATTCAGAC 403
| | | | |
Db 41 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTrpGlnSer 60
QY 404 CTAGCCACCTGCTCTTCTTAATATGACAGAAACCCATCCAGAGTTTACGCCCTGGGA 463
| | | | |
Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY 464 GCCTTTCTGAGCTATCAAGTTTACAGAGCTGTGGCTGGAGCAAAATCTAGACATCT 523
| | | | |
Db 81 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 100
QY 524 CTAGAGAACTTCCCATTTGGAACATCTCAAACTTTGAAAGAACTTATGTGCTCAAA 583
| | | | |
Db 101 LeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 120
QY 584 CTATCCAACTTTTCAAAATTAAGCTGTGATTTTCTTAATCTGACCAATCTAGAGCACTTG 643
| | | | |
Db 121 LeuIleGlnSerPheLysLeuProGlnLysPheSerAsnLeuThrAsnLeuGlnHisLeu 140
QY 644 GACCTTCCAGAACAAAGATTCAAGATTATTCACAGACTTGCGGGGTTCTACATCAA 703
| | | | |
Db 141 AspLeuSerSerAsnLysIleGlnSerIleTrpCysThrAspLeuArgValLeuHisGln 160
QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAATCTTAGAACTTTATCCAAACA 763
| | | | |
Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY 764 GGTGCACTTAAAGAAATTTAGGCTTCTTAAGCTGACCTTTAAGAAATATTTGATAGTTTA 823
| | | | |
Db 181 GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
QY 824 AATGTAATGAAAACCTGTATTCAGAGCTGGGCTGTGAAGTCCATGGTTGGTGTCTG 883
| | | | |
Db 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 220
QY 884 GGAGAAATTTAGAAATGAGAAACTTGAAAGTTTGACAAATCTGCTAGAGGCGCTG 943
| | | | |
Db 221 GlyGlnPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 240
QY 944 TGCATTTTGAACATTTGAAGAAATTCGATTAAGCATTTGACCTACTGATCTGATGATTT 1003
| | | | |
Db 241 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTrpLeuAspTrpTrpLeuAspAspIle 260

QY 1004 ATTGACTTATTTATTTGACAAATGTTCTTCATTTTCCCGAGGAGTGACATT 1063
 |||||
 Db 261 ILeuSpLeuPheuSncysLeuThnAsnValSerSerPheSerLeuValSerValThnIle 280
 |||||
 QY 1064 GAAAGGGTAAAGAATTCTTTCTTAATTTGGATGGACATTAGATTAACTGT 1123
 |||||
 Db 281 GluArgValLysAspPheSerTyrAsnPheGlyTyrPcInHisLeuGluValAsnCys 300
 |||||
 QY 1124 AAATTTGGACAGTTTCCCACTTGAATGAACTCAATCTCTCAAAAAGGCTTACTTCACTTCC 1183
 |||||
 Db 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 |||||
 QY 1184 AACAAAGGTGGAGATGCTTTTTCAGAGTTGATCTACCAAGCCCTGAGTTCTTAGATCTC 1243
 |||||
 Db 321 AsnLysGlyGlnAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu 340
 |||||
 QY 1244 AGTAGAAATGGCTTGAATTTCAAGGTGGCTGTCTTCCAAAGTGAATTTTGGAGACAACGAC 1303
 |||||
 Db 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerInSerAspPheGlyThrThrSer 360
 |||||
 QY 1304 CTAAAGTATTTAGATCTGACCTTCAATGTTGTTATTCATGAGTTCAAACTTTGGGC 1363
 |||||
 Db 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
 |||||
 QY 1364 TTGAGACAACTAGAACATCTGGAATTTCCAGACTTCCAAATTTGAAACAAGAGGAGTTT 1423
 |||||
 Db 381 LeuGlnGlnLeuGlnLysLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 400
 |||||
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 Db 401 SerValPheLeuSerLeuAspAsnLeuIleTyrLeuAspIleSerHisThrHisThrArg 420
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Search completed: March 29, 2005, 17:00:01
 Job time : 309.49 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 42.7671 Seconds
(without alignments)
16993.973 Million cell updates/sec

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Perfect score: 8579
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Searched: 513545 segs, 7464904 residues
Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	4197	48.9	844	4	US-09-949-016-9438
2	629.5	7.3	661	1	US-08-514-014-4
3	629.5	7.3	661	2	US-08-833-823-4
4	599.5	7.0	784	4	US-09-982-308B-23
5	539	6.3	775	4	US-09-949-016-8799
6	316	3.7	605	3	US-09-063-950-5
7	305	3.6	623	4	US-09-949-016-10995
8	303.5	3.5	907	4	US-09-170-496D-264
9	303.5	3.5	907	4	US-09-170-496D-278
10	303	3.5	605	1	US-08-190-802A-49
11	303	3.5	605	1	US-08-477-346-49
12	303	3.5	605	3	US-08-473-089-49

13	303	3.5	605	4	US-08-487-072A-49	Sequence 49, Appl
14	303	3.5	605	4	US-09-538-092-1087	Sequence 1087, Ap
15	299.5	3.5	662	4	US-09-538-092-1325	Sequence 1325, Ap
16	299.5	3.5	662	4	US-09-949-016-6619	Sequence 6619, Ap
17	299.5	3.5	665	4	US-09-949-016-10710	Sequence 10710, A
18	299	3.5	1525	3	US-09-191-647-2	Sequence 2, Appl1
19	299	3.5	1525	3	US-09-540-245A-2	Sequence 2, Appl1
20	299	3.5	1525	3	US-09-540-153-2	Sequence 2, Appl1
21	296	3.5	603	1	US-08-190-802A-50	Sequence 50, Appl
22	296	3.5	603	1	US-08-477-346-50	Sequence 50, Appl
23	296	3.5	603	3	US-08-473-089-50	Sequence 50, Appl
24	296	3.5	603	4	US-08-487-072A-50	Sequence 50, Appl
25	289.5	3.4	1112	3	US-09-353-585-3	Sequence 3, Appl1
26	289	3.4	1529	4	US-09-312-283C-336	Sequence 36, App
27	286.5	3.3	1166	4	US-10-101-464A-900	Sequence 900, App
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44	272	3.2	1480	5	PCT-US91-09055-2	Sequence 2, Appl1
45	271	3.2	1139	4	US-09-513-505-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Alignment Scores:
Pred. No.: 0
Score: 4197.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 48.92%
DB: 4
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RESULT 2
 US-08-514-014-4
 / Sequence 4, Application US/08514014
 / Patent No. 5707829

GENERAL INFORMATION:
 / APPLICANT: Jacobs, Kenneth
 / APPLICANT: McCoy, John
 / APPLICANT: Kelleher, Kerry
 / APPLICANT: Carlin, McKeough
 / TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 / TITLE OF INVENTION: ENCODED THEREBY
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 / STREET: 87 Cambridgepark Drive
 / City: Cambridge
 / STATE: Massachusetts
 / COUNTRY: USA
 / ZIP: 02140

COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/514,014
 / FILING DATE:

CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Brown, Scott A.
 / REGISTRATION NUMBER: 32,724
 / REFERENCE/DOCKET NUMBER: G16000
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (617) 498-8224
 / TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 661 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-514-014-4

Alignment Scores:
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 Score: 629.50 Matches: 199
 Percent Similarity: 45.90% Conservative: 109
 Best Local Similarity: 29.66% Mismatches: 274
 Query Match: 7.34% Indels: 89
 DB: 1 Gaps: 24

US-09-396-985b-1 (1-4868) x US-08-514-014-4 (1-661)

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 Db 103 LeuSerThrIleuValIleuThrIleuGlnAsnProIleIlePheMetAlaIleuThrSerIleuAsn 122
 QY 473 GGAATATCAAGTTTACAGAGAGCTGTGCTGTGAGACAAATCTAGCATCTTACAGAAC 532
 |||||
 Db 123 GlyProIysSerIleuYshIleuPheIleuIleGlnThrGlyIleSerAsnIleuGlnPhe 142
 QY 533 TTCCCATTTGACATCTCAAACTTTGAAGAAGCTTAATGTGCTCAATCTTATCCAA 592
 |||||
 Db 143 IleProValIleAsnIleuGlnAsnIleuGlnSerIleuYrIleuGlySerAsnIleSer 162
 QY 593 TCTTCAATTAACCTGATATTCTTCTAATCTGACCAACTAGACCTGAGACTTTC 652
 |||||
 Db 163 SerIleIlePheProIysAspPhePro--AlaArgAsnIleuYsValIleuAspPheGln 181
 QY 653 AGCAACAAGATTCAAGATTATTATGACAGAGACTTGCGGGTCTTACATCAAAATGCCCTTA 712
 |||||
 Db 182 AsnAsnAlaIleIshIerYrIleSerArgGluAspMetArgSerIleuGln-----Ala 199
 QY 713 CTCATCTCTCTTTAGACCTGTCCTGATTCCTATGACCTTATCCAAAGCTGACTTT 772
 |||||
 Db 200 IleAsnIleuSerIleuAsnIleuAsnIleuValIleuGlyIleGlnIleuGlyAlaPhe 219
 QY 773 AAGAATTAAGCTTCATAGCTGACTTAAAGAAATATTGATGATTAAATGTAAG 832
 |||||
 Db 220 AspSerThrValPheGlnSerIleu-----AspPheGlyGlyThrProAsnIleu 235
 QY 833 AAAACTTGTATTCAAGTCTGCTGCTTTAGAGTCCATGCTTGTGCTGGAGAAATT 892
 |||||
 Db 236 SerValIlePheAsnIleuGlnIleuAsnSerThrThrGlnSerIleuThrPheGlyThrPhe 255
 QY 893 AGAAATGAAGAACTTGAAAAAGTTTGACAAATCTGCTTAGAGGCGCTTGCAATTG 952
 |||||
 Db 256 GluAspIleAspAsp---GluAspIleSerSerAlaMetIleuIleuGlyIleuYsGluMet 274
 QY 953 ACCATTGAAGATTCGATTAGCATTAAGCTTACCTGATGATGATTTATGAC--- 1009
 |||||
 Db 275 SerValGluSerIleuAsnIleuGln-----GluIleAspPheSerAspIleSerThr 292
 QY 1010 TTAATTATGTTTGAAGATGTTCTTCAATTTCCCTGATGAGTGTGACTATGAAAG 1069
 |||||
 Db 293 ThrPheGlnCysPheThrGlnIleuGlnIleuAspIleuThrAlaIleuIleuIleuYsGly 312
 QY 1070 GTAAAAAGACTTTTCTTATATTTCCGATGCGCAACATTTGAAATTAGTTAAC----- 1120
 |||||
 Db 313 LeuProSer-----GlyMetIleuGlyIleuAsnIleuIleuYsIleuVal 327
 QY 1121 -----TGTAATTT-----GACAGTTTCCCACTG 1147
 |||||
 Db 328 LeuSerValAsnIlePheAspGlnIleuYsGlnIleSerAlaIleAsnIlePheProSerIleu 347
 QY 1148 -----AACTCAATCTTCAAAAGGCTTACTTTCATCTTCCAAAC 1186
 |||||
 Db 348 ThrIleIleuYrIleuGlyAsnValIleuYsIleuIleuIleuIleuValIleuGlyIleuGln 367
 QY 1187 AAAAGTGGAAATGCTTTTTCAGAAAGTGAATGATGTAACAAGCTTGAATTTGATCTCAAT 1246
 |||||
 Db 368 IysIleuGlyAsn-----LeuGlnThrIleuAspIleuSer 378


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Db      163 SerIleYsbPheProLysAspPhePro---AlaArgAsnLeuValLeuAspPheGln 181
QY      653 AGCAACAAGATTCAAAGATTTATTTGTCACAGACTCGGGGTTTACATCAAAATGCCCTTA 712
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182 AsnAsnAlaIleHisIyrIleSerArgGluAspMetArgSerLeuGln-----Ala 199
QY      713 CTCATCTCTCTTTAGACCTGTCCTCGAATCTTATGACCTTTATCCAACCGAGTCGATTT 772
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      200 IleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValGlyGlyLeuLeuGlyAlaPhe 219
QY      773 AAGAAATTAAGGCTTATAGCTGATCTTAAGAAATTAATTTGATAGTTAAATGAAG 832
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      220 AspSerThrValPheGlnSerLeu-----AsnPheGlyGlyThrProAsnLeu 235
QY      833 AAAACTTGATTCAGAGCTCGGCTGGTTTGAAGTCATCGTTGGTTCGGAGAAATTT 892
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      236 SerValIlePheAsnGlyLeuGlnAsnSerThrThrGlnSerLeuThrPhe 255
QY      893 AGAAATGAAGAACTTGAAAGATTGCAAAATCTGCTCTAGAGGCGCTGTCGAAATTTG 952
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      256 GluAspIleAspAsp---GluAspIleSerSerAlaMetLeuGlyGlyLeuGlyMet 274
QY      953 ACCATTGAAGAAATTCGATTAAGTACTTAACTACTGATCTGATGATATTATTGAAC--- 1009
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      275 SerValGluSerLeuAsnLeuGln-----GluHisArgPheSerAspIleSerSerThr 292
QY      1010 TTAATTAATTTGTTTGAAGATTTCTTCAATTTCCCTGGTGAAGTGAATGAAG 1069
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      293 ThrPheGlnCysPheThrGlnLeuGlnGluLeuAspLeuThrAlaThrHisLeuGly 312
QY      1070 GTAAAGACTTTCTTATTAATTTGCGAAGTGGCAACTTTAGAAATTTAGTAAAC----- 1120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      313 LeuProSer-----GlyMetGlyGlyLeuAsnLeuLeuGlySlyLeuVal 327
QY      1121 -----TGTAATTT-----GGACAGTTTCCACATTTG 1147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      328 LeuSerValAsnHisPheAspGlnLeuGlyGlnIleSerAlaIleAsnPheProSerLeu 347
QY      1148 -----AACTCAATCTCTCAAAAGGTTACTTTCACCTTCCATCCATC 1186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      348 ThrHisLeuTyrIleArgGlyAsnValIlySlyLeuHisLeuGlyValGlyCysLeuGln 367
QY      1187 AAAGTGGAGATCTTTTTCAGAAAGTGAATCTAACAGCTTGAGTTCTAGATCTCACT 1246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      368 LysLeuGlyAsn-----LeuGlnThrLeuAspLeuSer 378
QY      1247 ACAAATGCTTGAATTTCAAAGTTCGTTCTCAAAAGTATTTGGACAACACCACTTA 1306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      379 HisAsnAspIleGluIleSerAspCysCysSerLeuGlnLeuGlyAsnLeuSerHisLeu 398
QY      1307 AAGTATTTGATCTGAGCTTCAATGCGTATTATACATGAGTTCAAAAC---TTCTTGGGC 1363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      399 GlnThrLeuAsnLeuSerHisAsnGluProLeuGlyLeuGlnSerGlnAlaPheLysGln 418
QY      1364 TTAGAACAACACTAGACATCTGATTTCCAG-----CATTCGAATTTGAACA 1411
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      419 CysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuHisIleAsnAlaProGln 438
QY      1412 ATGAGTAGATTTTCA-----GTATTCGTATCACTCAAGAACTCATTTAC-----CTT 1459
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      439 ---SerProPheGlnAsnLeuHisPheLeuGlnValLeuAsnLeuThrThrCysPheLeu 457
QY      1460 GACATTTCTCATATCAACACACAGAGTTGCTTTCATAGGAGATCTTCAATGCTTGGCACT 1519
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      458 AspThrSerAsnGlnHis-----LeuLeuAlaGlyLeuProVal 470
QY      1520 CTCGAAGTCTTGAATAATGCTGCAATCTTTTCCAGAAACAACTCTCT-----CCAGAT 1573
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      471 LeuArgHisLeuAsnLeuGlyAsnHisPheGlnAspGlyThrIleThrLysThrAsn 490
QY      1574 ATCTTCACAGAGCTGAAGAACTTGACCTTCTGAGACCTTCTCAAGTGTCACTGAGACAG 1633
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      491 LeuLeuGlnThrValGlySerLeuGlnValLeuIleLeuSerSerCysGlyLeuLeuSer 510

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QY      1634 TTGTCTCAACAGACATTTAATCACTCTCCAGCTTTCAGAGTCTTAATATATGAGCCAAAC 1693
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      511 IleAspGlnAlaAlaPheHisSerLeuGlyLysMetSerHisValAspLeuSerHisAsn 530
QY      1694 AACTTCTTT-----TCATGATACGTTTCTTTAT-----AAG 1726
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      531 SerLeuThrCysAspSerIleAspSerIleAspSerLeuSerHisLeuGlyIleTyrLeuAsnLeu 550
QY      1727 TGTCTGAATCCCTCCAGGTTTGTATTTACATGTCCTCAATCAGATATGACTTCCAAA 1786
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      551 AlaAlaAsnSerIleAsnIleIleSerProArgLeuProIleLeu-----566
QY      1787 CAGAAACTCAGACATTTTCCAGTACTGATCTTAAATCTTAACTTCAAGATGACTTT 1846
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      567 -----SerGlnGlnSerThrIleAsnLeuSerHisAsnProLeu 579
QY      1847 GCTTGATCTTGTGAACACCAAGATTTCTGCAATGATGACAGACAGGACGCTTTG 1906
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      580 AspCysThrCysSerAsnIleHisPheLeuThrIlePtyrGlyGlyAsnLeuHisSlyLeu 599
QY      1907 GTGGAAGTTGAACGAATGGAATGTGACACCTTCAGATTAACAGGCGATGCTGCGTG 1966
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      600 GluGlySerGlnGluThrThrCysAlaAsnProProSerLeuArgIlyValLysLeuSer 619
QY      1967 AGTTGAATATATCAGCTGTCAGATGAATAGACATCATGATGATGTCGCTGCTCACTG 2026
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      620 AspValLysLeuSerCysGlyIle-----ThrAlaIleGlyIlePhePheLeuIleVal 637
QY      2027 CTGTGATATCTGTTGTAGCACTTGTGTTAT 2059
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      638 PheLeuLeu---LeuLeuAlaIleLeuLeuPhe 647

RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB06010C
; CURRENT APPLICATION NUMBER: US/09/982,308B
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.: 1,166-55 Length: 784
Score: 599.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 6,99% Indels: 219
DB: 4 Gaps: 38

US-09-396-985B-1 (1-4868) x US-09-982-308B-23 (1-784)
QY      245 ATCCCGACAACTCCCTTCTCAACCAAGAACTGACCTGAGCTTATATCCCTGAGG 304

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Db      46  ILeProSerGlyLeuThrGluAlaValLysSerLeuAspLeuSerAsnAsnArgIleThr 65
Qy      305  CATTTAGGACGACTATAGCTCTTCACTTCCAGAACTGCAAGCTGCTGATTTATCCAG 364
Db      66  TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
Qy      365  TGTGAATCCAGCATTTGAAAGTGGGGCATATCAAGCCTAAGCCACTCTCTACTCTTA 424
Db      86  AsnGlyIleAsnThrIleGlnGlnAspSerPheSerSerLeuGlySerLeuGlnIleu 105
Qy      425  ATATTGACAGAAACCCCATCCAGAGTTTAAAGCCCTGGAGCCCTTTCTGCACTATCAAGT 484
Db      106  AspLeuSerTyrAsnTyrIleuSerAsnLeuSerSerSerTyrPheLysProLeuSerSer 125
Qy      485  TTRCAGAAAGCTG-----GTGGCTGTGGAG 508
Db      126  LeuThrPheLeuAsnLeuLeuGlnLysAsnProTyrLysThrLeuGlnLysLThrSerLeuPhe 145
Qy      509  ACAAACTAGCATCTAGAGAACTTCCCATTTGGACATCTCAAACT----- 556
Db      146  SerHisLeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
Qy      557  -----TTGAAAGAACTTATGTGGCTCAAACTT 586
Db      166  GlnArgLysAspPheAlaGlyLeuThrPheLeuGlnLysLeuGlnIleAspAlaSerAsp 185
Qy      587  ATCCAACTCTTCAAAATTTACTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTGAGC 646
Db      186  LeuGlnSerTyrGln--ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
Qy      647  CTTTCAGAGAAAG-----ATTCAAGAAAT 673
Db      205  LeuHisMetLysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal 224
Qy      674  TATTGACAGACTTGGGGTTTCTATCAATGACCCCTACTCAATCTCTTTAGACCTG 723
Db      225  GluCysLeuGlnLeuArg-----AspThr 232
Qy      734  TCCCTGATCTTATGAACCTT-----ATCAACACAGTGCATTTTAAAGAAATTAAGCTT 787
Db      233  AspLeuAspThrPheHisPheSerGlnLeuSerThrGlyLysThrAsnSerLeu---Ile 251
Qy      788  CATTAAGTGCCTTAAAGAAAT-----AATTGATAGTTTA---AATGTAATGAA 835
Db      252  LysLysPheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLys 271
Qy      836  ACTTGT-----ATTCAAGGTCTGGCTGTGTTTAAAGTCCATGCTTGGTTCTG----- 883
Db      272  LeuLeuAsnGlnIleSerGlyLeuLeuGlnLeuGlnPheAspArgCysThrLeuAsnGly 291
Qy      884  ---GGAGATTTTGAAATGAGAAACTTGAAAAAGTTTGACAAATCTGCTCTAGAGGCG 940
Db      292  ValGlyAsnPheArgLysAspAsnAspArgValIleAspProGlyLysValGln--- 310
Qy      941  CTGTGCAATTTGACCTTGAAGAATCCGATTTAGCA-----TACTTAGACTCTACCTC 994
Db      311  -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
Qy      995  GATGATATTATGACTATTATTAATTTGTTGACAAATTTTCTCATATTTCCCTGGTAGT 1054
Db      327  ---AspLeuSerThrIleuTyrSerLeuThrGlnArgValLys-----Arg 340
Qy      1055  GTGACTATTGAAAGGGTAAAGACTTTTCTTATATATTCGGATGGCAACATTTAGAAATTA 1114
Db      341  IleThrValGlnAsnSerLysValPhe-----Leu 350
Qy      1115  GTTAACTGTAATTTGACAGTTTCCACATGTGAATCTCAATCTCAAAAGGCTTACT 1174
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1175  TTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAAATGATCTCAACAGCTTGAGTTT 1234

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Db      358  -----HisLeuLysSerLeuGlnTyr 364
Qy      1235  CTAGATCTCAGTAGAAAT-----GGCTTGAGTTTCAAGGTTGCTGTCT 1279
Db      365  LeuAspLeuSerGlnAsnLeuMetValGlnGlnTyrLeuLysAsnSerAlaCys----- 382
Qy      1280  CAAAGTATTTTGGGACAAACAGCCCTAAAGTATTTAGATCTGAGCTTCAATGATGTATT 1339
Db      383  -----GlnAspAlaIleProSerIleuGlnThrLeuIleLeuAsnGlnAsn----- 397
Qy      1340  ACCATGAGTTCAAACTTCTGGGCTTGAACAACTTGAACATCTGATTTCCAGCACTTCC 1399
Db      398  -----HisLeu-----Ala 400
Qy      1400  AATTGAAACAAATGATGATGATTTTCAATTTCTATCATCTGACAACTTCAATTAACCTT 1459
Db      401  SerLeuGlnLysThrGlyGln-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 418
Qy      1460  GACATTTCTCATATCTACACACAGAGTGTCTTCAATGGCATCTTCAATGGCTTGTCAGT 1519
Db      419  AspIleSerLys----- 422
Qy      1520  CTCGAAGTCTGAAAAATGGCTGGCAATTCTTTCAGAAAACTTCTTCAGATATCTTC 1579
Db      423  -----AsnSerPheHisSer-----MetProGlnThrCys 432
Qy      1580  ACAGAGCTGAGAAACTTGACCTTCCGTGACCTCTCTCACTGTCATCTGACAGCACTTGCT 1639
Db      433  GlnThrProGlnLysMetLysTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
Qy      1640  -----CCAACAGCATTTTAACCTACCTCCAGACTTCCAGTACTAATATGAGCCAC 1690
Db      453  GlyCysIlePro-----LysThrLeuGlnIleuAspAlaSerAsn 466
Qy      1691  AAC-----ACCTCTTTCATTTGAT 1711
Db      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArg 486
Qy      1712  -----ACGTTTCT---TATTAAGTGTGAACTCCCTCCAGGTTCTTGATTAC 1756
Db      487  AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuLysIle 506
Qy      1757  AGTCTCAATCACATATGACTTCCAAAAACAGAACTCAGACATTTTCCAAAGTACTCTA 1816
Db      507  SerArgAsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe---HisThrLeu 525
Qy      1817  GCTTCTTAATCTTACTCAGAAATGACTTGTCTGTGATCTTGGAACACAGAGTTTCTCTG 1876
Db      526  LysThrLeuGlnAlaGlyLysAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 545
Qy      1877  CAATGATCAAGGACACAGAGGAGCTTGTGGGAAGTT-----GAAACA 1921
Db      546  Gln-----GlnGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn 561
Qy      1922  ATGGAATGTGCAACACTTCCAGATTAAGAGGACATCTGTGCTGAGTTTGAATATCAC 1981
Db      562  TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
Qy      1982  -----TGTCAATGATTAAGACCAATCATTTGTGTGTGCTCTCAGTGTGCTTGTGA 2032
Db      582  ValSerGlnCysHisIleArgIleAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
Qy      2033  GTATCTGTGTGACAGTTCTGTGCTATAGTTCTAT-----TTTCACTGATGCTTCTT 2086
Db      602  IleLeuLeuThrGlyAlaLeuCysHisIleArgPheHisGlyLeuTyrTrpLysMetLys 621
Qy      2087  GCTGCTGCAATAAGTATGCTAGA-----GTTGAAACATC---TAT 2125
Db      622  TrpAlaIleThrLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 641
Qy      2126  GATGCTTTTGTATCTACTCAAGCCAGATGAGCACTGGGTAAAGATGACTGATGAAG 2185
Db      642  AspAlaPheValSerTyrSerGlnArgAspAlaTyrTrpValGlnAsnLeuMetValGln 661

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OY 2186 AATTGTAAGAAGGGGTGCTCCATTTCAGTCTGCTTCACAGACGACTTATTC 2245
Db 662 GTLGGTGAAspNheasnpProphleuYsleuNHisYakYasppheilepro 681
OY 2246 GGTGTGGCCATTGCTGCCAATCATCATCTGAAGGTTTCCATTAAGCCGAAGGTGATT 2305
Db 662 GilystrpIleileasppheilelele---AapserileglulysserHisYstrVal 700
OY 2306 GTTGTGGTGTCCAGACTTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCT 2365
Db 701 pheValleuSerGluAsnphValYysSerGutpCylysYstrGluLeuaspPheSer 720
OY 2366 CAGACCTGGACGTTTCTGAGCAGTGTGCTGTGATCATCTTCATCTTCCTCCGAGAGGTG 2425
Db 721 HisPheValGluLeupheaspGluAsnAsnAspAlaIleleuIleuLeuGluProIle 740
OY 2426 GAGAAGACCTCTCTCAGGACAGAG--GTGAGAGCTTACCGCTTCCAGCAGGAACACT 2482
Db 741 GilystrYsAlaIleproGlnArgPheCylysLeuArgYsIleMetAsnThrYsThr 760
OY 2483 TACCTTGAGTGGGAGAGACAGTGTCTCGGGGGCGGCACATCTTCTGAGAGACATCAGAAA 2542
Db 761 TyrLeuGluTutpProwetaspGluAlaGlnArgGluGlyPheThrValAsnLeuArgAla 780
OY 2543 GCCCTG 2548
Db 781 AlaIle 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMANS DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRN
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores:
Pred. No.: 4,72e-49 Length: 775
Score: 539.00 Matches: 218
Percent Similarity: 41.22% Conservative: 120
Best Local Similarity: 26.59% Mismatches: 264
Query Match: 6.28% Indels: 218
DB: 4 Gaps: 37

US-09-396-985B-1 (1-4668) x US-09-949-016-8799 (1-775)
OY 245 ATCCCGGACAACTCCCTTCATCAACCAAGAACTGAGCTTATATCCCTCGAGG 304
Db 81 IleProSerGlyLeuThrGluAlaValYsSerLeuAspLeuSerAsnHisArgIleThr 100
OY 305 CATTATGAGCAATATGCTTCTTCAGTTTCCAGAACTCGAAGTGCAGATTATATCCAG 364
Db 101 TyrIleSerAsnSeraspLeuGlnArgCyValAsnLeuGlnAlaLeuValLeuThrSer 120
OY 365 TGTGAATCCAGACAAATTGAAGATGGGGCATATCAGAGGCTTAAGCCACTTCTTACCTTA 424

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Db	121	AsnGlyIleAsnThrIleGlnGlnAspSerPheSerSerIleGlySerIleGlnHisIleu	140
Qy	425	ATATTGACAGAAACCCCATCCAGATTTACCCCTGGAGCCTTTTGTGACTACAGT	484
Db	141	AspLeuSerIlyrAanIlyrLeuSerAsnLeuSerSerItrPheIysProLeuSerSer	160
Qy	485	TTACAGAACTG-----GTGGCTGTGGAG	508
Db	161	LeuThrPheLeuAsnLeuLeuGlyAsnProIlyrIlyrThrLeuGlyGlnThrSerLeuPhe	180
Qy	509	ACAATATCTAGCATCTCTAGAGAACTCCCATCTGGACATCTCAAAACT-----	556
Db	181	SerHisLeuThrIlyrIleuGlnIleLeuArgValGlyIleAsnMetAspThrPheThrIlyrIle	200
Qy	557	-----TTGAGAAGAACTTAACTGGCTCACAACTCT	586
Db	201	GlnArgIysAspPheAlaGlyLeuThrPheLeuGlnGlnIleuGlnIleAspAlaSerAsp	220
Qy	587	ATCCAAATCTTTCAAAATTAACCTGAGATATTTTCTATCTGACCAATCTTAGACACTTGGAC	646
Db	221	LeuGlnSerIlyrGln-----ProIlyrSerLeuIysSerIleGlnAsnValSerHisLeuIle	239
Qy	647	CTTTCAGCAACAAG-----ATTCAAAAGTAT	673
Db	240	LeuHisMetIysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal	259
Qy	674	TATTGCACAGACTGTCGGGTCTTCAATCAAAATGCCCTTACAAATCTCTCTTGAACCTG	733
Db	260	GlnIySerLeuGlnIleuAspG-----AspThr	267
Qy	734	TCCCTGAATCTTATGAACCTT-----ATCCAAACAGGTGCATTTAAAGAAATTAAGCCTT	787
Db	268	AspLeuAspThrPheHisPheSerGlnIleuSerThrGlyGlnThrAsnSerLeu---Ile	286
Qy	788	CATAGCTGACTTTAAAGAAAT-----AATTGATAGTTA---AATGTAAATGAA	835
Db	287	IyIyIysPheThrPheArgAsnValIlyIleThrAspGlnSerLeuPheGlnValMetIyIys	306
Qy	836	ACTTGT-----ATTCAAGGTCTGGCTGTTTGAAGTCCATCGTTTGCTGCTG-----	883
Db	307	LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleuGlnIleuPheAspAspCysThrLeuAsnGly	326
Qy	884	---GGAGAAATTTAGAAATGAAGAACTTGAAAGATTGACAAATCTGCTCTAGAGGCG	940
Db	327	ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIyValGln---	345
Qy	941	CTGTGCATTTGACCATTTGAAGAAATCCGATTAGCA-----TACTTAGACTACTACCTC	994
Db	346	-----ThrLeuThrIleArgArgLeuHisIleProArgPheIyLeuPheIytr-----	361
Qy	995	GATGATATTTATGACTATTTAATTTATGTTTGGCAAAATGCTTCTCATATTTCCCTGGTGA	1054
Db	362	---AspLeuSerThrLeuIyIySerLeuThrGlnArgValIys-----Arg	375
Qy	1055	GTGACTATTTGAAGAGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTTAGAAATTA	1114
Db	376	IleThrValGlnAsnSerIyValPhe-----Leu	385
Qy	1115	GTTAACGTGAATTTGGACAGCTTTCCACATGAAACTCAAACTCTCAAAAGGCTTACT	1174
Db	386	ValProCysIleuLeuSerGln-----	392
Qy	1175	TTGACTTCCAAACAAGGTGGAAATGCTTTTTCAGAAGTGATCTTACCAAGCCTTGAGTTT	1234
Db	393	-----HisLeuIySerLeuGlnIytr	399
Qy	1235	CTAGATCTCAGTAGAAAT-----GCTTGAAGTTTCAAAAGGTGCTGTCTT	1279
Db	400	LeuAspLeuSerGlnIleuAsnLeuMetValGlnGlnIyIyIreIyIyAsnSerAlaCys-----	417
Qy	1280	CAAAAGTATTTTGGGACCAACGCTTAAAGTATTTTAATCTGAGCTTCAATGCTGTATTT	1339

418 -----GluAspAlaItrProSerLeuGlnThrLeuIleuValArgLysAsn----- 432
QY 1340 ACCATAGTTCAAACTCTTGGCTTAGAACAACTGATGATTTCCAGCATTC 1399
Db 433 -----HisLeu-----Ala 435
QY 1400 AATTGAACAATAGATGATTTTCAGTATTCCTACATCAGAACCTCATTTACCT 1459
Db 436 SerLeuGlnIleuThrLeuGln-----ThrLeuIleuThrLeuValAsnLeuThrAsnIle 453
QY 1460 GACATTTCTCATATCTGACACGAGTTGCTTCAATGGCATTTCAATGGCTTGTCACT 1519
Db 454 AspIleSerLys----- 457
QY 1520 CTCGAAGTCTGAAAATGGCTGGCAATCTTTCCAGAAAACCTCTCCAGATATCTTC 1579
Db 458 -----AsnSerPheHisSer-----MetProGluThrCys 467
QY 1580 ACAGAGCTGAGAAACTTGACCTTCTGAGACCTCTCAGTGTGACAGAGAGCTGTGCT 1639
Db 468 GlnTrpGluIleuThrLeuValSerThrArgIleHisSerValThr 487
QY 1640 -----CCAAACAGATTTTAATCTGCTCCAGTCTTCAAGTACTAATATAGCCAC 1690
Db 488 GlyCysIlePro-----LysThrLeuGlnIleuLeuAspValSerAsn 501
QY 1691 AAC-----AAGCTTTTCATTTGAT----- 1711
Db 502 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArg 521
QY 1712 -----ACGTTTCTCT-----TATTAAGTGTCTGAACTCCCTGACGATTTTGAATAC 1756
Db 522 AsnIleuLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle 541
QY 1757 AGTCTCAATCACTAATAGCTTCCAAAAACAGAACTACAGATTTTCCAGTACTGTA 1816
Db 542 SerArgAsnAlaIleThrThrPheSerLysGlnLeuAspSerPhe---HisThrLeu 560
QY 1817 GCTTTCTTAATATCTACAGATGATGATGATGATGATGATGATGATGATGATGATG 1876
Db 561 LysThrLeuGlnIleuValGlnLysAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 580
QY 1877 CAATGATCAAGACAGACAGACAGCTCTGCTGAGATTT-----GAAACA 1921
Db 581 Gln-----GlnGlnGlnAlaLeuAlaLysValIleuIleAspTrpProAlaAsn 596
QY 1922 ATGGAATGCAACACCTTCAGATAGCAGGAGCTGCTGCTGATGATTTGAATATCAC 1981
Db 597 TyrLeuCysAspSerProSerHisValArgGlnGlnIleValIleAspValArgLeuSer 616
QY 1982 -----TGTGAGATGAATAGACCATATGATGATGATGATGATGATGATGATG 2032
Db 617 ValSerGlnCysHisArgThrAlaLeuValSerLysMetCysValAlaLeuPheLeuLeu 636
QY 2033 GATAGCTTTGTAGACGTTCTGCTGATATAGTTCTAT-----TTTCACTGATGCTTCT 2086
Db 637 IleLeuLeuThrGlnValLeuCysHisArgPheHisIleLysLeuTrpLysMetLysMetMet 656
QY 2087 GCTGGCTGATAAAGTATGCTAGA-----GGTAAAATC-----TAT 2125
Db 657 TrpAlaItrPheGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 676
QY 2126 GATAGCTTTGTATCTATCTGACGAGATGAGACCTGGGTAAGATGAGATGAGATGAG 2185
Db 677 AspAlaIleValSerLysArgLysArgAspAlaTyrTrpValGlnAsnLeuMetValGln 696
QY 2186 AATTAGAAGAGGGGCTCCATTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2245
Db 697 GlnLeuGlnAsnProPheAsnProPheLysLeuHisLysValArgPheIlePro 716
QY 2246 GGTGTGGCCATTTGCTGCAACATCATCATGAAAGTTTCCATAAAGCCGAAAGTGAT 2305
Db 717 GlyLysTrpIleIleAspAsnIleIle---AspSerIleGlnLysSerHisLysThrVal 735

QY 2306 GTTGTGTGTCCAGACCTTATCCAGACCGCTGTGTATCTTGAATATGAGATTTGCT 2365
Db 736 PheValIleuSerGlnAsnPheValLysSerGlnTyrCysLysGlnLeuAspPheSer 755
QY 2366 CAGACCTGGCAGCTTTCTGAGCAGTGTGCTGTATCATCTTCAATGCTCCGAGAGGTG 2425
Db 756 HisPheArgLeuPheAspGlnLysAsnAsnAspAlaIleIleuIleLeuGlnIleProIle 775
RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: HOLLIMAN, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 605
; TYPE: PRF
; ORGANISM: Papilio hamadryas
US-09-063-950-5
Alignment Scores:
Pred. No.: 9,46e-25 Length: 605
Score: 316.00 Matches: 157
Percent Similarity: 39.04% Conservative: 94
Best Local Similarity: 24.42% Mismatches: 242
Query Match: 3,68% Indels: 150
Gaps: 23
US-09-396-985B-1 (1-4868) x US-09-063-950-5 (1-605)
QY 200 GTTCCATATATTAATCATATGATGATGATGATGATGATGATGATGATGATGATG 259
Db 53 ValAsnGlnLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspGlnIle 72
QY 260 CCGTTCTCAACAAGAACCTGAGACCTTAAATCCCTGAGGATTTAGGACAGCTAT 319
Db 73 ProGlnGlnThrGlnAlaLeuThrLeuAspSerAsnAsnLeuSerIleProProAla 92
QY 320 AGCTTCTTCAAGTTTCCAGACCTGACAGTGTGATTTTCCAGGTGTAAATCCAGACA 379
Db 93 AlaPheArgAsnLeuSerSerLeuAlaPheLeuAsnLeuGlnGlnGlnLeuGlnSer 112
QY 380 ATTGAAGATGGGGCATATACAGACCTTAAGCAGCTCTCTAATATATTTGACAGGAAC 439
Db 113 LeuGlnProGlnAlaLeuLeuGlnLysGlnLysLeuCysHisIleuHisLeuGlnLysArgAsn 132
QY 440 CCCATCAGAGTTTAACTCCCTGGAGCCTTTCT----- 472
Db 133 GlnLeuArgSerLeuAlaValGlnThrPheAlaTyrThrProAlaLeuAlaLeuLeuGln 152
QY 473 -----GGATATCAAGTTTA 487
Db 153 LeuSerAsnAsnArgLeuSerArgLeuGlnLysArgLysPheGlnLysLeuGlnLysLeu 172
QY 488 CAGAACCTGTGGCTGTGAGACCAATCTAGCATCTCTAGAGAACTTCCCATTTGACAT 547
Db 173 TrpAspLeuAsnLeuGlnTyrTrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGln 192
QY 548 CTCAAACCTTTGAGAAAGCTTAAATGCTGCTCAATCTTATTCGAATCTTCAATTTAC 607
Db 193 LeuGlnGlnLeuArgLysLeuValLeuAlaGlnAsnArgLeu---AlaTyrLeuGlnPro 211
QY 608 GAGTATTTTCTTATATCTGACCAATCTAGACAGCTTGACCTTTCCAGCAACAGATTTCA 667
Db 212 AlaLeuPheSerGlnLysLeuAlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArg 231

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QY 668 AGATTTATTCACAGACTTGGGGTTCTACATCAATGCCCCCTTCAATCTCTCTTTA 727
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Db 232 AAlaLe-----LysAlaAsnValPheAlaGlnLeuProAlaGlnLeu-----LysLeu 247
QY 728 GACCTGTCCTGGAATCTTGAAGAACTTTATCCACAGAGTGTCTTAAAGAAATAGG--- 784
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Db 248 TyTLeuAspArgLeuIleAlaValAlaProGlyAlaPheLeuGlyLeuLysAla 267
QY 785 CTTCATAGCTGACTTTTAAAGAAATATTTGATAGTTTAAATGTAATGAAATCTGTAT 844
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Db 268 LeuArgTyrLeuAspLeuSerHisAsn---ArgValAlaGlyLeuLeuGluAspThrPhe 286
QY 845 CAAGGTGTGCTGTGTTTAAAGATTCATCGTTGGTCTGGAGAAATTTAGAAATGAAGA 904
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   |||
Db 287 ProGlyLeuLeuGlyLeuArgValLeuArgLeu----- 297
QY 905 AACTTGGAAAAATTTGACAAATCTGCTTGAAGGGCTGTGCAATTTGACCATTGAAGA 964
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Db 298 -----SerHisAsnAlaIleAlaSerLeuArgProArgThrPheGluAsp 312
QY 965 TTCCGATTAGCATTAAGACTACTACTGATGATATTTATTTGATTTAATTTGTTTG 1024
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Db 313 Leu-----HisPheLeuGlnGluLeu----- 319
QY 1025 ACAATGTCTTCATTTTCCCTGGTGAAGTGTGACTATTGAAAGGTAAAGACTTTTCT 1084
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Db 320 -----GlnLeuGlyHisAsnArgIleArgGlnLeuAlaGluArgSer 333
QY 1085 TATTAATTCGAGANGGCAACATTTAGAAATTAAGTAACTGTAAATTTGACAGTTTCCACA 1144
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Db 334 PheGlu---GlyLeuGlyGlnLeuGlyValLeuThrLeuAspHisAsnGlnLeuGln 352
QY 1145 TTGAAATCTCAAAATCTCAAAAGCTTACTTCTCC-----AACAAAGTGGGAAT 1198
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Db 353 ValLysValGlyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsn 372
QY 1199 GCTTTTTCAGAAAGTTGATCTTACCAAGCTTGAAGTTCTAGATCTCAGTAA---AATGAC 1255
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Db 373 CysLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGlyLysLeuHisSer 390
QY 1256 TTGAGTTTCAAAAGTGTCTGT-----TCTCAAAAGTGAATTTGGACAAACC 1300
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Db 391 LeuHisLeuGlnGlySerCysLeuGlyArgIleArgProHisThrPheAlaGlyLeuSer 410
QY 1301 AGCTTAAAGTATTTAGATCTGAGCTTCAATGCTGTATTTACACATGAGTTCAACTTTTG 1360
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Db 411 GlyLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGlnGlnSerLeu 430
QY 1361 ---GGCTTAGAACAACTAGAACATCTGATTTCCAGATTCCAATTTGAAACAAATGAGT 1417
   |||
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   |||
Db 431 TyrGlyLeuAlaGlyLeuLeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
QY 1418 GAGTTTTCAGTATTCCTATCACTCAGAAACCTCATTTACCTTGACATTTCTCATACTAC 1477
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Db 447 -----ThrHis 448
QY 1478 ACCAGAGTTCCTTCAATGCGATCTTAAATGCTTGTTCAGTCTCGAAGTCTGAAAATG 1537
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Db 449 LeuPro-----HisGlnLeuPheGlnGlyLeuGlyLysLeuGlnGlyLeuLeu 465
QY 1538 GCTGGCAATCTTTCAGGAAACCTGCTTCCA---GATATCTTCACAGAGGCTGAGAAAC 1594
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   |||
Db 466 SerHisAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeuGlnArg 483
QY 1595 TTGACTTCTCTGAGACTCTCTCTGAGTTCAACTGGAGAGAGTGTCTCCACAGCAATTTAAC 1654
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Db 484 AlaPheTyrLeuAspValSerHisAsnArgLeuGlnAlaLeuProGlySerLeuLeuAla 503
QY 1655 TCACTCTCCAGTCTTCAAGTACTTAAATATAGACCAACAACTTTCTTTATTTGAGTACG 1714
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Db 504 SerLeuGlyArgLeuArgTyrLeuAsnLeuArgAsn-----SerLeuArgThr 520

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QY 1715 TTTCCTTAATAGTGTCTGAATCTCCCTCCAGGTTCTTGATTACAGTCTCAATCAATATG 1774
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Db 521 PheThrProGln----- 524
QY 1775 ACTTCAAAAAAAGAGAACTACAGACTTTTCCAGAGTACTTCTTAAATCTTACT 1834
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Db 525 -----ProProGlyLeuGlnArgLeuTyrLeuGln 534
QY 1835 CAGAAATGACTTGTCTTACTTGTGAACACAGAGT----- 1870
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Db 535 GlyAsnProTyrAspCysSerCysProLeuLysAlaLeuArgAspPheAlaLeuGlnAsn 554
QY 1871 -----TTCTGCAATGATC-----AAGACCAAGGCAAGCTC 1903
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   |||
Db 555 ProSerAlaValProArgPheValGlnAlaIleCysGlnGlyLysAspCysGlnProPro 574
QY 1904 TTGCTGGAAGTTGAAGATGGAATGTGCAACCTTTCAGATTAAGACGGCATGCTGTG 1963
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Db 575 ValTyrThrTyrAsnAsnIleThrCysAlaSerProGlyValAlaGlyLeuAspLeu 594
QY 1964 CTGAGTTTG 1972
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Db 595 ArgAspLeu 597

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-10995

Alignment Scores:
Pred. No.: 1,546-23 Length: 623
Score: 305.00 Matches: 171
Percent Similarity: 37.87% Conservative: 96
Best Local Similarity: 24.26% Mismatches: 260
Query Match: 3.56% Indels: 178
DB: Gaps: 28

US-09-396-985b-1 (1-4868) x US-09-949-016-10995 (1-623)
QY 113 GCCTCGCGCTGGCT-----GGAGCTTGATCCAGCCATGCGCTTCTCTCTG 163
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Db 16 AlAcArgArgMetAlaLeuArgLysGlyAlaLeuAlaLeuAlaLeuLeuLeuSerTyr 35
QY 164 GTGAGA-----CCAGAAAGCTGGAG----- 184
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   |||
Db 36 ValAlaLeuGlyProArgSerLeuGlnGlyAlaAspProGlyThrProGlyGlnAlaGln 55
QY 185 -----CCCTGCGGTG-----GAGGTGGTCTCTAATATTACT 214
   |||
   |||
   |||
Db 56 GlyProAlaCysProAlaAlaCysValCysSerTyrAspAspAspAlaAspGlnLeuSer 75
QY 215 TATCAATGATGAGAGCTGAATTTTCAAAATCCCGACAACTCCCTTCTCAACCAAG 274
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; LENGTH: 907
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-170-496D-264

Alignment Scores:
Pred. No.: 2,97e-23 Length: 907
Score: 303.50 Matches: 194
Percent Similarity: 36.00% Conservative: 116
Best Local Similarity: 22.53% Mismatches: 285
Query Match: 3.54% Indels: 266
DB: 4 Gaps: 36

US-09-396-985b-1 (1-4868) x US-09-170-496D-264 (1-907)

QY 32 TCMAAGCGTATGCAACGACGCG-----ATTGACGGGCGACTGCTGCACAA 82
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Db 19 AlarhcdlyglserProargserGlyValleuLeuarglyCysProthrhlsCys 38
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 ACCAGTGGAGTATGCGCAGGATGATGTCTGCGCGCTGGCGTGGAGCTGTATCCA 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 HiscyglubproaspGlyArgMetLeu----- 47
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 143 GCCATGGCCTTCTCTCTGCGTGAGACCAAAAGCTGGAGCCCTGCGTGGAGTGTT 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ----- 47
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QY 203 CTAATATTACTTATCAATGATGAGTGAATTTCTACAAATCCCGCAACCTGCC 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 48 -----LeuArgValaspCysSerAspLeuGlyLeuSerGlyLeuProSerAsnLeuSer 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 263 TTCTCAACCAAGAACCTGACCTGAGCTTAAATCCCTGAGCATTTAGCAGCTATAGC 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ValpheThierSerlyrLeuaspLeuSerMetAsn----- 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 323 TTCTTCAAGTTCCCAAGACTGACAGTGCATTTATTCAGGTGAAATTCAGACAAAT 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 -----AsnIleSerGlnLeu 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 383 GAAGATGGGCGATATGACGCTTAAGCCACTCTCTTACTTATATTGACAGAAACCC 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 LeuProAsnProleuProSerLeuArgPheLeuGlnGlnLeuArgLeuAlaGlyAspAla 101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 443 ATCAGAGTTTAAAGCCCTGGAGGCTTTCTGACTATCAAGTTTACAGAGCTGGTGGCT 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 LeuThrylIleProlyserGlyAlaPheThrylLeuThrylSerLeuIleValLeuMetLeu 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 503 GTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAA 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GlnAsnAsnGlnLeuArgHisValProThrglnAlaLeuGlnAsnLeuArgSerLeuGln 141
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QY 563 GAACCTTAATGTGGCTGACATCTTATGCAATCTTTCAATTAAGTATTTTCTTAAT 622
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Db 142 SerLeuArgLeuAspAlaAsnHisIle--SerlyrValProProSerCysPheSerGly 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 623 CTGACCAATCTAGAGCACTTGGACCTTTCAGCAACAAGATTCAGAGTATTATTTGACA 682
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Db 161 LeuHisSerLeuArgHisIleThrylPheLeuAspAspAsnAlaLeuThrglnIleProValGln 180
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QY 683 GACTTGGGGTCTTACATCAAAATGCCCCCTACTCAATCTCTTTAGACTGTCCTGAAT 742
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Db 181 AlaPheArgSerLeuSerAlaLeuGln-----AlaMetThrLeuAlaLeuAsn 196
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QY 743 CCAATGAACCTTATCCACACAGGTGCATTTAAAGAAAT--AGCTTCAATAGCTGACT 799
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Db 197 LysIleIleHisIleIleProAspTyrAlaPheGlyAsnLeuSerSerLeuValIleLeuHis 216
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QY 800 TTAGAAGATATAT--TTGATAGTTTAAATGTATGAAGCTGTATTTCAAGGCTGGCT 856
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 LeuHisAsnAsnArgIleHisSerLeuGly-----LysLysCysPheAspArgIleLeuHis 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 857 GGTTAGAAGTCAATCGTTGGTTCTGGAGAAATTTAGAATGAAGAACTTGAAGAG 916
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Db 235 SerLeuGlnThrLeuAspLeu-----AsnTyrAsnAsnLeuAspGln 248
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QY 917 TTGACAAATCTGCTCTAGAGGCGCTGTGCAATTTGACATTGAAGATTCGATTAGCA 976
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 Phe--ProThrAlaIleArgThrLeuSerAsn-----LeuLys 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 977 TACTTAAGTACTACCTCGATGATATATTATGACTTA-----TTTAATGTTTG 1024
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 GlnLeuGlyPheHisSerAsnAsnIleArgSerIleProGlnLysAlaPhe----- 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1025 ACAATGTTTCTTCAATTTCCCTGCTGAGTGTGACTATT--GAAGGGTAAAGACTTT 1081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 -----ValGlyAsnProSerLeuIleThrIleHisPheTyrAspAsnProIleGlnPhe 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1082 TCTTATATTTGGAGGCAACATTTAGAATTAAGTTAACTGTAAATTTGGACGTTGCC 1141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 ValGlyArgSerAlaPheGlnHisLeuPro-----GlnLeuArg 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1142 ACATTGAACCTCAAAATCTCTCAAAAGCTTACTTTCATTCCAAACAAAGTGGAAATGCT 1201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 ThrLeuThrLeuAsnGlyAlaSerGlnIleThr----- 319
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1202 TTTTCAAGATGATATACCAAGCCTTGAGTTTCTAGATCTCAGTGAATGAGCTTGAGT 1261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 -----GlnPheProAspLeuThr----- 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1262 TTCAAAAGTTTGCTGTTCGAAAGTATTTGGGACCAACGCTTAAGTATTAGATCTG 1321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 -----GlyThrAlaAsnLeuGlnSerLeuThrLeu 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1322 AGCTTCANAGTGTTATTTACATGAGTTCAACTTCTTGAGC--TTGAACAACATAGAA 1378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 ThrGlyAlaGlnIleSerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGln 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1379 CATCTGATTTCCAGCATTCATTTGAACAAGATGAGTTCAGTATCTTATCA 1438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 ValLeuAspLeuSerTyrAsnLeuLeuGlnAspLeuProSerPheSerValCysGlnLys 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1439 CTCAGAAACCTCATTTACCTTCAATTTCTCACTACACACAGATTCCTTCAATGGC 1498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 LeuGlnLys-----IleAspLeuArgHis----- 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1499 ATCTTCAAGGCTTGTCCAGATCTCGAAGTCTGGAAGATGCGCAATTTCTTCCAGGAA 1558
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 -----AsnGlnIleThrylLeuIleVal----- 391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1559 AACTCTCTTCCAGATATCTTCAACAGCTGAGAAACTTGACCTTCTGACCTCTCTCAG 1618
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 -----AspThrPheGlnGlnLeuLeuSerLeuArgSerLeuAsnLeuAlaTyr 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1619 TGTCAACTGAGACAGTGTCTCCACAGAGATTTACTGCTCTCCAGTCTTCAAGTACTA 1678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 AsnLysIleAlaIleIleHisProAsnAlaPheSerThrLeuProSerLeuIleLysLeu 427
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1679 AATATGAGCCACAAACATTTCTTTTCACTGGAATACTTCTTATTAAGTGTGAACTCC 1738
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 AspLeuSerSerAsn-----LeuLeuSerSerPheProIleThrglyLeuHisGly 444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1739 CTCGAGTCTTGATTACGTCTCAATCAATCAATGACTTCCAAAAGAGAACTACAG 1798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 LeuThrHisLeuLysLeuThrglyAsnHisAlaLeuGlnSerLeuIleSerSer--Glu 463
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1799 CATTTTCCAGATGATCTAGCTTCTTAATCTTACTCAAGAAAGACTTTCCTGTACTGT 1858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 AsnPheProGln-----LeuLysValIleGlnMetProTyrAlaTyrGlnCys 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1859 -----GAACACACAGATTTCTTCCATGATGATCAAG----- 1888
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 CysAlaPheGlyValCysGlnAsnAlaTyrLysIleSerAsnGlnIleThrasnLysGlyAsp 499
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1889 -----GACGAG 1894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 AsnSerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGln 519
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY      1895 AGGCAGCTC-----TTGGTGGAGATTGAACGAATG 1924
      ||| |||
Db      520 hrgAspIeuGlusAphleuLeuAapPhegluGlusApleuysalaLeuHisSerVal 539
QY      1925 GAATGTGCACACCTTCAGATTAAGCAGGCGATCCTT----- 1960
      ||| |||
Db      540 Glncys---SerProSerProGlyProPheIyProCysegluHisLeuLeuAerGlyTyr 558
QY      1961 -----GTGCTGAGTTGAATATCACTCTGTCAGATGAATTAAG 1996
      ||| |||
Db      559 LeuIleArgIleGlyValTPrThrIleAlaValLeuAlaLeuThrCys-----AsnAla 576
QY      1997 ACCATCATTTGTTGTCGCTCCTCAGTGTCTGTGATGATCTTTGATGAGCATTTGCTGTC 2056
      ||| |||
Db      577 LeuValThrSerThrValPheAArgSerProLeuTyrIleSerProIleIysLeuLeuIle 596
QY      2057 TATTAAGTTCTATTTCACCTGATGCTT-----CTTGCTGCTGCTG 2095
      ||| |||
Db      597 GlyValIleAlaAlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyVal 616
QY      2096 ATTAAGTAT-----GGTAAGCT 2113
      ||| |||
Db      617 AspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTPrTPrGluAsnGlyValGly 636
QY      2114 GAAACATCTATGATGCTTGTATCTACTCAAGCCAGCATGAGCATGGATAGGAAT 2173
      ||| |||
Db      637 CysHisValIleGlyPheLeuSerIlePheAlaSerGluSerSerValPheLeuLeuThr 656
QY      2174 GACCTAGTAAAGATTAGAGAAGGGG--TGCTTCATTTGACTGCTGCTTCATAC 2230
      ||| |||
Db      657 -----LeuAlaIleLeuGlu-ArgGlyPheSerValIyTyrSerAlaIyAspHeGluTh 674
QY      2231 AGAGACTTATTTCCCGGTGGCCATTGCTGCCAATCATCCATGAAGTTTCCATAA 2290
      ||| |||
Db      674 rIyysAla-----ProPheSerSerLeuIyValIleIle-- 685
QY      2291 AGCCGAAAGGTGATGTTGTGTGTCGCCAGACTTCATCCAGACCGCTGCTGATCTTT 2350
      ||| |||
Db      686 -----LeuLeuCySaIaLeuAlaLeuThrMechAlaAlaValProle 700
QY      2351 G 2351
      ||| |||
Db      700 u 700

RESULT 9
US-09-170-496D-278
; Sequence 278, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170, 496D
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 278
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-278

Alignment Scores:
Pred. No.: 2,97e-23 Length: 907
Score: 303.50 Matches: 194
Percent Similarity: 36.00% Conservative: 116
Best Local Similarity: 22.53% Mismatches: 285
Query Match: 3.54% Indels: 266
DB: 4 Gaps: 36

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US-09-396-985B-1 (1-4868) x US-09-170-496D-278 (1-907)
QY      32 TCMAAGCGTGATAGCAACACAGC-----ATTCAACAGGCGCACCTGCTGCACAA 82
      ||| |||
Db      19 AlArhGlyGlySerSerProArgSerGlyValLeuLeuAlaGlyCysProThrHisCys 38
QY      83 ACCAGTAGAGATGAGCCAGATGATGTGCTGCGCTGCGCTGCGAGCATCTGATCCCA 142
      ||| |||
Db      39 HisCysegluProAspGlyArgMetLeu----- 47
QY      143 GCGATGCGCTTCTCTCTGCTGAGACCAAGAGCTGGAGCCCTGCTGAGGTGCTT 202
      ||| |||
Db      47 ----- 47
QY      203 CCTAATATTACTTATCAATGATGAGCTGATTTCTACAAATGCCGAGAACCTTCCCC 262
      ||| |||
Db      48 -----LeuArgValAspCysSerAspLeuGlyLeuSerGluLeuProSerAsnLeuSer 65
QY      263 TTCTCAACCAAGAACCTGAGCTGAGCTTAAATCCCTGAGGCAATTAGCAGATATAGC 322
      ||| |||
Db      66 ValPheThrSerTyrLeuAspLeuSerMetAsn----- 76
QY      323 TTCTTCAAGTTCCAGAACTGCAAGTGTGATTTATCCAGGTGGAATTCAGACAAAT 382
      ||| |||
Db      77 -----AsnIleSerGluLeu 81
QY      383 GAAAGATGGGGCATATCAGACGCTTAAGCCACTCTCTACTTAAATATGACAGAAACCCC 442
      ||| |||
Db      82 LeuProAsnProLeuProSerLeuIyArgPheLeuGluGluLeuArgLeuAlaGlyAsnAla 101
QY      443 ATCCAGAGTTAGACCTGAGGACCTTTTGTGACTATCAAGTTTACAGAACTGAGTGCST 502
      ||| |||
Db      102 LeuThrTyrIleProIySelIyAlaPheThrGlyLeuTyrSerLeuIyValLeuMetLeu 121
QY      503 GTGGAGACAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTGGAA 562
      ||| |||
Db      122 GluAsnAsnGluIleuAsnArgHisValProThrGluAlaLeuGluAsnLeuArgSerLeuGlu 141
QY      563 GAATTTAATGTGGCTACAAATCTTATCCAAATCTTTCAAATTCAGAGATTTTCTAAT 622
      ||| |||
Db      142 SerLeuArgLeuAspAlaAsnHisIle--SerTyrValProProSerCysPheSerGly 160
QY      623 CTGACCAATCTAGAGACTTGGACTTTCSCAGCAACAGATTCMAAGTATTATTATTCACA 682
      ||| |||
Db      161 LeuHisSerLeuAsnArgHisLeuThrIyLeuAspAspAsnAlaLeuThrGluIleProValGlu 180
QY      683 GACTTGCGGGTTCTATCATCAAAATGCCCTTACTCAATCTCTTTAGACTGTGCCGTAAT 742
      ||| |||
Db      181 AlaPheArgSerLeuSerAlaLeuGlu-----AlaMetThrLeuAlaLeuAsn 196
QY      743 CCTATGAACCTTATCCAAACAGGTGATTTAAAGAAAT--AGGTTGATTAAGCGACT 799
      ||| |||
Db      197 LyuIleHisHisIleProAspTyrAlaPheGlyAsnLeuSerSerLeuValIleuHis 216
QY      800 TTAAGAAATTAAT--TTGATAGTTTAAATGTAATGAAGAACTTGATTAAGGTGCTGCT 856
      ||| |||
Db      217 LeuHisAsnAsnArgIleHisSerLeuGly-----LyuIyCysePheAspGlyLeuHis 234
QY      857 GGTTTAGAAATCCATCGTTGGTTGCTGAGAGATTAGAAATGAAGAACTTGAAGAAAG 916
      ||| |||
Db      235 SerLeuGluThrLeuAspLeu-----AsnTyrAsnAsnLeuAspGlu 248
QY      917 TTGACAAATCTGCTTAGAGGCGCTGTCGAATTTGACATTTGAGAAATTCGATTAAGCA 976
      ||| |||
Db      249 Phe--ProThrAlaIleArgThrLeuSerAsn-----LeuIyS 260
QY      977 TACTTACATGACTGATGATGATATATTAATGACTTA-----TTAATGTGTTG 1024
      ||| |||
Db      261 GluIleGlyPheHisSerAsnAsnIleArgSerIleProGluIyAlaPhe----- 277
QY      1025 ACAAAATGTTCTTCAATTTTCCCTGCTGAGTGTGACTAAT--GAAAGGGTAAAGACTTT 1081
      ||| |||

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Db 278 -----ValGlyAsnProSerLeuIleThrIleHisPheTyraAsnProIleGlnPhe 295
 QY 1082 TCTTAATAATTCCGATGCAACATTTAGATTAAGTAAATTGGACAGTTTCCC 1141
 Db 296 ValGlyArgSerAlaPheGlnHisLeuPro-----GluLeuArg 308
 QY 1142 ACATTGAATCAAAATCTCTCAAAAGGCTTTCATTTCACAAAGGTGGGAAATGCT 1201
 Db 309 ThrLeuThrLeuAsnGlyAlaSerGlnIleThr----- 319
 QY 1202 TTTTCAGAACTGATCTACCAAGCCTTGAGTTCTAGATCTCAGTAGAAATGGCTTGAGT 1261
 Db 320 -----GluPheProAspLeuThr----- 325
 QY 1262 TTCAAAGTTGCTGTTCTCAAAAGTATTGGAGCAACAGCCTTAAAGTATTAGATCTG 1321
 Db 326 -----GlyThrAlaAsnLeuGlnSerLeuThrLeu 335
 QY 1322 AGCTTCATGTTGTTATTACATGAGTTCAAACTTTGGGC---TTAGAACAACTAGAA 1378
 Db 336 ThrGlyAlaGlnIleSerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGln 355
 QY 1379 CATCTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGGTTTCAGTATTCCTATCA 1438
 Db 356 ValLeuAspLeuSerTyraAsnLeuGlnAspLeuProSerPheSerValCysGlnLys 375
 QY 1439 CTCAGAACTCATTTACCTTCGATTTCTCATCTACACACAGAGTTGCTTCATATGGC 1498
 Db 376 LeuGlnLys-----IleAspLeuArgHis----- 383
 QY 1499 ATCTTCATGCTGTTGCCAGCTTCGAGGCTTGAATAATGCTGGCAATTTCTTCCAGGAA 1558
 Db 384 -----AsnGlnIleTyraGlnIleLysVal----- 391
 QY 1559 AACTCTCTTCCAGATATCTTCAGAGAGCTGAGAACTTGACCTTCTGCACCTCTCTCAG 1618
 Db 392 -----AspThrPheGlnGlnIleLeuSerLeuArgSerLeuAsnLeuAlaTyr 407
 QY 1619 TGTCACTGGAGAGATGTCTCCAAAGCATTTTAACCTGCTCCAGTCTTCAGTAGTA 1678
 Db 408 AsnLysIleAlaIleIleHisProAsnAlaPheSerThrLeuProSerLeuIleLysLeu 427
 QY 1679 AATATGAGCCACAACAATCTTTTTCATGATGATGCTTCTTAAATGATGCTGAACTCC 1738
 Db 428 AspLeuSerSerAsn-----LeuLeuSerSerPheProIleThrGlyLeuHisGly 444
 QY 1739 CTCAGAGTTCTTGAATTAAGTCAATCACAATATGACTTCCAAAACAGAACTACAG 1798
 Db 445 LeuThrHisLeuLysLeuThrGlyAsnHisAlaLeuGlnSerLeuIleSerSer---Glu 463
 QY 1799 CATTTCCAGTAGTCTAGCTTCTTAAATCTTACACAGAACTGCTTGTCTGTACTGT 1858
 Db 464 AsnPheProGln-----LeuLysValIleGlnLeuProTyraIleTyraGlnCys 479
 QY 1859 -----GAACACACAGAGTTTCTCGAATGATGATCAAG----- 1888
 Db 480 CysAlaPheGlyValCysGlnAsnAlaTyraLysIleSerAsnGlnIleProAsnLysGlyAsp 499
 QY 1889 -----GACCAG 1894
 Db 500 AsnSerSerMetAspAspLeuHisLysLysAspAlaGlyMetPheGlnAlaGlnAspGlu 519
 QY 1895 AGGCAGCTC-----TTGGTGAAGTTGAACGAATG 1924
 Db 520 ArgAspLeuGlnAspPheLeuLeuAspPheGlnGlnAspLeuLysAlaLeuHisSerVal 539
 QY 1925 GAATGTGCAACACCTTCAGATAAGCAGGCGATGCT----- 1960
 Db 540 GlnCys---SerProSerProGlyProPheLysProCysGlnHisLeuLeuAspGlyTyr 558
 QY 1961 -----GTGCTGAGTTTGAATATCACTGCTGCATGAAATTAAG 1996
 Db 559 LeuIleArgIleGlyValTyrThrIleAlaValLeuAlaLeuThrCys-----AsnAla 576

QY 1997 ACCATCATTTGTTGTGCGTCCCTCACTGTGCTTGTAGTATCTGTTCAGACAGTTCTGTC 2056
 Db 577 LeuValThrSerThrValPheArgSerProLeuTyrlleSerProIleLysLeuIle 596
 QY 2057 TATTAAGTTCTAATTTTCACCTGATGCTT-----CTTGCTGCTGC 2095
 Db 597 GlyValIleAlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyVal 616
 QY 2096 ATTAAGTAT-----GGTAGAGGT 2113
 Db 617 AspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTrpTrpGlnAsnGlyValGly 636
 QY 2114 GAAACATCTATGATGCTTTGTTTATCTACTCAAGCAGAGATGAGGATGGGTAGAGAT 2173
 Db 637 CysHisValIleGlyPheLeuSerIlePheAlaSerCluSerSerValPheLeuLeuThr 656
 QY 2174 GAGCTAGTAAAGATTTAGAGAGAGGG---TGCCTTCATTTGAGCTTGCTTCATC 2230
 Db 657 -----LeuAlaLeuGln-ArgGlyPheSerValLysTyraSerAlaLysPheGln 674
 QY 2231 AGAGACTTATTCCTCCGCTGCGCATTTGCTGCCAATCATCATGAGGTTTCCATPAA 2290
 Db 674 LysAla-----ProPheSerSerLeuLysValIleIle-- 685
 QY 2291 AGCCGAAAGTGATTTGTTGTGCTGCCAGCACTTCATCCAGCCGCTGTGTATCTTT 2350
 Db 686 -----LeuLeuCysAlaLeuLeuAlaLeuThrMetAlaValProle 700
 QY 2351 G 2351
 Db 700 u 700

RESULT 10
 US-08-190-802A-49
 ; Sequence 49, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Theoreof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 605 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
; US-08-190-802A-49

Alignment Scores:
Pred. No.: 2,5e-23 Length: 605
Score: 303.00 Matches: 157
Percent Similarity: 38.57% Conservative: 91
Best Local Similarity: 24.42% Mismatches: 243
Query Match: 3.53% Indels: 152
DB: 1 Gaps: 24

US-09-396-985B-1 (1-4868) x US-08-190-802A-49 (1-605)

QY 221 TGCATGAGAGCTGATTTCTACAAATATCCCGACACCTCCCTTCTCAACCAAGAACTTG 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 60 CysSerSerArgSerLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 281 GACCTGAGCTTTAATCCCTGAGGACATTTAGGACGATATGACTTCTTCAGTTTCCAGAA 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 TrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 341 CTGCAGGTGCTGATTTATTCAGGTGTGAATCCAGACATTTGAAGATGGAGCATATCAG 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 401 AGCCTAAGCACCCTCTCACTTAATATTGACAGAAACCCCATCCAGATTGACCCCTG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 120 GlyLeuGlnAsnLeuGlySerIleuH1sLeuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 461 GGAGCCCTTTCT----- 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 GlyThrPheAlaH1sThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 473 -----GACATATCAAGTTTACAGAAAGCTGGTGGCTGTGAG 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 ArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGlyTrp 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 509 ACAATATCAATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTT 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 180 AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlnLeu 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 569 AATGTGCTCAACATCTTATCCATCTTCTTCAATTCCTGAGATTTTCTATCTGACC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 ValLeuAlaGlyAsnArgLeu---AlaIyLeuGlnProAlaLeuPheSerGlyLeuAla 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 629 AATCTAGAGCAGCTTGACCTTTCACAGAACAAAGATTCAAGATTATTTATGACAGACTTG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLeu-----LysAla 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 689 CGGGTTCTACATAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAATCCATG 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 AsnValPheValGlnLeuProArgLeuGln---LysLeuIyLeuAspArgAsnLeuIle 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 749 AACTTTATCCAACAGGATTTTAAAGAAATTAG---CTTCATAAGCTGACCTTAAAGA 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 255 AlaAlaValAlaProGlyAlaPheLeuGlyLeuIyAlaLeuArgTrpLeuAspLeuSer 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 806 AATAATTTTGATAGTTTAAATGTATGATGAAAACCTGTATTCAGAGTCTGCTGTTTGA 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 HisAsn---ArgAlaAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeuArg 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 866 GTTCATCGTTTGTGTTCTGGGAGAAATTGAAATGAAGAAACCTTGAAAAGTTTGACAA 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 294 ValLeuArgLeu-----SerHis 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 926 TCTGCTCTAGAGGCGCTGTGCAATTTGACCATTTGAAGAAATCCGATTAGCATATTAGAC 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 300 AsnAlaIleAlaSerLeuArgProArgThrPheIyAspLeu----- 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 986 TACTACTCGATGATATATTGACTTATTTAATTTGTTTGAACAATGTTTCTCATTTTCC 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 314 HisPheLeuGlnGlyLeu-----Gln 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 CTGGTAGGTGTACATTTGAAAAGGTAAGAACTTTCTTATATTTTGGATGGCAACAT 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 LeuGlyHisAsnArgIleArgGlnLeuAlaGlnArgSerPheGln---GlyLeuGlyGln 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1106 TTGAATTTAGTTAATCTGTAATTTTGGACAGTTTCCACATTTGAAACTCAAACTCTCAAA 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 LeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValIyAlaGlyAlaPheLeu 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1166 AGCCTTACTTTCACCTTC-----AACAAAGGTGGAAATGCTTTTTCAGAGTTGATCTA 1219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 GlyLeuThrAsnValAlaValIeAsnLeuSerGlyAsnGlyLeuArg-----AsnLeu 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1220 CCAAGCCTTGAAGTTTCTAGATTCAGATGAGA---AATGCTTGAAGTTTCAAGGTTGCTGT 1276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 ProGlnGlnValPheArgGlyLeuArgGlyLeuGlyIySerLeuH1sLeuGlnGlySerCys 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1277 -----TCTCAAGTGATTTTGGACACACAGCCTTAAAGTATTAGATCTG 1321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 LeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPheLeu 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1322 AGCTTCAATGTGTATTATACATGAGTTCAAACTTCTTG---GGCTTGAACAATGAGA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 418 LysAspAsnGlyLeuValGlyIleGlnGlnIySerLeuThrProGlyLeuAlaGlnLeu 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1379 CATCTGGAATTTCCAGATTTCCAAATTTGAAACAAATGAGTGAATTTCAATATTCATCA 1438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 GlnLeuAspLeuThrSerAsnGlnLeu----- 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1439 CTCAGAAACCTATTTACCTTGACATTTCTCATACTACACACAGAGTTGCTTTCATGAC 1498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 -----ThrHisLeuPro-----HisArg 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1499 ATCTTCATATGCTTGTCCAGTCTGAGTCTTGAAGTCTTGAAGATCTGGCAATTTCTTCAGAA 1558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 LeuPheGlnGlyLeuGlyIySerLeuGlyIyLeuLeuLeuSerArgAsnArgLeuAlaGln 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1559 AACTTCCTTCCA---GATATCTTCACAGAGCTGAGAAACTTTGACCTCTCGACCTCTCT 1615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 473 -----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrAspValSer 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1616 CAGTGTCACTGAGAGAGTTGTCTCCACAGCATTTTACTCACTCTCCAGTCTTCAAGTA 1675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 HisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuAlaGlyTrp 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1676 CTAAATATGAGCCACAACTTCTTTTCATTGATACGTTTCTTATATAGTGTCTGAAC 1735
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1736 TCCCTTCAGGTTCTTGATTACAGTCTCAATCACTATATATGATTTCCAAAAACAGAACTTA 1795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 524 ----- 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1796 CAGCATTTTCCAAGTAGTCTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTGTACT 1855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCysGly 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1856 TGTGAACACAGAGTTTCTGCAATGATCAAGAC----- 1891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 CysPro-----LeuIyAlaLeuArgAspPheAlaLeuGlnAsnProSerAla 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1892 ---CAGAGCAGCTCTTGGTGAAGTTGAACGAATGGAATGTGCAACACTTCAAGTAAAG 1948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 558 ValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaIyTrp 577
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QY 1949 CAGGCAATGCTGTGCTGATTTGAATATCACTGTCAATGATAATGAACCATCTGTGT 2008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 578 TyrAsn-----AsnIleHnGlyAsnLeuSerProProGlnValIyGly 591
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QY 2009 GTGTCCGATC 2017
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Db 592 LeuaspLeu 594

RESULT 11
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 626223
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Alignment Scores:
Pred. No.: 2.5e-23 Length: 605
Score: 303.00 Matches: 157
Percent Similarity: 38.57% Conservative: 91
Best Local Similarity: 24.42% Mismatches: 243
Query Match: 3.53% Indels: 152
DB: 3 Gaps: 24

US-09-396-985b-1 (1-4868) x US-08-477-346-49 (1-605)

QY 221 TGCATGGAGCTGATTTCTACAAATCCCGACAACTCCCTTTCACACCAAGACCTG 280
Db 60 CysSerSerArgSerLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
QY 281 GACCTGAGCTTTATCCCTGAGGCACTTAGGCAAGCTATGCTTCTTCAGTTTCCAGAA 340
Db 80 TrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
QY 341 CTGCAAGGTGCTGATTTATCCAGGTGTGAATCCAGCAATTGAAGATGGGGCATATCAG 400
Db 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeuLeu 119

QY 401 AGCTTAAGCCACCTCTCTACATTTATATTGACAGAAACCCATCCAGACTTAGCCCTG 460
Db 120 GlyLeuGlnAsnLeuGlnCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
QY 461 GGAGCTTTTCT----- 472
Db 140 GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
QY 473 -----GGACTATCAAGTTTACAGAAAGCTGGGCTGGAG 508
Db 160 ArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGlyTrp 179
QY 509 ACAAAATGACATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTT 568
Db 180 AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlnLeu 199
QY 569 AATGGGCTCACATCTTATCCAAATTTTCAAAATTTACTGAGATTTTCTAATCTGACC 628
Db 200 ValLeuAlaGlyAsnArgLeu--AlaTrpLeuGlnProAlaLeuPheSerGlyLeuAla 218
QY 629 AATCTAGACACTTGAGACCTTTCAGCAACAAGATTCAAAGTATTATTGACAGACTTG 688
Db 219 GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLeu-----LysAla 235
QY 689 CGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTGCTCCGTAATCTGATG 748
Db 236 AsnValPheValGlnLeuProArgLeuGln--LysLeuTrpLeuAspArgAsnLeuLeu 254
QY 749 AACTTATCCAAACAGGTGATTTAAAGAAATTAGG--CTTCATATAGCTGACTTTAAG 805
Db 255 AlaAlaValAlaProGlyAlaPheLeuGlyLeuValaLeuArgTrpLeuAspLeuSer 274
QY 806 AATTAATTTGATAGTTTAATTAATGAAGAACTTGATTCAGAGCTGGCTGATTTAGAA 865
Db 275 HisAsn--ArgValaAlaGlyLeuLeuGlnAspTrpPheProGlyLeuGlnGlyLeuArg 293
QY 866 GTTCATCGTTGGTTCTGGAGAAATTTAGAAATGAAGAAACTTGAAAAATTTGACAAA 925
Db 294 ValLeuArgLeu-----SerHis 229
QY 926 TTGCTCTGAGGGGCTGTGCAATTTGACCAATTGAAGAAATTCGATTAGCATTTAGAC 985
Db 300 AsnAlaIleAlaSerLeuArgProArgTrpPheLeuAspLeu----- 313
QY 986 TACTACCTCGAGATTTATTTAGCTTATTTAATGTTTGAACAATGTTTCTTATTTC 1045
Db 314 HisPheLeuGlnGlnLeu-----Gln 320
QY 1046 CTGGTGAAGTGTGACTTTGAAAGGTAAGAACTTTCTTAATTTGAGATGGCAACAT 1105
Db 321 LeuGlyHisAsnArgIleArgGlnLeuAlaGlnArgSerPheGln--GlyLeuGlnGln 339
QY 1106 TTGAAATTAAGTAACTGTAATTTGAGACAGTTTCCACATTTGAACCTCAAAATCTTCAAA 1165
Db 340 LeuGlnValaLeuThrLeuAspHisAsnGlnLeuGlnGlnValaLysAlaPheLeu 359
QY 1166 AGGCTTACTTCACTTCC-----AACAAAGGTGGGAAGCTTTTCAGAAAGTTGATCTTA 1219
Db 360 GlyLeuThrAsnValaAlaValaLeuAsnLeuSerGlyAsnCysLeuArg-----AsnLeu 377
QY 1220 CCNAGCCTGAGTTTCTAGATCTCAGTAGA---AATGGCTTGAAGTTTCAAGAGGTTCTGT 1276
Db 378 ProGlnGlnValaPheArgGlyLeuGlnGlyValaHisSerLeuHisLeuGlnGlySerCys 397
QY 1277 -----TTCNAAAGTGAATTTTGAGCAACAAGCCTTAAGATTTAGATCTG 1321
Db 398 LeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPheLeu 417
QY 1322 AGCTTCAATGCTGTTATTTACATGAGTTCAAACTTCTG---GGCTTAGAACAATAGAA 1378
Db 418 LysAspAsnGlyLeuValaGlyIleGlnGlnGlnSerLeuTrpGlyLeuAlaGlyLeuLeu 437
QY 1379 CATCTGATTTCCAGCATTCCAATTTGAACAATGAGTGAATTCAGATTTCTTATCA 1438

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Db      438  GlnLeuAspLeuThrSerAenGlnLeu----- 446
Qy      1439  CTCGAAACCTCATTTACCTTGACATTTCTCATACTCACACGAGAGTTGCTTCAATGGC 1498
Db      447  -----ThHHisLeuPro-----HisArg 452
Qy      1499  ATCTCAATGCTTGTTCAGATCTCGAAGTCTTGAAATGGCTGGCAATCTTTCAGGAA 1558
Db      453  LeuPheGlnGlyLeuGlyLeuGlyLeuLeuSerArgAsnArgLeuAlaGlu 472
Qy      1559  AACTCTCTTCCA--GATATCTTCACAGAGCTGAGAACTTGAACCTTCGACCTCTCT 1615
Db      473  LeuProAlaSerAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspValSer 490
Qy      1616  CAGTGTCACTGAGAGAGTTGTCTCCACAGAGATTAATCACTCTCCAGTCTTCAGAGTA 1675
Db      491  HisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArgTyr 510
Qy      1676  CTAAATATGAGCCACCAACACTCTTTCATTTGAGTATGCTTCTTATTAAGTGTGAGC 1735
Db      511  LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
Qy      1736  TCCTCCAGGCTTCTTGATTAACAGTCTCAATCACATATGACTTCCAAAAACAGAGACTA 1795
Db      524  ----- 524
Qy      1796  CAGCATTTTCAGATGACTGCTTCTTAAATCTTAATCTGAGATGACTTGTGCTTACT 1855
Db      525  ProGlnGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCysGly 541
Qy      1856  TGTGACACACAGAGTTTCTGCAATGATGATCAAGAGC----- 1891
Db      542  CysPro-----LeuYsAlaLeuArgAspPheAlaLeuGlnAsnProSerAla 557
Qy      1892  ---CAGAGCAGCTCTTGTGTGAGTGAAGTGAACGAGATGTCACACCTTCAGATTAAG 1948
Db      558  ValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaTyrThr 577
Qy      1949  CAGGAGCATGCTGTGCTGAGATTTGAATATACCTGTCAAGTGAATGAACCATCATTTGT 2008
Db      578  TyrAsn-----AsnIleThrCysAlaSerProGlnValValGly 591
Qy      2009  GTGTGCGTC 2017
Db      592  LeuAspLeu 594

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RESULT 12
 US-08-473-089-49
 / Sequence 49, Application US/08473089
 / Patent No. 6342368
 / GENERAL INFORMATION:
 / APPLICANT: Mochly-Rosen, Daria
 / APPLICANT: Ron, Dorit
 / TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 / TITLE OF INVENTION: Theroef
 / NUMBER OF SEQUENCES: 265
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Morrison & Foerster
 / STREET: 2000 Pennsylvania Avenue, NW
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20006-1812
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/473,089
 / FILING DATE: 07-JUN-1995
 / CLASSIFICATION: 435

```

/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 2550-0025.22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 605 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor binding
/ INDIVIDUAL ISOLATE: protein complex, Fig. 32
/ US-08-473-089-49

```

Alignment Scores:
 Pred. No.: 2.5e-23 Length: 605
 Score: 303.00 Matches: 157
 Percent Similarity: 38.57% Conservative: 91
 Best Local Similarity: 24.42% Mismatches: 243
 Query Match: 3.53% Indels: 152
 DB: 3 Gaps: 24

US-09-396-985B-1 (1-4868) x US-08-473-089-49 (1-605)

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Qy      221  TGCATGAGCTGATTTCTACAAATCCCGCAACCTCCCTTCAACCAAGACCTG 280
Db      60  CysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
Qy      281  GACCTGAGCTTAACTCCCTGAGGCACTTATGAGCAGTATAGCTTCTTCCAGTTCCAGAA 340
Db      80  TrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
Qy      341  CTGCAAGCTGCTGATTTATCCAGGTGTGAATCCAGCAATGAATGAGGAGCATATCAG 400
Db      100  LeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLeuGlnProGlnAlaLeuLeu 119
Qy      401  AGCTTAAGCCACTCTCTACCTTAATATTGACAGGAAACCCCATGCAAGTTAGCCCTG 460
Db      120  GlyLeuGlnAsnLeuCysHisIleuHisIleuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
Qy      461  GAGACCTTTCT----- 472
Db      140  GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
Qy      473  -----GGACTATCAAGTTTACAGAGCTGTGCTGTGGAG 508
Db      160  ArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuTrpAspLeuAsnLeuGlyTyr 179
Qy      509  ACAATCTAGCATCTCTAGAGAACTTCCCATTTGAGCATCTGCAAACTTGAAGAAGACTT 568
Db      180  AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlnLeu 199
Qy      569  AATGTGCTCAACAATTTATCCAAATCTTCAAAATTAACCTGAGATTTTCTTAATCTGACC 628
Db      200  ValLeuAlaGlyAsnArgLeu--AlaTyrLeuGlnProAlaLeuPheSerGlyLeuAla 218
Qy      629  AATCTAGACACCTTGACCTTTCCAGCAACAGATTCAAAGTATTATTTGACAGACTTG 688
Db      219  GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaIle-----LysAla 235
Qy      689  CGGTTCTACATCAATGCCCCCTACTCAATCTCTTTGACCTGTCCCTGAACTCTTAT 748
Db      236  AsnValAlaPheValGlnLeuProArgLeuGln--LysLeuTyrLeuAspArgAsnLeuIle 254
Qy      749  AACTTATCCAAACAGGTGCATTTAAAGAAATTAGG--CTTCATATAGCTGACTTTAAG 805
Db      255  AlaAlaValAlaProGlyAlaPheLeuGlyLeuLysAlaLeuArgTrpLeuAspLeuSer 274

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QY 806 AATAATTTGATGATTAATAATGAAAACTTGATTCAGAGCTGCGGTGTTAGAA 865
   |||
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   |||
Db 275 Hisasn---ArgValAlaGlyLeuLeuGlnAspThrProGlyLeuLeuGlyLeuArg 293
QY 866 GTCCATCGTTGGTCTCGGAGAAATTGAAATGAAGAAAATTGAAAAGTTTGACAA 925
   |||
   |||
   |||
Db 294 ValLeuArgLeu-----SerHis 299
QY 926 TCGCTCTAGAGGCGCTGTCATTTGACCATTTGAAGAAATTCGGATTAGCATTAAGAC 985
   |||
   |||
   |||
Db 300 AsnAlaIleAlaSerLeuArgProAlaGlyThrPheLeuAspLeu----- 313
QY 986 TACTACCTCGATGATTAATTGACTTATTAATTGTTGACAAATGTTCTCATTTTCC 1045
   |||
   |||
   |||
Db 314 HisPheLeuGlnGluLeu-----Gln 320
QY 1046 CTGGTAGTGTCATATGAAAGGTAAGAACTTTCTTAATAATTCGGATGCAACAT 1105
   |||
   |||
   |||
Db 321 LeuGlyHisAsnArgIleArgGlnLeuAlaGlyAspSerPheGlu---GlyLeuGlyGln 339
QY 1106 TTGGAATAGTAACTGTAATTTGAGACAGTTCCCATTTGAAATCTCAATCTTCGAA 1165
   |||
   |||
   |||
Db 340 LeuGlyValLeuThrLeuAspHisAsnGlnLeuGlnGlyValLeuAlaPheLeu 359
QY 1166 AGGCTTACTTCACTTCC-----AACAAAGTGCGGAATGCTTTTCAGAAAGTTGATCTA 1219
   |||
   |||
   |||
Db 360 GlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----AsnLeu 377
QY 1220 CCAAGCCTGAGTTTCTAGATCTCAGTGA---AATGGCTTGAAGTTCAAGGTCGTGT 1276
   |||
   |||
   |||
Db 378 ProGlnGlnValPheArgGlyLeuGlyLeuGlnSerLeuHisAsnLeuGlnGlySerCys 397
QY 1277 -----TCTCAAGTGAATTTGGGACAAACCGCTTAAGTTTAAATCTGT 1321
   |||
   |||
   |||
Db 398 LeuGlyArgIleArgProHisIleThrPheThrGlyLeuSerGlyLeuArgGlyLeuPheLeu 417
QY 1322 AGCTCAATGGTGTATTAATCAATGATGATTTCAAACTTCTG---GAGCTTGAACAATAGAA 1378
   |||
   |||
   |||
Db 418 LysAspAsnGlyLeuValGlyIleGlnGlnSerLeuThrProIleValAlaGluLeuLeu 437
QY 1379 CATCTGGATTTCCAGCATTCCAATTGAAACAAATGAGTGTTCAGTATTCCTATCA 1438
   |||
   |||
   |||
Db 438 GluLeuAspLeuThrSerAsnGlnLeu----- 446
QY 1439 CTGAGAACTCTATTAACCTTGACATTTCTCATATCTCACCCAGAGTTGCTTCAATGGC 1498
   |||
   |||
   |||
Db 447 -----ThrHisLeuPro-----HisArg 452
QY 1499 ATCTCAATGGCTTTCGACGTCGAAGCTTTGAAATGGCTGGAATTTCTTCCAGGAA 1558
   |||
   |||
   |||
Db 453 LeuPheGlnGlyLeuGlyLysLeuGlnGlyLeuLeuLeuSerArgAsnArgLeuAlaGlu 472
QY 1559 AACTCTCTTCCA---GATATCTTCACAGAGCTGAGAAATCTGACTTCCGACCTCTCT 1615
   |||
   |||
   |||
Db 473 -----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrPheLeuValSer 490
QY 1616 CAGTGTCACTGAGACAGTGTCTCCAAACAGCATTTTAATCACTTCCAGCTTCCAGGTA 1675
   |||
   |||
   |||
Db 491 HisAsnArgLeuGlnIleLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuAspGly 510
QY 1676 CTAAATATGAGCAACAACAATCTTTTCACTTGATAGACGTTTCTTAATAAGTCTGAAAC 1735
   |||
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Db 511 LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
QY 1736 TCCTCCAGGTTCTTGATTAAGCTTCAATCACATATAGACTTCCAAAAACAGAACTA 1795
   |||
   |||
   |||
Db 524 ----- 524
QY 1796 CAGCATTTTCAAGTATGCTTACTTTTAATCTTAATCTTAATCAAGATGACTTGTGTACT 1855
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   |||
   |||
Db 525 -----ProProGlyLeuGlnArgLeuThrIleLeuGlnGlyAsnProThrAspCysGly 541

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QY 1856 TGTGAACACCAAGAGTTTCTCGAATGATCAAGAC----- 1891
   |||
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   |||
Db 542 CysPro-----LeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSerAla 557
QY 1892 ---CAGAGCAGCTCTTGTGTGAAGTTGAACAAATGAATGTGCAACACTTCAGATGAG 1948
   |||
   |||
   |||
Db 558 ValProArgPheValGlnAlaIleLeuCysGlnGlyAspAspCysGlnProProAlaTyrThr 577
QY 1949 CAGGCGATCCGTGTGTGATGTTGAATATATACCTGTGCACATGATGAATGAACCATTTGAT 2008
   |||
   |||
   |||
Db 578 TyrAsn-----AsnIleThrCysAlaSerProProGlnValValGly 591
QY 2009 GTGTCCGTC 2017
   |||
   |||
   |||
Db 592 LeuAspLeu 594

RESULT 13
US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Alignment Scores:
Pred. No.: 2.5e-23
Score: 303.00
Percent Similarity: 38.57%
Best Local Similarity: 24.42%
Query Match: 3.53%
DB: 4
Gaps: 24

US-09-396-985B-1 (1-4868) x US-08-487-072A-49 (1-605)
QY 221 TGCATGAGCTGAATTTCTACAAATCCCGACAACTCCCTCTCAACGAAGACCTG 280

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QY 1949 CAGGCGATGCTGTGATGATTGAATATCATCTGTCAGATGATGAACCATCATTTGAT 2008
 Db 578 TyrAsn-----AsnIleThrCysAlaSerProProGluValValGly 591
 QY 2009 GTGTGGTC 2017
 Db 592 LeuAspLeu 594

RESULT 15

US-09-538-092-1325
 ; Sequence 1325, Application US/09538092
 ; Patent No. 675314
 ; GENERAL INFORMATION
 ; APPLICANT: Glot, Loic
 ; APPLICANT: Mansfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT APPLICATION NUMBER: US/09/538,092
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,965
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CuratSeqFormatter Version 0.9
 ; SEQ ID NO 1325
 ; LENGTH: 662
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (0)..(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q14392
 US-09-538-092-1325

Alignment Scores:

Pred. No.: 6,44e-23 Length: 662
 Score: 299.50 Matches: 187
 Percent Similarity: 38.97% Conservative: 94
 Best Local Similarity: 25.94% Mismatches: 259
 Query Match: 3.49% Indels: 181
 DB: 4 Gaps: 35

US-09-396-985b-1 (1-4868) x US-09-538-092-1325 (1-662)

QY 185 CCCGCTGAGAGGTCTCTAATATCTAATCAAGTCAGATGAAATTTCTACAA 244
 Db 25 ProCysIysMetValAspIlylValSer-----CysGlnValLeuGlyLeuGln 42
 QY 245 ATCCCGACAACTCCCTCTCTCAACCAAGACTGAGCTTTAATCCCTGAG 304
 Db 43 ValProSerValLeuProProleuPheThrGlnThrLeuAspSerGlyAsnGlnLeuArg 62
 QY 305 CATTAGCAGCTATAGCTTCTTCAAGTTCCCAAGACTGAGCTGATTTATCCAG 364
 Db 63 SerIleuAlaSerProleuGlyPheTyThrAlaLeuArgHisIleuAspLeuSerThr 82
 QY 365 TGTGAATTCAGACAAATTGAAGATGGGCAATATAGAGCTTACCCCTCTACTTA 424
 Db 83 AsnGlnIleSerPheLeuGlnProGlyAlaPheGlnIleuThrHisLeuGlnHisLeu 102
 QY 425 ATATTGACAGGAACCCCATCCAGAGTTTACCTCGGAGGCTTTCTGGATTCAGT 484
 Db 103 SerIleuAlaHisAsnAlaGlyLeuAlaMetAlaThrAlaLeuSerAlaGlyGlyLeuGlyPro 122
 QY 485 TTACAGAGCTGTGCTGTGAGACAAATCTAGCATCT-----CTAGAG 529
 Db 123 LeuProArgValThrSerIleuAspLeuSerGlyAsnSerIleuTySerGlyLeuLeuGln 142
 QY 530 AACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAATGTGGCTCACAATCTTATC 589
 Db 143 ArgIeu---LeuGlyGlnAlaProSerIleuHisThrLeuSerIleuAlaGlnAsnSerIleu 161

QY 590 CAATCTTCAAAATTACCTGAGTAT---TTTCTAATCTGACCAATCTAGAGCACTTGAC 646
 Db 162 Thr-----ArgLeuThrArgHisThrPheArgAspMetProAlaLeuGlnGlnLeuAsp 179
 QY 647 CTTTCCAGCACAACAAGTATTTATTTATTCACAGACTTCGGGTTTATCATCAAAATG 706
 Db 180 LeuHisSerAsnValLeuMetAspIleGluAspGlyAlaPheGlnGlyLeuProArgLeu 199
 QY 707 CCCCTACGATCTCTCT----- 724
 Db 200 ThrHisLeuAsnIleuSerArgAsnSerIleuThrCysIleSerAspPheSerIleuGlnGln 219
 QY 725 -----TTAGACCTGTCCCTGAATCCTAGAACTTTATC-----CAACCA 763
 Db 220 LeuArgValLeuAspLeuSerCysAsnSerIleGluAlaPheGlnThrAlaSerGlnPro 239
 QY 764 GGTGCACTTTAAAGAAATTAGGCTTCAAGCTGACTTAAAGAAATAT----- 811
 Db 240 GlnAla-----GluPheGlnLeuThrTrpLeuAspLeuArgGluAsnIlyLeuLeuHis 257
 QY 812 TTTGATAGTTTAAATGTAATGAAACTGTATTCAGAGCTGCGCTTTAGAGTCAT 871
 Db 258 PheProAspLeuAlaAlaLeuProArgLeuIleTyTrpLeuAsnLeuSerAsnAsnLeuIle 277
 QY 872 CGTTTGGTTCTGGGAGAAATTAGAAAT----- 898
 Db 278 ArgLeuProThrGlyProProGlnAspSerIlyGlyIleAlaProSerGlyGlyTrp 297
 QY 899 -----GAGGAAACTTGAAAGTTTGACAAATCTGCTCTA 934
 Db 298 SerAlaLeuProleuSerAlaProSerGlyAsnAlaSerGlyArgProleuSerGlnLeu 317
 QY 935 GAGGCGCTGTGCAATTTGACATTTGACAAATCCGATTTGACADACTTAGACTACTACCTC 994
 Db 318 LeuAsnLeu---AspLeuSerTyArgAsnIleGlnLeu---IleProAspSerPheLeu 335
 QY 995 GATGATATTAATTTGACTTATTT-----AATTGTTGACAAATGTTTCT 1036
 Db 336 GlnHisLeuThrSerIleuCysPheLeuAsnLeuSerArgAsnCysLeuArgThrPheGln 355
 QY 1037 TCATTTTCCCTGTGAGTGTGACTATTTGAAGGGTAAAGACTTTTCTTATATTTGGCA 1096
 Db 356 AlaArgArgLeuGlySerIleuProCysLeuMetLeuLeuAspLeuSerHisAsn---Ala 374
 QY 1097 TGGCAACATTTGAATTAAGTAACTGTAATTTGGACAGTTCCCACTTGAAGTCAAA 1156
 Db 375 LeuGlnThrLeuGlnLeuGlyAlaArgAlaLeuGlySerLeuArgThrIleuLeuGln 394
 QY 1157 TCTCTCAAAAGCTTACTTTCATCTTCCAAAGAGTGGAGATGCTTTTTCAGAAATGTT 1213
 Db 395 -----GlyAsnAlaLeuArgAspLeuPro 402
 QY 1214 -----GATTCACAGCTTGAAGTTTCTAGATCTCAGTGAAGATGGCTTG 1258
 Db 403 ProTyThrPheAlaAsnLeuAlaSerIleuGlnArgLeuAsnLeuGlnIlyAsnAlaGlyVal 422
 QY 1259 AGT-----TTCAAAAGTTTGCTGCTTCAAAAGTATTT 1291
 Db 423 SerProCysGlyGlyProAspArgIleuProGlyProSerGlyCysValAlaPheSer----- 440
 QY 1292 GGGACAAACAGCCTAAAGATTATTTAGATCTGAGCTTCAAGTGGTGTATTTACAGTACTCA 1351
 Db 441 GlyIleThrSerIleuArgSerIleuSerIleuValAspAsnGlnIle----- 455
 QY 1352 AACTTCTTGGCTTTAGAACACTAGAACACTTGGATTTCCAGATTTCCAAATTTGAAACA 1411
 Db 456 -----GluLeuLeuArgAlaGlyAlaPheLeuHisThrProLeuThrGln 470
 QY 1412 ATGAGTGAATTTTCAATATTCATATCAGCAAGAACTCATTTAATCCTTGAATTTCTCAT 1471
 Db 471 -----LeuAspLeuSerSer 475
 QY 1472 ACTCACACAGAGTGTCTTCAATGAGCATCTTCAATGAGCTTG---TCCAGTCTCGAAGTC 1528

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Db      476 AsnProGlyLeuGluValAlaThrGlyAlaLeuGlyGlyLeuGluAlaSerLeuGluVal 495
QY      1529 TTGAAATGCGCTGGCAATTTCTTCCAG-----GAAACCTTCTTCAGATATCTTCACA 1582
Db      496 LeuAlaLeuGlnGlyAsnGlyLeuMetValLeuGlnValAlaSerLeuProCysPheIleCys 515
QY      1583 GAGCTGAGAAACTTGTACCTCTGACCTCTCTCAAGTCACTGGAGCAGTGTCTCCA 1642
Db      516 -----LeuIysArgLeuAsnLeuAlaGluAsnArgLeuSerHisLeu----- 529
QY      1643 ACAGCATTTAACTCACTCTCCACTTTCAGGTAATAATATGAGCCAACTTCTTT 1702
Db      530 ProAlaIlePheThrGlnAlaValSerLeuGluValLeuAspLeu--ArgAsnAsnSerPhe 548
QY      1703 TCATTGATACGTTTCTTCTTAAGTCTGAACCTCCCTCAGGTTCTTGATTACAGTCTC 1762
Db      549 SerLeu-----LeuProGlySerAlaMetGlyGlyLeuGlu----- 560
QY      1763 AATCACAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTAGTCTAGCTTTC 1822
Db      561 -----ThiSerLeuArgArg 565
QY      1823 TTAAATCTTACTGCAATGACTTGTCTTGTACTTGTGAACACGAGTTTCTGCAATGG 1882
Db      566 LeuTyrLeuGlnGlyAsnProLeuSerCys--CysGlyAsn-----GlyTyr 580
QY      1883 ATCAGAGACCGAG--AGGCGCTCTGTGTGAAGTTGAACGATGCA-----TGT 1930
Db      581 LeuAlaIleGlnLeuHisGlnGlyArgValAspValAspAlaThrGlnAspLeuIleCys 600
QY      1931 GCAACACCTTCAGATAAGCAGGGCGATGCTGTGCTGATTGAATATCACCC----- 1981
Db      601 ArgPheSerSerGlnGlnGlu-----ValSerLeuSerHisValArgProGlu 616
QY      1982 ---TGTCAATGAAT-----AAGACCATCATTTGTGTGTGCGTCTCACTGTGCTTGT 2032
Db      617 AspCysGlnIleGlyGlyLeuIysAsnIleAsnLeuIleIleLeuThrPheIleLeu 636
QY      2033 GTATCTGTTGTACGAGTTCTGTGCTTAAGTTCTATTTTCACTGATGCTTCTTGCTGGC 2092
Db      637 ValSerAlaIleLeu-----LeuThrThrLeuAlaAla 647
QY      2093 TGC 2095
Db      648 Cys 648
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Search completed: March 29, 2005, 17:36:27
Job time : 100.767 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus.n2p model

Run on: March 29, 2005, 11:51:33 ; Search time 50.705 Seconds
(without alignments)
18474.848 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaatactacctgcctcaaa.....caaaaaaaaaaaaaaa 4868

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 segs, 96215763 residues
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ n2p.model -DEV=x1h
-Q=cg21/USFTO_epool/US0396985/runat_28032005_155743_21159/app_query.fasta_1.85098
-DB=PIR_79 -QPM=Iaaban -SUFX=rxpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum2 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=psco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0396985 @CCN 1.1 1364 @runat_28032005_155743_21159 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -TREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: PIR_79:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	7.7	661	2	I56258 RPI05 - mouse
2	474	5.5	786	2	T08654 Toll protein-like
3	454	5.3	1097	2	A29943 Toll protein precu
4	433	5.0	1389	2	T13852 gene wheeler prote
5	421	4.9	1385	2	T13887 clr protein - fru1
6	396	4.6	1166	2	T15864 hypohetical prote
7	333.5	3.9	1134	1	A29944 hypohetical prote
8	328.5	3.8	1280	1	B34087 hypohetical prote
9	326.5	3.8	712	2	S23650 retrovirus-related
10	320.5	3.7	1275	2	T38588 reverse transcript
11	319.5	3.7	1275	2	B28096 line-1 protein ORF
12	319.5	3.7	1275	2	S65824 reverse transcript
13	316	3.7	605	2	JC5239 insulin-like growt
14	307.5	3.6	1531	2	T42218 slit-1 protein hom

15	305	3.6	853	2	T17461 disease resistance
16	303.5	3.5	907	2	JB0176 orphan G protein-c
17	303	3.5	605	2	A41915 insulin-like growt
18	302	3.5	603	2	T24315 hypothetical prote
19	299.5	3.5	662	2	S42799 garp precursor - h
20	297	3.5	994	2	H96510 probable disease r
21	296.5	3.5	845	2	T07039 Hcr9-0 protein - t
22	296	3.5	603	2	JC1282 insulin-like growt
23	295	3.4	907	2	JG0193 G protein-coupled
24	290	3.4	603	2	JC6128 insulin-like growt
25	290	3.4	855	2	T07015 Cf-4a protein - to
26	289.5	3.4	1112	2	T10504 disease resistance
27	289	3.4	855	2	T17460 disease resistance
28	285.5	3.3	1134	2	T04587 hypohetical prote
29	285	3.3	622	2	JC7973 synleutin - human
30	285	3.3	1091	2	A58532 glial cell membran
31	284	3.3	1259	4	GNH011 retrovirus-related
32	282.5	3.3	1027	2	B85089 receptor protein k
33	280	3.3	890	2	T00800 disease resistance
34	278.5	3.2	1019	2	C96519 probable disease r
35	276.5	3.2	768	2	T17462 disease resistance
36	276	3.2	983	2	G84524 probable disease r
37	275.5	3.2	1523	2	T13953 MEGF3 protein - ra
38	272	3.2	1469	2	B36665 slit protein 2 pre
39	272	3.2	1480	2	A36665 slit protein 1 pre
40	271	3.2	1143	2	T10636 hypohetical prote
41	270.5	3.2	1109	2	T19536 receptor-like prot
42	269.5	3.1	275	2	S21348 probable pol polyp
43	268	3.1	910	2	G84648 probable disease r
44	267	3.1	766	2	T01817 hypohetical prote
45	267	3.1	1784	2	C96615 hypohetical prote

ALIGNMENTS

RESULT 1
I56258
RPI05 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 09-Jul-2004
R:Accession: I56258
C:Accession: I56258
R:Make, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kinoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RPI05, a novel B cell surface molecule implicated in B cell activation, is a m
A:Reference number: I56258; MIMD:95204928; PMID:7897216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: UNIPROT:Q62192; GB:D37797; MIMD:9761711; PIDD:BA07043.1; PIDD:9761711

Alignment Scores:
Pred. No.: 4,51e-42
Score: 663.00
Percent Similarity: 45.68%
Best Local Similarity: 28.70%
Query Match: 7.73%
DB: 2
Length: 661
Matches: 196
Conservative: 116
Mismatch: 289
Indels: 82
Gaps: 16

US-09-396-985B-1 (1-4868) x I56258 (1-661)
QY 143 GGCATGGCTTCTCTCTCTGCG---GTGAGACCAAGAGCTGGAGCCCTGGCGAGG 199
DB 12 AAlaenPhelaulaerCyasgalatThrTherSerAspGlnyScyStleGluys 31
QY 200 GTTCTTAATATTAATATATGATGATGAGCTGATTTTACAAATCCCGACCACTC 259
DB 32 GluValAsnIyTherThyAsnCySgluAsnLeuGlyLeuAsnGlnIleProGlyThrLeu 51
QY 260 CCTTTTCAACCAAGAACTGAGCTGAGCTTTAATCCCTGAGGACATTAGGACACT 319
DB 52 ProAsnSerThrGluCyLeuGluPheserPheAsnValLeuProThrIleGlnAsnThr 71

QY	320	AGCTTTCTCAAGTTCCCGAAATCGAGGCTGGATTTATCCAGGTGGAAATCGAACA	379
Db	72	ThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIleTyrTrp	91
QY	380	ATTGAAGAGGAGGGCATATCAGAGCTGAAGCCACCTCTCACTTAATATGACAGGAAC	439
Db	92	IleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThrAlaAsn	111
QY	440	CCCATCTCAGAGTTTAGCCCTGGGAGACCTTTTCTGGACATATCAATTAACAGACCTGATG	499
Db	112	ProLeuIlePheMetAlaGluThrAlaLeuSerGluProValAlaLeuTyrHisIleLeuPhe	131
QY	500	GCTGGGAGACAAATCTAGCATCTCTGAGAAACTCCCATTTGGACATCTCAAAACTTGG	559
Db	132	PheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnIleSerThrLeu	151
QY	560	AAAGAAGCTTAATAGTGGCTCACAACTCTTATCCAACTCTTCAAAATTAACCGAGATTTATCT	619
Db	152	GluSerLeuTyrLeuGlySerAsnHisIleSerSerIleLysLeuProLysGlyPhePro	171
QY	620	AATCGACCAATCTAGACACTTTGGACCTTTCCAGCAACAAGATCTCAAGATTTATATGC	679
Db	172	Thr---GluLysLeuIleValLeuAspPheGlnAsnMetAlaIleHisTyrLeuSerLys	190
QY	680	ACAGACTTGGGGGTTCTACATCAAAATGCCCTCAATCTCTCTTTAGACTGTCCCTG	739
Db	191	GluAspMetSerSerLeuGlnGln----AlaThrAsnLeuSerLeuAsnLeuAsnGly	208
QY	740	AATCCTATGAACCTTATCCAAACCGAGTGCATTTAAAGAAATTAGCGTTCAATCAACTGACT	799
Db	209	AsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu--	227
QY	800	TTAAGAAATTAATTTTGATAGTTTAATTAATGAAGAAACTGTGATTAACAAGCTGGCTGCT	859
Db	228	-----AsnPheGlnGlyThrGlnAsnLeuValIlePheLysGlyLeuLysAsn	244
QY	860	TTAGAAGTTCATCGTTGGTCTGGGAGAAATTTGAAGATGAAGAACTTGAAAAGTTT	919
Db	245	SerThrIleGlnSerLeuTrpLeuGlyThrPheGluAspMetAspAsp---GluAspIle	263
QY	920	GACAAATCTGCTCTAGAGGGCTGGCGCAATTTGACATGAAGAAATCCGATTAGCATAC	979
Db	264	SerProAlaValPheGlnGlyLeuGlySerGluMetSerValGluSerIleAsnLeu--Gln	282
QY	980	TTAGACTACTACCTGATGATATTTATGACTTAATTTATGACAAATGTTTCTTCA	1039
Db	283	LysHisTyrPhePheAsnHisIleSerSerAsnThrPheHisCysPheSer-----	298
QY	1040	TTTTCCCTGGTGAGTGATGATATTGAAGGGTAAAAGACTTTTCTTATTAATTTGGATGG	1099
Db	299	-----GlyLeu	300
QY	1100	CAACATTTAGAAATTAGTAACTGTAAATTTTGACAGCTTCCACAC-----TTGAAATC	1153
Db	301	GlnGluLeuAspLeuThrAlaThrHisIleLeuSerGlnLeuProSerGlyLeuValGlyLeu	320
QY	1154	AAATCTCTCAAAAGCTTACTTCACTTCCCAACAAAGGTGGGAAT-----GCTTTTCA	1207
Db	321	SerThrLeuLysGlyLeuValLeuSerAlaAsnLysPheGlnAsnLeuCysGlnIleSer	340
QY	1208	GAAAGTTGATCTAACAGGCTTGAGTTT-----	1234
Db	341	AlaSerAsnPheProSerLeuThrHisIleLeuSerIleLysGlyAsnThrLysArgLeuGlu	360
QY	1235	-----CTAGATCTCAGTGAAGAAAT	1252
Db	361	LeuGlyThrGlyCysLeuGlnAsnLeuGlnAsnLeuArgGluLeuAspLeuSerHisAsp	380
QY	1253	GCGTGAAGTTCAAAAGGTTCGCTGCTCAAAAGTGATTTTGGGAGCAACAGCGCTTAAAGAT	1312
Db	381	AspIleGlnThrSerAspCysAsnLeuGlnLeuAlaGlnLeuSerHisIleuGlnSer	400
QY	1313	TTAGATCTGAGGCTTCAATGTTGTATTACCATGATTCGAAC--TTCTTGGGCTTTGAA	1369

[illegible]

Pred. No.: 1.06e-27 Length: 786
 Score: 474.00 Matches: 204
 Percent Similarity: 41.80% Conservative: 130
 Best Local Similarity: 25.53% Mismatches: 303
 Query Match: 5.53% Indels: 162
 DB: 2 Gaps: 32

US-09-396-985b-1 (1-4868) x T08664 (1-786)

QY 470 TCTGACCTACAGTTTACGAGCTGGCTGTGAGACAAATCTGACATCTCTAGAG 529
 DB 34 AenGlyLeuLleHisValProLysAspLeuSerGlnLysThrThrLleuAenLleSer 53
 QY 530 AACTCCCCATGGACATCTCAAACT-----TTGAAGAAG 565
 DB 54 GlnAsnTrpLleSerGlnLeuTrpThrSerAspLleuSerLeuSerLysLysGlyLe 73
 QY 566 CTTAATGTGGCTGACAACTTTATTCAAATCTTGAATTAAGTATTTTCTAATCTG 625
 DB 74 LeuLleLleSerHisAsnArgLleGlnTrpLeuAspLleSerValPheLysPheAsn-- 92
 QY 626 ACCAATCTAGAGACTTGGACCTTTCCAGCAAGAAATTCAAAGTATTTTGGACAGAC 685
 DB 93 GlnGlnLeuGlnLysLeuAspLeuSerHisAsnLysLeuValLysLleSerCys----- 110
 QY 686 TTGCGGGTTCTACATCAATGCCCCCTACTCATCTCTCT-----TTAGACCTGCTCCGTAAT 742
 DB 111 -----HisProthrValAsnLeuLysHisLleuAspLeuSerPheAsn 124
 QY 743 CCTATGAACTTATTC-----CAACGAGTGCATTTTAAAGAAATTAAGCTTCAT 790
 DB 125 AlaPheAspLalaLeuProLleCysLysGlnPheGlyAsnMetSerGlnLeuLysPheLeu 144
 QY 791 AAGCTACCTTAAAGAAATATTTGATAGTTTAAATGTAAGAAATCTGATTAAGCT 850
 DB 145 GlyLeuSer-----ThrThrHisLeuGlnLysSerSerValLlePro 158
 QY 851 CTGGCTGGTTTGAAGTCATCGTTGGTTGCTG-----GGAGAAATT 892
 DB 159 LLeLHisLleuAsnLleSerLysValLeuLeuValLeuGlnLysGlnLysLys 178
 QY 893 AGAAATGAAGAACTTGAAGAAATTTGACAAATCTGCTAGAGCGCTGTCACAAATTG 952
 DB 179 GlnAspProGlyLysLeuGlnAspPheAsnThrGlnSerLleHisLleValPheProthr 198
 QY 953 ACCATTGAAGAATTCGATTGACATTAAGTACTACTGCTGATGATTAATTAGCTTA 1012
 DB 199 AsnLysGln----- 201
 QY 1013 TTTAATGTTTGAACAATGTTTCTTCATTTCCCTGGTAGTGACATTAAGAGGTA 1072
 DB 202 PheHisPheLleuAspValSerValLysThrValAlaAsnLeuGlnLeuSerAsnLle 221
 QY 1073 AAAGACTTTCCTTAATATTCGATGACCAATTTAGAAATTAAGTATTAATTTGGA 1132
 DB 222 LysCysValLeuGlnLysPheLysCysSerTrpPheLeuSerLleLeuAlaLysLeuGln 241
 QY 1133 CAGTTTCCCACTTGAAGCTCAATCTCTCAAAAGGCTTACTTTCACCTTCAACAAA--- 1189
 DB 242 ThrAspProLysLeuSerSerLleThrLleuAsnAsnLleGlnLysThrTrpAsnSerPhe 261
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 DB 262 LLeArgLleLeuGlnLeuValTrpHisSerThrValTrpTrpLysSerSerLleSerAsnVal 281
 QY 1214 GATCTACCA---AGCCTTGAGTTTCTAGATCTGAGTAAGAAATGCTTGAAGTTCAAAAGT 1270
 DB 282 LysLeuGlnGlnLysLleuAspPheArgAspPheAspTrpSerGlyHisSerLleuLysAla 301
 QY 1271 TGTGTTTCTCA-----AGTAT----- 1288
 DB 302 LeuSerLleHisGlnValLysSerAspValPheGlyPheProGlnSerTrpLleTrpGln 321

QY 1289 ---TTTGGACAACAGCCTTAAG----- 1309
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 QY 1310 -----TATTAAGATCTGAGCTTCAATGGCTGTAAT----- 1339
 DB 342 LeuCysProSerLysLleSerProPheLHisLleuAspPheSerAsnLeuLeuThr 361
 QY 1340 ---ACCATGAGTTCAACATTTCTGGGCTTGAACAACCTGAACATCTGATTTCCAGCAT 1396
 DB 362 AspThrValPheGlnLysCysGlyHisLleuThrGlnLeuGlnLysThrLleuLleGlnMet 381
 QY 1397 TCCAAATTTGAACAATGATGATGAGTTTGA---GTAATCTTACCTGACAGAACTCAT 1453
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 QY 1454 TACCTGACATTTTCATATCTCACACAGAGTTGCTTTCAAT-----GGCATCTTC 1504
 DB 402 GlnLeuAspLleSer-----GlnAsnSerValSerTrpAspGlnLysGlyAspCys 419
 QY 1505 AATGGCTTGCCAGCTGCGAAGCTTGAAGAAATGGCGCAATCTTCCAGGAAACTTC 1564
 DB 420 SerTrpThrLysSerLeuSerLysLeuAsnMetSerSerHisLleuThrAspThrLle 439
 QY 1565 -----CTTCCAGATATCTTCAACAGAGCTGAGAACTTGACCTTCCGACCTCTCT 1615
 DB 440 PheArgCysLeuProPro-----ArgLleLysValLeuAspLeuHis 453
 QY 1616 CAGTGTCAACTGAGAGAGTTGCTCCACAGCATTTAAGTACTTCCAGTCTTCAAGTA 1675
 DB 454 SerAsnLysLleLysSerLle---ProLysGlnValValLysLeuGlnLalaGlnGln 472
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 QY 1724 AAGTGTCTGAACCTCCCTCAGGTTCTTGATTAAGCTCAATGACATTAATGACTTCCA 1783
 DB 490 SerSerLeuSerValLeuLleLleAspHisAsnSerValSerHisProSerAlaAspPhe 509
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 DB 510 PheGlnSerCysGlnLysMetArgSer-----LleLysAlaGlyAspAsnPro 525
 QY 1844 TTTGCTTGTATCTTGAACAACAGATTTCTGCAATGATGATCAAGACAGACGACCTC 1903
 DB 526 PheGlnCysThrCysGlnLeuGlnLysLys-----ValLysAsnLleAspGlnVal 542
 QY 1904 TTGCTGGAAGTT-----GAACGAATGAATGTGCAACACCTTCAGATTAAG 1948
 DB 543 SerSerGlnValLeuGlnLysLysTrpProAspSerTrpLysCysAspTrpProGlnSerTrp 562
 QY 1949 CAGGCG-----ATGCTGTGCTGATTTGAATATCACTGCTGAC 1987
 DB 563 ArgGlyThrLeuLeuLysAspPheHisMetSerGlnLeuSerCysAsnLleThrLleuLeu 582
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 DB 583 LLeValThrLleValAlaThrMetLeuValLleAlaValThrValThrSerLeuCysLle 602
 QY 2048 GTTCTGTCTAATGAATTTCTAATTTTCACTGATGCTTCTGCTGCTGCTGCTGCTGCT 2107
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 QY 2108 AGAGTGAAACATC-----TATGATGCTTTGTT 2137
 DB 622 ArgAlaArgAsnLleProLeuGlnLysLysLysLysLysLysLysLysLysLysLysLys 641
 QY 2138 ATCTACTCAGCAGATGAGACTGGGTGAAGAAATGAGCTGTAAGAAATTTGA--- 2194
 DB 642 SerTrpSerGlyHisAspSerPheTrpValLysAsnGlnLeuLeuProAsnLeuGlnLys 661
 QY 2195 GAAGGGGTGCTTCATTTCAAGCTGTGCTTCACTACAGAGACTTATTCCTGGGTGTGGCC 2254

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Db      662  GLUGlyMet-----GlnIleCybLeuHISGLuabgAsnPhenValProGlyLysSer 678
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Db      679  ILeValGLuAsnIleIle---ThrcyVleGLuLysSerTyRlysSerIlePhenVal 697
QY      2315  TCCCAACACTTCATCCAGAGCCCGTGTATCTTCATTAATATGATGATGCTGACACTGG 2374
Db      698  SerProAsnPhenValGlnSerGluTyrPCyshiTyGluLeuTyRheAlaHisAsn 717
QY      2375  CAGTTTCTGAGCAGCTGCTGTGATCATCTTCATTCCTTCGAGAGGTC---GAGAG 2431
Db      718  LeuPhenIleGluLysSerAsnSerLeuIleLeuIleLeuLeuGluProIleProGlnTy 737
QY      2432  ACCCTGCTCAGGAGCAGGAGCTGTACCCGCTTCACGACGAAACATTACCTGAG 2491
Db      738  SerIleProSerSerTyRHisLysLeuLysSerLeuMetAlaArgTrpThrTyRLeuGlu 757
QY      2492  TGGGAGGACAGTGTCTCTGGGCGCACATCTTCGAGACGACTCGAAGAAAGCCCTG 2548
Db      758  TrpProLysGluLysSerLysArgGlyLeuPhenTrpAlaAsnLeuArgAlaIle 776

RESULT 3
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C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, an
A:Reference number: A29943; PMID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M1969; GB:J02682; MID:G158640; PIDN:AAA28941.1;
C:Gene: FLYBase:TL
A:Cross-references: FLYBase:FBgn003717
C:Keywords: Transmembrane protein
P:1-17/Domain: signal sequence #status predicted <SIG>
P:18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 3.78e-26 Length: 1097
Score: 454.00 Matches: 219
Percent Similarity: 38.97% Conservative: 129
Best Local Similarity: 24.52% Mismatches: 291
Query Match: 5.29% Indels: 254
DB: Gaps: 43

US-09-396-985b-1 (1-4868) x A29943 (1-1097)
QY      206  AATATTACTTATCATGATGAGCTGATTTCTACAAA--ATCCCGCAACCTTCCC 262
Db      270  AsnValThrAspIleAsnLeuSerAlaAsnLeuPhenArgSerLeuProGlnGlyLeuPhe 289
QY      263  TTCTCAACCAAGAACTGAC-----CTGACGTTTAAAT-----CCCTGAGGCAT 307
Db      290  AspHisAsnLysHisIleuAsnGluValArgLeuMetAsnAsnArgValProLeuAlaThr 309
QY      308  TTAGGAGCATATGCTTCTTCAGTTTCCAGAGCTGAGAGGCTGAGATTATCCAGGTG 367
Db      310  LeuProSerArgLeuPhenAlaAsnGlnProGluLeuGlnIleLeuArgLeu---ArgAla 328
QY      368  GAAATCCAGCAATTTGAAGATGGGGCATATCAGAGCTTAAGCCACTCTACCTTATA 427
Db      329  GluLeuGlnSerLeuProGlyAspLeuPhenGluHisSerThrGlnIleThrAsnIleSer 348
QY      428  TTGACAGGAAACCCCATCCAGAGTTTACCCCTGGAGCCCTTTCTGAGATATCAAGTTTA 487
Db      349  LeuGlyAspAsnLeuLeuLysThrLeuProAlaThrLeuLeuGlnHisGlnValAsnLeu 368

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QY      488  CAGAGCTGTGCTGTGAGACAAATCTAGCATCTTAGAGAACTTCCCATTTGACAT 547
Db      369  LeuSerIleAspLeuSerAsnAsnArgLeuThrHisIleuProAspSerLeuPhenAlaHis 388
QY      548  CTCMAAATCTTGAAGAACTTAATGTGGCTCAACATCTTATCCAACTTTCAATTAACCT 607
Db      389  ThrThrAsnLeuThrAspLeuArgLeuGluIuAspAsnLeuLeuThrGlyLysSer---Gly 407
QY      608  GAGTATTTTCTTAATGTACCAATCTTAGAGCACTTGAGACCTTTCACGACAAAGATTCA 667
Db      408  AspIlePheSerAsnLeuGlyAsnLeuValThrLeuValMetSerArgAsnArgLeuArg 427
QY      668  AGTAT-----TATTCACAGACTTGGGGTTTGCAT----- 700
Db      428  ThrIleAspSerArgAlaPheValSerThrAsnGlyLeuArgHisIleuHisIleuAspHis 447
QY      701  -----CAAAATGCCCTTACTCAATCTCTCTTAAAGCTGTGCTGCTGAAT--- 742
Db      448  AsnAspIleAspLeuGlnGlnProLeuLeuAspIleMetLeuGlnThrGlnIleAsnSer 467
QY      743  CCTATGAACTTATCCACACAGTGATTTAAAGAAATTAAGCTTCATATAGCTGATT 802
Db      468  ProPheGlyTrpMetHis-----GlyLeuLeuThrLeuAsnLeu 480
QY      803  AGAAATPAAATTTGATGATTAAATGTAATGAAAACTTGATTCAGAGCTGTGCTGCTT 862
Db      481  ArgAsnAsn-----SerIleIle----- 486
QY      863  GAAATCCATCGTTGTGCTGTGAGAAATTTAGAAATGAAGAAACTTGAAGAAATTTGAC 922
Db      487  -----PheValTyRAsnAspTrpLysAsn----- 494
QY      923  AATATGCTTAGAGGCGCTGTGCAATTTGACATTTGAAGAAATTCGATTAAGCATCTTA 982
Db      495  -----ThrcMetLeuGlnLeuArgGluLeuAspLeuSerTyR--- 506
QY      983  GACTATACCTGATGATATTAATTCATTAATTTGACAAATGTTTCTTCATTT 1042
Db      507  -----AsnAsnIleSerSerLeu 512
QY      1043  TCCCTG-----GTGAGTGTGACTATTTGA 1066
Db      513  GlyTyRGLuAspLeuAlaPheLeuSerGlnAsnArgLeuHisIleValAsnMetThrHisAsn 532
QY      1067  AGGCTAAAGACTTTCT-----TATATTTCCGA 1096
Db      533  LysIleArgArgIleAlaLeuProGluAspValHisIleuGlyGluGlyTyRAsnAsnAsn 552
QY      1097  TGGCAACATTTGAATTA-----GTTAACTGTAAATTTTGACAGATT 1138
Db      553  LeuValHisValAspLeuAsnAsnAsnProLeuValCysAspCysThrIleLeuTrpPhe 572
QY      1139  CCCCACTG-----AAACTCAAACT 1159
Db      573  IleGlnLeuValArgGlyValHisLysProGlnTyRSerArgGlnPheLysLeuArgTrp 592
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QY      1217  -----CTACCAAGCCTTGAATTTTCTAGATCTCAGTGAATAGGCTTGAAGTTTC 1264
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QY      1265  AAAGTTGC---TGTTCTCAAAATGATTTTGGACCAACCAAGCTTAAGTATTAAGTCTG 1321
Db      633  ArgGlyCysAsnCyHisIleValArgThrTyRAsp-----LysAlaLeuValIle 648
QY      1322  AGCTTCAATGGTGTATTATCATGATTTCAAACTTTTGGGCTTGAACAACAATGAACAT 1381
Db      649  AsnCyHisIle-----SerGlyAsnLeuThrHisIleValProArgLeuProAsn 663

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QY 1382 CTGATTTCCAGCATTCCTCAATTGAAACAATGAGTGGATTTTCATGATTTCTATCATCTC 1441
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 QY 1442 AGAAACCTCATTTATCTTGACATTTCTCATATCATCACACAGAGTGGCTTTCATGAGCATC 1501
 Db 676 GlnAsnAsnThrLeuLeuArgLeuProSerAlaAsnThr----- 688
 QY 1502 TTCATAGGCTTTGTCAGCTTCGAAAGCTTTGAAAACTTGCAATTTCTTTCCAGAAAAAC 1561
 Db 689 ---ProGlyLysArgLysSerValThrSerLeuHisLeuAlaGlyAsn----- 702
 QY 1562 TTCCTTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTCTCGACCTCTCTCAGTGT 1621
 Db 703 -----AsnLeuThrSerLeuAspValAspGlnLeu 712
 QY 1622 CAACCTGAGCAGATGTGTCCAAAGCATTTAACTCACTCTCCAGCTTTCAGGATCTAAAT 1681
 Db 713 -----ProThr-----Asn 715
 QY 1682 ATGAGCCACAACAACCTTTTCAATGATACGTTCTTATAAGTGTGAACTCCCTC 1741
 Db 716 LeuThrHis----- 718
 QY 1742 CAGGTTCTTGATTAACATCTCAATACATATGATCTTCAAAAAACAGAACTACAGCAT 1801
 Db 719 ---LeuAspLysSerTrpAsnHisLeu-----GlnMetLeuAsn--- 730
 QY 1802 TTTCCAAAGTACTAGCTTTCTTAAAT-----CTTACT 1834
 Db 731 ---AlaThrValLeuGlyPheLeuAsnArgThrMetLysTrpArgSerValLysLeuSer 749
 QY 1835 CAGAAATGACTTTGCTGTACTGTGAAACACACAGATTTCCGCAATGATCAAGACCAAG 1894
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 QY 1895 AGGACAGCTCTTGATGGAAGTTGAAACGAATGGAATGTGCAACACCTTCAGATTAAGCAGGC 1954
 Db 770 PheGlnArgLysLeuGlyAspArgAsnGlnMetMetCysValAsnAlaGlnMetProThrArg 789
 QY 1955 ATGCTCTGTGCTGATTTGAATATCACTGTCAATGATTAAGACATC---ATTGGTGTG 2011
 Db 790 MetValGlnLeuSerThrAsnAspLysCysProAlaGlnLysGlyValPheIleAlaLeu 809
 QY 2012 TCGGATC-----CTCAGTGTGCTGTAGTATCTGTGTAGACGTTCTGCTGTCTTAAG 2062
 Db 810 AlaValValIleAlaLeuThrGlyLeuLeuAlaGlyPheThrAlaAlaLeuLysTrpLys 829
 QY 2063 TTC-----TATTTTCACCTGATGCTTCTTGCTGGCTGCAT 2098
 Db 830 PheGlnThrGlnLysLysIleTrpLeuLysAlaHisAsnLeuLeu----- 845
 QY 2099 AAGTATGTAGAGGTGAAAAATC-----TATGATGCTTTTGTATCTAC 2143
 Db 846 TrpPheValThrGlnGlnAspLeuAspLysAspLysPheAspAlaPheIleSerLys 865
 QY 2144 TCAGAGCAGATGAGAGCTGGGTAAAGATGACCTGATTAAGAATTGAAGAAAGGGGTG 2203
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 QY 2264 AACATCATCATAGAGGTTTCCATAAAGCCGAAAGGTGATTTGTGTGTGCTCCAGCAC 2323
 Db 906 AsnIleMet---ArgSerValAlaAspSerArgArgThrIleLeuValLeuSerGlnAsn 924
 QY 2324 TTGATCCAGAGCGCGGTGTATCTTTGATATGAGATTTGCTGAGACCTGCGAGTTTCTG 2383
 Db 925 PheIleLysSerGlnLysTrpAlaArgLeuGlnPheArgAlaAlaHisValArgSerAlaLeuAsn 944
 QY 2384 AGCAGTGTGTGCTGTATCATCTTCAATGTC-----CTGCAAGAAAGTGAGAAAGACC 2434

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 QY 2495 GAGGACAGTCTCTGGGCGGCACATCTTCTGGAGACGACTCAGAAAGCCCTGCTGGAT 2554
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 RESULT 4
 T13852
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 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 09-Jul-2004
 C:Accession: T13852
 R:Bidom, E.; Kooyer, S.; D'aveylyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Belien, H.
 Development 120, 885-899, 1994
 A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simi
 A:Reference number: Z17796; PMID:95324375; PMID:7600965
 A:Accession: T13852
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1389 <ELD>
 A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:G415682; PID:G1019104; PIDN:AAA792
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 Pred. No.: 1,57e-24 Length: 1389
 Score: 433.00 Matches: 217
 Percent Similarity: 39.93% Conservative: 138
 Best Local Similarity: 24.41% Mismatches: 356
 Query Match: 5.05% Indels: 178
 DB: 2 Gaps: 34
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 QY 575 GCTCACAATCTTAATCCAACTTTCAATTAATTAATTAATTTCTTAATTTGACCAATCTA 634
 Db 437 SerSerAsn-----GlnLeuThrGlnValProGlnAlaValAlaGlnAspLeuSerMetLeu 454
 QY 635 GAGCACTTGGACCTTTTCCAGCAACAAGATTCAAAAGATTATTTATTTGACAGACTTGGGGTT 694
 Db 455 LysThrLeuAspLeuGlyGlnLysGlnIleSerGlnPheLysAsnAsnThrPheArgAsn 474
 QY 695 CTACATCAAAATGCCCTACTCAATCTC----- 721

Db 475 Leu^{en}glnLeu^{thr}glnLeu^{arg}Leu^{leu}Leu^{asn}Arg^{ile}glnVal^{leu}Thr^{Val}Gly 494
QY 722 -----TCCTTGAACCTGTCCCTGAATCCCTATGAACTTT 754
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QY 812 TTGTATACGTTAAATGTAATGAAACCTGTATTAAGGTCGTGGCTGGTTTGAAGTCAT 871
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QY 1208 -----GAAATTGATCTA 1219
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QY 1220 CCAACCTTGAGTTCTA-----GAT 1240
Db 708 Gln^{Asn}ile^{ile}Gln^{Cys}Leu^{Met}Pro^{His}Asp^{Arg}Ser^{Ala}Pro^{Leu}Arg^{Pro}Leu^{Ala}Asp^{ser} 727
QY 1241 CTCAGTAGAAATGGCTTGAGTTGCAA-----GGTTGC 1273
Db 728 Leu^{Ser}Ala^{Asp}Asp^{Phe}Val^{Cys}Ala^{Ser}Tyr^{Leu}Ser^{His}Val^{Ser}Pro^{Thr}Cys^{His}Cys^{Val} 747
QY 1274 TGTTCCTCAAGTATTTGGGCAACAACAGCTTAAGATTTGATCTGAGCTTCATAGT 1333
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QY 1334 GTTATTAACATGATTCAAACTTCTTG-----GGCTTAGAACAACTAGAACATCTGCAT 1387
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QY 1388 TTCAGACATTCCAATTTGAAACAAATGAGTGAAGTTTCAGATTCCTATCACTGCAAAAC 1447
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QY 1448 CTCATTTACCTTGACATTTCTCATCTACACCAAGAGTGGCTTTCATAGGATCTTCAT 1507
Db 804 Met^{Pro}Gln^{ile}Gln^{Val}Ala^{gly}His^{leu}Thr^{Arg}Val^{Arg}Asn^{Leu}Ala^{Arg}ile^{Tyr}Leu^{Arg} 823
QY 1508 GGCCTTGTCACATCTCGAAAGCTTGAATAATGCTGGCAATCTTTCACAGAAAATCTCTT 1567

Db	Asn1AserLeuMetThrLeuGlnAenGlySer-----	835
Qy	1568 CCAATATCTTCACAGAGCTGAGAACTTAACTCTTGGACCTCTCTCACTGTCAACTG	1627
Db	836 -----Leu1AgiLeuVal1AsnLeuAArgVal1Ileu1Val1eue1uAen1uVal1eu	852
Qy	1628 GAGCAGTTCCTCCAAAGCATTTAACTCACTCCAGTCTCCAGTCTCCAGTCACTAAATATAGC	1687
Db	853 Thr1ALeuGluGlyThrGluPheArgSerLeuGlyLeuLeuArgGlyLeuGlyTyrLeuHis	872
Qy	1688 CACAACAACTCTTTTATGGATACCTTTCTTATAGTGTCTGAACCTCCCTCCAGGT	1747
Db	873 AsnMetLeuThrHisIleSerAenAlaThrPheGluProLeuValSerLeuGluVal	892
Qy	1748 CTGATTAACAGTCACTCAATCAATATGACTTCCAAAACAGAACTACAGCATTTTCCA	1807
Db	893 Leu1ArgLeuAraAenAenArgLeuSerSerLeuProHisLeuGlnTyrArgHis-----	910
Qy	1808 AGTAGTCACTGTTCTTAACTTAACTCAAGATTAACCTTGGCTCTGACTTGTGAACAC---	1864
Db	911 ---SerLeuGlnGlyLeuThrLeuGlyAArgAenAlaTyrSerCysArgCysGlnGlyLeu	929
Qy	1865 CAGAGTTTCTCCATGAGATCAAGACACAGAGGACAGCTCTTGCGTGAAGTTGAACGATG	1924
Db	930 ArgGluLeuAlaGlnPheValSerAraAenAlaMetValValAArgAraPheHisAraPhe	949
Qy	1925 GAATGTGCACACCTTCAGATTAAGCAGGACCTGCTGCTG-----	1966
Db	950 TyrCysLeuAraPhe1Agi1Ile1AraArg1uLeuGluLeu1IleGlyAenLeuAlaAenGly	969
Qy	1967 -----AGTTGAATATCACTCTCAGATGAATTAAG	1996
Db	970 ProAraPysSerAraPheLeuAraPheAlaSerAlaSerAenIleSerSerGlnAraPheLeu	989
Qy	1997 ACC---ATCATTTGCT-----GTGCGCGCTCACTGTCCTTGTAGTA	2035
Db	990 AlaGlyAla1IleGlyCysProCysTyrProAlaValLeuValLeu1IlePheLeuValVal	1009
Qy	2036 TCTGTGTGACAGTTCGTGCTATTAAGTCTTATTTTCACTGATGCTTTGCTGAGCTGC	2095
Db	1010 ValLeu1Ile1Val1PheVal1PheAraGluSerVal1ArgMetTyrLeuPheAla-----	1027
Qy	2096 ATTAAGTATGCT-----AGAGGTAAAC-----ATCTATGAT	2128
Db	1028 ---His1TyrGlyValAraGlyValCysGluProAraPheGlnAraPhe1Agi1LysLeuTyrAraP	1046
Qy	2129 GCGTTTGTATCTACTCAAGCCAGAGGACGAGCGGAGATGAGATGAGCTGTAAAGAT	2188
Db	1047 Ala1Ile1IleuHis1SerGlnLysAraPyrGluPheVal1CysAraAen1IleAla1Glu	1066
Qy	2189 TTAGAAGAGGGGGCCCTCAATTCAGTCTGCCCTTCACTACAGACATTTATCCCGGT	2248
Db	1067 LeuGluHis1GlyAraProProPheAraGluLeuCys1IleGlnGlnAraGaaP---LeuProPro	1085
Qy	2249 GTGGCCATTCGTGCCAATCATCATCAAGAGGTTCCATAAAGCCGAAAGGTATGTT	2308
Db	1086 Gln1AsaSerHisLeuGlnLeuVal---GlnGly1AaAraGlnAsaSerAArgLys1Ile1Leu	1104
Qy	2309 GTGGTGTCCCAAGCTTCATCCAGACGCCGGGTGTACTTTGAATTAAGATTGCTCAG	2368
Db	1105 ValLeuThrAraGlnLeuLeuAlaThrGluTyrAenAraGly1GluPheAraGlnAla---	1123
Qy	2369 ACCTGGCAGTTTCTGACAGAGTCCGTGCTGTATCACTTTCATTCCTGCGACAGAG---	2422
Db	1124 -----PheHis1GluSerLeuAraGlyLeu-----AlaGlnLysLeuVal	1136
Qy	2423 ---GTGAAGAAGACCTGCTCAGGACAGACAGGTGAGCTGTACCGCTTCTCAGAGAAAC	2479
Db	1137 1Ile1IleGluGluThrSerValSerAlaGlu1AgiLysAraValAla1AgiLeuSer-----	1154
Qy	2480 ACTTAACTTCAGAGTGGAGAGACAGTGTCTGGGGCGGCACATC-----	2521
Db	1155 ProTyrLeuLys-----SerVal1ProSerAraAraGluLeuThrCysAraPArgTyr	1171

Oy	2522	TTCTGAGACGACTCAGAAAAAGCCCTG	2548
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Db	1172	PhetTpgIuylsleuArGTYrAlaile	1180

RESULT 5

c1r protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: F13887
 R:Chiang, C.; Beachy, P. A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
 A:Reference number: Z17805; MUID:95151581; PMID:7848870
 A:Accession: F13887
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: UNIPROT:Q24591, EMBL:S76155, NID:g913247, PID:g913248, PIDN:AA83383
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0004364
 A:Note: c1r

Alignment Scores:	
Pred. No.:	1,286-23
Score:	421.00
Percent Similarity:	35.60%
Best Local Similarity:	23.96%
Query Match:	4.91%
DB:	2
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	length: 1385
	Matches: 213
	Conservative: 139
	Mismatches: 359
	Indels: 178
	Gaps: 33

Qy	27	CTGAGCTGAGCTTTTATCCCGTGAAGGATTTAGGACCTATTAAGCTCTTCAGTTTCCA	337
Db	338	LeuAsnSerAsnAsnAlaLeuThrArgIleGlySerLysThrPheLysGluLeuTyr	357
Qy	338	GAATCGAGGTGCTGATTTATTCAGAGTGTGAATTCAGACAATTTGAAGATGGGCGATAT	397
Db	358	PheLeuGlnIleLeuAspMetArgAsnAsnSerIleGlyHisIleGluGluGlyAlaPhe	377
Qy	398	CAGAGCCCTAAGCCACCTCTCTAATTATATGACAGGAAACCCCATCTGACAGATTTAGCC	457
Db	378	LeuProLeuTyrAsnLeuHisThrLeuAsnLeuAlaGluAsnArgLeuHisThrLeuAsp	397
Qy	458	CTGGAGACCTTTTCTGAGATATACAAATTTCAGAGAGCTGTGGCTGTGGAGACAATCTA	517
Db	398	AsnArgIlePheAsnAlaLeuLeuValLeuThrLysLeu---ThrLeuAsnAsnAlaLeu	416
Qy	518	GCATCTCTA---GAGAACTTCCCAATGGACATCTCAAAACTTTGAAAGAACTTAATGTG	574
Db	417	ValSerIleValGlnSerGlnAlaPheArgAsnCybSerAspLeuLysGluLeuAspLeu	436
Qy	575	GCTCAACATCTTAATCCAAATCTTTCAAAATTACCTGAATATTTTCTAATTCGACCAATCTA	634
Db	437	SerSerAsn-----GlnLeuThrGluValProGluAlaIleGlnAspLeuSerMetLeu	454
Qy	635	GAGACCTTGGACCTTTCCAGACAACAAGATTCAAAATATTATTGACACAGACTTCGGGCTT	694
Db	455	LysThrLeuAspLeuLysGluAsnGlnIleSerGluPheLysValAsnAsnThrPheArgAsn	474
Qy	695	CTCATCAATGAGCCCTCACTCAATGTC-	721
Db	475	LeuAsnGlnLeuThrGlyLeuLeuArgLeuIleAspAsnArgIleGlyAsnIleThrValGly	494
Qy	722	-----TCTTTAGACTGTCCCTGAATTCCTAATGACTTT	754
Db	495	MetPheGlnAspLeuProArgLeuSerValLeuAsnLeuAlaLysAsnArgIleGlnSer	514
Qy	755	ATCCAAACCGGTGCAATT---AAAGAAATTAGCGCTTCAAGCTGCACTTTAAGAAATAT	811
Db	515	IleGluArgGlyAlaPheAspLysAsnThrGluIleGluAlaIleLeuGluLeuAspLys	534

Qy	812	TTTGAATGATTAAATGTAATGAAAACCTGTAATTCAGAGTCGGCTGGTTTGAAGTCCAT	871
Db	535	Phe-----LeuThrAspIleasnGlyIlePheAlaThrLeuAlaSer	548
Qy	872	CGTTTGGCTCGGGAGATTAGAAATGAA-----	901
Db	549	LeuLeuTripleuAsnLeuSerGluAsnHisLeuValTrpPheAspTrpAlaPheIlePro	568
Qy	902	GGAACCTTGAAAAAGTTTGAC-----AAATCTGCTCTAGAGGGCTGTGCAATTTC--	952
Db	569	SerAsnLeuLeuSerTrpLeuAspIleHisGlyAsnTrpIleGluAlaLeuGlyAsnTrpTyr	588
Qy	953	---ACCAATTGAAGAATTCGCAATTGACACTTACTTACACTTAATCTCCGATGATTAATTAGAC	1009
Db	589	LyseLeuGlnGluGluTrpLeuArgValThrThrLeuAspAlaSerHisAsnArgIleThrGlu	608
Qy	1010	TTATTTAATTGTTTGACAAATGTTTCTCAATTTTCCCTGGGAGCTGGACATTAAGAAAG	1069
Db	609	Ile---GlyAlaMetSerValProAsnSerIleGluLeuLeuPheIleAsnAsnIle	627
Qy	1070	GTAAAGAATTTTCTTAATAT-----TTGCGATGGCAACATTGAAATTAGTAATCTGT	1123
Db	628	IleGlyGlnIleGlnAlaAsnThrPheValAspTrpThrArgGluAlaArgValAspLeu	647
Qy	1124	AAATTGGACAGTTTCCCACTGAAATCTAAATCTCTCAAAAGGCTTACTTCACTTCC	1183
Db	648	TyrAlaAsnValLeuSerTrpIleSerLeuAsnAlaArgValAlaProvalSerAla	667
Qy	1184	AACAA-----GGTGGAAATGCTTTTCA-----	1207
Db	668	GluIysProValProGluPheTrpGluGlyGlyAsnProPheGluCysAspCysSerMet	687
Qy	1208	-----GAAGTGAATCTTA	1219
Db	688	GluTrpLeuGlnArgIleAsnAsnLeuThrThrArgGlnHisProHisValValAspLeu	707
Qy	1220	CCAAAGCTTGAGTTCTA-----GAT	1240
Db	708	GlyAsnIleGluCysLeuMetProHisSerArgSerAlaProLeuArgProLeuAlaSer	727
Qy	1241	CTCAATGGAATGGCTTGAAGTTCAAA-----GGTTGC	1273
Db	728	LeuSerAlaSerAspPheValCysLeuTrpGluSerHisCysProProThrCysHisCys	747
Qy	1274	TGTTTCCAAAGTGATTTTGGGACAAACAGGCTTAAAGATTAGACTGAGCTTCAATGGT	1333
Db	748	CysGluTrpTrpGluGlnCysGluCysGluValIleLeuSerProGluAsnCysSerCysPheHis	767
Qy	1334	GTTATTACATGAGTTCAACTTCTTG-----GGCTTGAACAACATGAACATCTGAT	1387
Db	768	AspAlaThrTrpAlaThrAsnIleValAspCysGlyArgGlnSerLeuAlaIleLeu---	786
Qy	1388	TTCCAGCATTCCAATTGAAACAAATGAGTGGATTTCAGTAATTCCTATGATCAACAAAC	1447
Db	787	-----ProAsnArgIleProGlnAspValSerAspLeuTrpLeuAspGluAsnAsn	803
Qy	1448	CTCAATTACCTTCGATCTCTCAATCTCAATCAACAGAGATTCCTTCATGCGATCTTCAT	1507
Db	804	MetSerProGluLeuGluValGlyHisLeuThrGlyArgTrpAsnLeuArgAlaLeuTrpLeu	823
Qy	1508	GGCTTGTCCAGTCTCCGAAGCTTGAATAGGCTGGCAATCTTTCCAGAAAATCTTCTT	1567
Db	824	AsnAlaSerHisMetThrLeuGlnAsnGlySer-----	835
Qy	1568	CCAGATATCTTCAACAGAGCTGAGAAATGATGACCTTCTGGACCTCTCTCACTGTCAAATG	1627
Db	836	-----LeuAlaGlnLeuValAsnLeuArgValLeuHisTrpLeuGluAsnAsnLeuLeu	852
Qy	1628	GAGCAGTGTCTCCACAGACATTTAACTACTCTCCAGTCTTACAGATCTAAATATAGAC	1687
Db	853	ThrAlaLeuGlnGlyThrGluPheArgSerLeuGlyLeuLeuArgGlyLeuTrpLeuHis	872

[illegible]

Chaptelin precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: photoreceptor cell-specific membrane protein
C:Species: *Drosophila melanogaster*
C:Date: 15-Dec-1988 #sequence revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29944; #accession A29944; A21123
R:Reinke, R.; Krantzh, D.E.; Yen, D.; Zipursky, S.L.
Cell 52. 291-301, 1988
A:Title: Chaptelin, a cell surface glycoprotein required for *Drosophila* photoreceptor ce
A:Reference number: A29944; MUID:68135762; PMID:3124963
A:Accession: A29944
A:Molecule type: DNA
A:Residues: 1-1134 <REI>
A:Cross-references: UNIPROT:P1024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M190
R:Zipursky, S.L.; Venkatesh, T.R.; Teplov, D.B.; Benzer, S.
Cell 36. 15-26, 1984
A:Title: Neuronal development in the *Drosophila* retina: monoclonal antibodies as molecu
A:Reference number: A21123; MUID:84106810; PMID:6420071
A:Accession: A21123
A:Molecule type: Protein
A:Residues: 31-43; 'HX', '46-49', 'H' <ZIP>
C:Genetics:
A:Gene: FlyBase:cbp
A:Cross-references: FlyBase:FBgn0000313
A:Intons: 1/3 80/3; 316/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C:Superfamily: Chaptelin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cell adhesion; glycoprotein; membrane protein
F:1-29/Domain: signal sequence #status predicted <IG>
F:30-1134/Product: chaptelin #status predicted <MUT>
F:80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:303-335/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
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F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
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F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
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F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
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F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
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F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
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F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
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F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

QY 1901 CTCCTGGTGAAGTTGACGAATGTCACACCTTCAGATAAGAG----- 1951
 DB 984 ---LeuthraenvalProleuMetThrGlnAlaLeuProHisLeuArgGluMetLeu 1002
 QY 1952 ---GGCATGCTGTGCTGAGATTGCAATATCACTCTGACATGTAATGAACCATTCATTGCT 2008
 DB 1003 SerGlyAsnProIleThrSerLeuAsn-----AsnAsnSerPheAspGly 1017
 QY 2009 GTGCGGTC---CTCAGTGGCTTGTATGCTTGTGTAGACAGTCTGCTATTAAGTTC 2065
 DB 1018 ValAsnLeuAspLeuGluMetLeuAspIleSerAsnPheArgLeuHisIleTyPheGluTyR 1037
 QY 2066 TATTTTCACTGATGCTTCTGTGCTGCTGCATA 2098
 DB 1038 -----GlyCysLeu 1040

RESULT 8
 B34087
 hypothetical protein (L1H 3' region) - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
 C/Accession: B34087
 R/Scott, A.F.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J.
 Genomics 1, 113-125, 1987
 A/Title: Origin of the human L1 elements: proposed progenitor genes deduced from a cons
 A/Reference number: A34087; MUID:88085185; PMID:3692483
 A/Accession: B34087
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-1280 <SC0>
 A/Cross-references: UNIPROT:Q9Y5K0
 C/Superfamily: pol polyprotein

Alignment Scores:
 Pred. No.: 1,33e-16 Length: 1280
 Score: 328.50 Matches: 95
 Percent Similarity: 53.95% Conservative: 28
 Best Local Similarity: 41.67% Mismatches: 70
 Query Match: 3.83% Indels: 36
 DB: 2 Gaps: 4

US-09-396-985B-1 (1-4868) x B34087 (1-1280)
 QY 3817 CATTTGGGAAGAGTGATGTTATTCATTGAGAAAACAATGTCGTGGAATTAATGGGGTT 3876
 DB 1084 HisPheSerLysGluAspIleTyzAlaAlaAsnLysHisMet----- 1097
 QY 3877 CTTATTAAGAAGGTTCCAGAAAAGAATGTTCAATTCAGCTTCTTCAGAAACAGAAACA 3936
 DB 1098 -----LysLysCysSerSerSerLeu----- 1104
 QY 3937 TTCAGGAAAAGACATCAATCAGATGTCATCAGGGAATGAATAATTAACCAATGAGACA 3996
 DB 1105 -----AlaIleArgGluMetGlnIleLysThrThrMetArg 1116
 QY 3997 TATACCTTATACAGGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
 DB 1117 TyrHisLeuThrProValAlaArgMetAlaIleIleLysLysSerGlyAsnAsn-ArgCysTr 1136
 QY 4045 TCAAGATATAGAAATGGAATTCCTTCTTCATCTGTCGAGGGAATGGAATAATGGTGTGA 4104
 DB 1136 pArgGlyCysGlyGlnIleGlyThrLeuLeuHisCysTrpTrpAspCysLysLeuValG 1156
 QY 4105 GCCGTTATGAAGAAACAGTACGAGGCTTCTCAAAA--TTAAATAATGAATGCTATATGA 4163
 DB 1156 nProLeuTrpLysThrValIleTrpArgPheLeuLysAspLeuGluLeuGlnIleProPheAs 1176
 QY 4164 TCAGCAATCTCACTTGTATATATATCCAAATATATTGAATTCAGATTTTCAAGAAA 4223
 DB 1176 pProAlaIleProLeuLeuGlyIleTyzProLysAspTyzLysSerCysTyzLysAs 1196
 QY 4224 TATTTACACTCCATGTTCAATGTCGACCTTTCACATCACTGTTCCAAAGTTATGA 4283
 DB 1196 pProAlaIleProLeuLeuGlyIleTyzProLysAspTyzLysSerCysTyzLysAs 1196

DB 1196 pThrCysThrArgMetPheIleAlaAlaLeuPheThrIle-----AlaLysThr-TyP 1214
 QY 4284 AACACCCAAATTCATTCATGGAATAATGAACAAAGGAATGTCATTAACGTACAA 4343
 DB 1214 snGlnProLysCysProSerMetIleAspTrpIleLysMetTrpHisIleTyzThrM 1234
 QY 4344 TGGGATATATATTCACCTTAATAAAAAGGGGGATCTCTGTTATTTATGACAAACATGAATGA 4403
 DB 1234 etGlnTyzTyzAlaAlaIleLysAsnAspGlnPheMetSerPheValGlyThrTrpMetL 1254
 QY 4404 ACCCGAGGCGCATTTATGCTATGTAATAATGACGAATGAACAAAGCAATTAAGTCTGA 4463
 DB 1254 yLeuGlnThrIleIleLeuSerLysLeuSerGlnGlnTyzThrLysArgMetP 1274
 QY 4464 TTTCAATTTATGAGGTCT 4483
 DB 1274 hSerLeuIleGlyGlyAsn 1280

RESULT 9
 S23650
 retrovirus-related hypothetical protein II - human retrotransposon LINE-1
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S23650
 R/Hohjoh, H.; Minakami, R.; Sakaki, Y.
 Nucleic Acids Res. 18, 4039-4104, 1990
 A/Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences whi
 A/Reference number: S23649; MUID:90332398; PMID:2165587
 A/Accession: S23650
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-712 <HOH>
 A/Cross-references: UNIPROT:O15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:000363; UNI
 PROT:Q14754; UNIPROT:Q9Y5K0; UNIPROT:O00366; UNIPROT:Q8TF30; UNIPROT:000375; EMBL:X5223
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
 C/Genetics:
 A/Mobile element: LINE-1
 A/Start codon: GTG
 C/Superfamily: pol polyprotein

Alignment Scores:
 Pred. No.: 1.65e-16 Length: 712
 Score: 326.50 Matches: 95
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 Best Local Similarity: 41.67% Mismatches: 71
 Query Match: 3.81% Indels: 36
 DB: 2 Gaps: 4

US-09-396-985B-1 (1-4868) x S23650 (1-712)
 QY 3817 CATTTGGGAAGAGTGATGTTATTCATTGAGAAAACAATGTCGTGGAATTAATGGGGTT 3876
 DB 516 HisPheSerLysGluAspIleTy----- 523
 QY 3877 CTTATTAAGAAGGTTCCAGAAAAGAATGTTCAATTCAGCTTCTTCAGAAACAGAAACA 3936
 DB 524 ---AlaAlaLysLysHisMetLysCysSerProSerLeu----- 536
 QY 3937 TTCAGGAAAAGACATCAATCAGATGTCATCAGGGAATGAATAATTAACCAATGAGACA 3996
 DB 537 -----AlaIleArgGluMetGlnIleLysThrThrMetArg 548
 QY 3997 TATCACCTTATACAGGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
 DB 549 TyrHisLeuThrProValAlaArgMetAlaIleLysLysSerGlyAsnAsn-ArgCysTr 568
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 DB 568 pArgGlyCysGlyGlnIleGlyThrLeuLeuHisCysTrpTrpAspCysLysLeuValG 588
 QY 4105 GCCGTTATGAAGAAACAGTACGAGGCTTCTCAAAA--TTAAATAATGAATGCTATATGA 4163
 DB 588 nProLeuTrpLysSerValIleTrpArgPheLeuArgAspLeuGlnProGlnIleProPheAs 608

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QY 4164 TCCAGCAATCTCACTTCTGTATATATACCCAAAATAATGAAATTCAGAAATTCAGAAAA 4223
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Db 608 pProba1a1eProleuLeuGly1leTyrrProlysaBserLyseCyseTyrrLyys 628
QY 4224 TATTTACACTCCCATGTTTCAATGTCGACTTTTTCAGATCACTGTTTCCAAAGTTATGA 4283
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Db 628 pThrCystrArgMetPhe1leAla1eLeuPheThr1le-----Ala1yThr- Trp 646
QY 4284 AACAAACCAATTCCTCATGTCGAAATTAATGACAAAGCAATGTCATTAACGTCACA 4343
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 smGlnProlyscysProthMet1leAspTrp1leTyBysMetTrpHis1leTyrrThm 666
QY 4344 TGGGGATATATATTCAGGCTAAAAGGGGGATCCGTTATTTATGACAACATGAAATA 4403
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 666 ecGluTyrrTyrrAla1a1eTyBysAsnBpGluBpVal1SerPheValGlyThrTrpMet 686
QY 4404 ACCCGAGGCAATTAATGCTATGTTAAATGACAAATGACAAAGCAATACGCTGTA 4463
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 686 yBleuGluThr1le1leLeuSerLyseSerGlnGluGlnTyBThrLySH1eCyB1leP 706
QY 4464 TTTCAATTTATATGAGTTCT 4483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 706 heSerLeu1leGly1yAsn 712
```

RESULT 10

```
138588
Reverse transcriptase homolog - human retrotransposon L1
N/Alternate names: ORF2 protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I38588
R/Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazanian, H.H.
Nature Genet. 7, 143-148, 1994
A/Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q
A/Reference number: I38587; MID:95004577; PMID:7920631
A/Accession: I38588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:g483914; PID:AAB60345.1; PTD:g4839
C/Superfamily: pol polyprotein
```

Alignment Scores:

Pred. No.:	5 39e-16	Length:	1275
Score:	320.50	Matches:	93
Percent Similarity:	53.51%	Conservative:	29
Best Local Similarity:	40.79%	Mismatches:	71
Query Match:	3.74%	Indels:	36
DB:	2	Gaps:	4

US-09-396-985b-1 (1-4868) x I38588 (1-1275)

```
QY 3817 CATTTTGGAGAGGTGATGTTATCATTTGAGAAAAAATGTGTCGAAATTAATGGGCTT 3876
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 HisPheSerLyseLubsp1leTy----- 1086
QY 3877 CTTATTAAGAAGGTTCCCAAGAAAGATGTTTCATTCAGCTTTCTTACGAAACAGACA 3936
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1087 ---Ala1a1yLyBysH1eMetLyBysCyseSerSerLeu----- 1099
QY 3937 TTCAGGAAAAAGCAATGATGTCATCAGGGAATGAATTAATAACACAAATGAGA 3996
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1100 -----Ala1eArgGluMetGln1leTyBThrTrpMetArg 1111
QY 3997 TATCACTTATACCAAGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1112 TyrrHisLeuThrProValArgMetAla1le1leTyBysSerGlyAsnAsn-ArgCyBrr 1131
QY 4045 TCAAGGATATAGAAATTTGAAACCTTTCTTCACTGTCGAGGGAATGAAATGCTGTA 4104
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1131 pArgGlyCyBglTyBThrLeuLeuH1eCyBrrTrpArgCyBysLeuValG1 1151
```

```
QY 4105 GCCGTTAGAAAAACAGTACGAGGTTTCTCAAAA-TTAAAAATAGACTCTATATGA 4163
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1151 nProleuTrpLyBserVal1TrpArgPheLeuArgBpLeuGluLeu1leProBys 1171
QY 4164 TCCAGCAATCTCACTTCTGTATATATACCCAAAATAATGAAATTCAGAAATTCAGAAAA 4223
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1171 pProba1a1eProleuLeuGly1leTyrrProGluBpTyrrLyseCyseTyrrLyys 1191
QY 4224 TATTTACACTCCCATGTTTCAATGTCGACTTTTTCAGATCACTGTTTCCAAAGTTATGA 4283
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1191 pThrCystrArgMetPhe1leAla1eLeuPheThr1le-----Ala1yThr- Trp 1209
QY 4284 AACAAACCAATTCCTCATGTCGAAATTAATGACAAAGCAATGTCATTAACGTCACA 4343
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1209 smGlnProlyscysProthMet1leAspTrp1leTyBysMetTrpHis1leTyrrThm 1229
QY 4344 TGGGGATATATATTCAGGCTAAAAGGGGGATCCGTTATTTATGACAACATGAAATA 4403
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1229 ecGluTyrrTyrrAla1a1eTyBysAsnBpGluBpVal1SerPheValGlyThrTrpMet 1249
QY 4404 ACCCGAGGCAATTAATGCTATGTTAAATGACAAATGACAAAGCAATACGCTGTA 4463
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1249 yBleuGluThr1le1leLeuSerLyseSerGlnGluGlnTyBThrLySH1eArg1leP 1269
QY 4464 TTTCAATTTATATGAGTTCT 4483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1269 heSerLeu1leGly1yAsn 1275
```

RESULT 11

```
B28096
line-1 protein ORF2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Accession: B28096
R/Skowronski, J.; Fanning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A/Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A/Reference number: A28096; MID:88246405; PMID:2454389
A/Accession: B28096
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1275 <SKO>
A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:O00363; UNIPROT:O00366; UNIPROT:O00375
C/Superfamily: pol polyprotein
```

Alignment Scores:

Pred. No.:	6.42e-16	Length:	1275
Score:	319.50	Matches:	93
Percent Similarity:	53.07%	Conservative:	28
Best Local Similarity:	40.79%	Mismatches:	72
Query Match:	3.72%	Indels:	36
DB:	2	Gaps:	4

US-09-396-985b-1 (1-4868) x B28096 (1-1275)

```
QY 3817 CATTTTGGAGAGGTGATGTTATCATTTGAGAAAAAATGTGTCGAAATTAATGGGCTT 3876
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 HisPheSerLyseLubsp1leTy----- 1086
QY 3877 CTTATTAAGAAGGTTCCCAAGAAAGATGTTTCATTCAGCTTTCTTACGAAACAGACA 3936
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1087 ---Ala1a1yLyBysH1eMetLyBysCyseSerSerLeu----- 1099
QY 3937 TTCAGGAAAAAGCAATGATGTCATCAGGGAATGAATTAATAACACAAATGAGA 3996
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1100 -----Ala1eArgGluMetGln1leTyBThrTrpMetArg 1111
QY 3997 TATCACTTATACCAAGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1112 TyrrHisLeuThrProValArgMetAla1le1leTyBysSerGlyAsnAsn-ArgCyBrr 1131
QY 4045 TCAAGGATATAGAAATTTGAAACCTTTCTTCACTGTCGAGGGAATGAAATGCTGTA 4104
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db	1131	parGILyuybElguIlleGIlythIleuLeuHleIScyStrIrrrPherCySylvLeuValGI	1151
Qy	4105	GCCTGATGAAAAcAGTAcGAGGTTTCTCAAAA-TTAAAAATGAACTGCTATATAGA	4163
Db	1151	nProleuTrpIysSerValTrpArgPheLeuArgAyrleuGIuIleuGIuIleProPheAs	1171
Qy	4164	TTCCAGCAATCTCACTTCGTGTATATATATACCCAAAATATGAAATCAGAAATTTCAAGAAA	4223
Db	1171	pProAlaIleProleuLeuGIlyIleTyPProAsnAspTyTrIySserCysCyStrIyLeAs	1191
Qy	4224	TATTTACACTCCCAAGTTCATTTGNGGCACTCTTCAATCACTGTTCCTCAAAAGTTATGGA	4283
Db	1191	pThCyethrArgMetPheIleAlaIlePheMetHlle-----AlaIyStrHr-TRpa	1209
Qy	4284	AACAACCCAAATTTCCATTTGGAAAAATAATAGACAAGAAAGAAATGCAATATAGATACAA	4343
Db	1209	sngInProIyCySerProHrMetIleAspTrIleIyAlIyLeuMetTrpHleIleTyThrm	1229
Qy	4344	TGGGAGATTTATTCAGCCTAAAAAAGGGGGAGATCTGTATATTTATGCAACATGAATAA	4403
Db	1229	etGIuTyTyAlAlaIleIyAsnAspGIuPheMetSerPheValGIyIrrTrpMetI	1249
Qy	4404	ACCCGAGGCCATTAATGCTATGATTAATAGACAAAGTAAcAGAAAGCAAAATATGCGCTGA	4463
Db	1249	ysLeuGIuThrHleIleLeuSerIySylvSerGIuGIuIleTyethIySerHlsArgIleP	1269
Qy	4464	TTTCATTATATGAGTTCT	4483
Db	1269	heserLeuIleGIyGIyAsn	1275

RESULT 12

Reverse transcriptase homolog - human transposon L1.1
C/Species: Homo sapiens (man)
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S65824
R/Dombroski, B.A.
submitted to the EMBL Data Library, January 1992
A/Description: Isolation of an active human transposable element.
A/Reference number: S65823
A/Accession: S65824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1275 <DOM>
A/Cross-References: UNIPROT:Q15604, EMBL:M80340, NID:G9339767, PIDN:AAAS1622.1, PID:G9339767
A/Superfamily: pol polypeptide

Alignment Scores:

Pred. No.:	6,42e-16	Length:	1275
Score:	319.50	Matches:	93
Percent Similarity:	53.07%	Conservative:	28
Best Local Similarity:	40.79%	Mismatch:	72
Query Match:	3.72%	Indels:	36
DB:	2	Gaps:	4

OY	3817	CATTTCGGGAAGATGATGTTCATTCATGAGAAGAAACATGCTCGAATTAATGAGGTT	3876
Db	1079	HtHfSeSerlysgluApplIeTy-----	1086
OY	3877	CTTATAAAGAAGCTTCCAGAAAAGAAATGTTTCATTCAGCTTCTTCAGAAAACAGAAACA	3936
Db	1087	---AlalAlalyblySHismetLylylCysSerterSerLeu-----	1099
OY	3937	TTCAGGAAAAAGCAATCAGAGTGCATCAGSAAATGAATAATAAACCACCATGAGA	3996
Db	1100	-----AlailleargglumetgnilleystnThrMetLarg	1111
OY	3997	TATCACCTTATACCAAGTAGTGCTACTATAA-----AATGAAGTCCA	4044
Db	1112	TyrHisIeuThrProValArgMetAlaIlellelyslysserGIyanden-ArgCysTr	1131

Qy	TCAGAGTATATAGAGAAATTGGAAACCTTCTCACTGCTGGAGGGAGAAATGAGTGA	4104
Db	1131 pargGlyCyseGlyGluIleGlyThrIleuLeuHISCystrPrpAsrCylysIeuValG1	1151
Qy	4105 GCCGTTATGAAAAACAGTACGAGGCTTCTCAAAA--TTAAAAATAGACCTGCTATATGA	4153
Db	1151 nProleuTrpIysSerValItrpArgPheIeuAspIeuGluIleuGluIleProPheAs	1171
Qy	4164 TCCAGCAATCATCTTCTGTATATATATCCAAAAATAATTGAATCAGAAATTTCAGAAAA	4223
Db	1171 pProAlIleProIeuIeuGlyIleTyrrProAsnGluTyrrLysSerCyseStrIyIysAs	1191
Qy	4224 TATTACACTCCCATGTTCAATTGTGGACACTCTTCACAATCACTGTTCCAAAGTTATGA	4283
Db	1191 pThrCystrHsrArgMetPheIleAlaIleuPheThrIle-----AlaIysThr--TrpA	1209
Qy	4284 AACAAACCCAAATTTCCATTGGAAAAATAAATGACAAAGAAATGCAATTAACGTACAA	4343
Db	1209 snGlnProIyAsCyseProThMetIleAspTrIleIyIyIysMetTrpHisIleTyrrThrm	1229
Qy	4344 TGGGAGATATATTACGCTAAAAAAGGGGGGAGTCTCGTATATTATGACAACATGAATAA	4403
Db	1229 etGluTyrrTyrrAlaAlaIleIyIysAsnAspGluPheIleSerPheValG1YThrTrpMetL	1249
Qy	4404 ACCCGAGGCCATTATGCTTATGTAATAATGACGAAGTACAGAAAGACAAATACTGCTGA	4463
Db	1249 yIsIeuGluThrIleIleIleuSerIyIysIeuSerGlnGluIyIyStrIyHisIArgIleP	1269
Qy	4464 TTTCATTTATATGAGGTTC 4483	
Db	1269 hseStrIeuIleGlyGlyAsn 1275	

RESULT 13

insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: J05239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: J05239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: J05239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insuline-like met

Alignment Scores:

Pred. No.:	9.97e-16	Length:	605
Score:	316.00	Matches:	15
Percent Similarity:	39.04%	Conservative:	94
Best Local Similarity:	24.42%	Mismatches:	24
Query Match:	3.68%	Indels:	150
DB:	2	Gaps:	23

US-09-396-985B-1 (1-4868) x JC5239 (1-605)

OY 200 GTTCTTAATATTACTTTATCATGATGCATGGAGCTGAATTTCTACAAATAATCCCGACAACCTC 259
||| :::: ||| ||| :::: ||| ||| ::
Db 53 ValAenGIUleuSerValPheCyseSerarIghnAenleuthrArGlneProApGlyIle 72
||| :::: ||| ||| :::: ||| ||| ::
OY 260 CCCCTTCACCAAGAACCCTGGACCTGACTTTAATCCCTGAGGCATTTAGSCAGCTAT 319
||| :::: ||| ||| :||| ||| :|||
Db 73 ProGIyGLThrGlnAlaLeutrpLeunSpberAnSnleuSerIleProProAla 92
||| :::: ||| ||| :||| ||| :|||
OY 320 AGCTTCTTCAGTTTCCCAGAACTGCAGGTGCTGGATTTATTCACGCTGTGAATTCAGACA 379
||| :::: ||| ||| :||| ||| :|||
Db 93 AlaPheArgAenleuSerSerIeunlAphleuAnSnleuIngIyGIgnleuGIysr 112
||| :::: ||| ||| :||| ||| :|||
OY 380 ATTGAAGATGGGGCATATCACAGCTTAAGCCAACCTCTTACCTTAAATATTGACAGGAAC 439
||| :::: ||| ||| :||| ||| :|||

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Db      113 LeuGIuProGIuAlaLeuLeuGIuLeuGIuAsnLeuCyHisLeuHisLeuGIuArgAsn 132
QY      440 CCCATCCAGATTAGCCCTGGAGGCGCTTTCT----- 472
Db      133 GlnLeuArgSerLeuAlaValGIuThrPheAlaIYrThrProAlaLeuAlaLeuLeuGIu 152
QY      473 ----- 487
Db      153 LeuSerAsnAsnArgLeuSerArgLeuGIuAspGIuLeuPheGIuLeuGIuYanLeu 172
QY      488 CAGAGCTGGTGGCTGTGGAGACAATCTAGCATCTCTAGAGAACTTCCCATTTGGACAT 547
Db      173 TrpAspLeuAsnLeuGIuYrTrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGIu 192
QY      548 CTCAAAACCTTTGAAGAAGCTTAATAGTGGCCACATCTTATCCAACTTTTCAAAATTACCT 607
Db      193 LeuGIuGIuLeuArgLeuValLeuAlaGIuAsnArgLeu--AlaIYrLeuGIuPro 211
QY      608 GAGTATTTTCTAATCTGACCAATCTAGAGCACTTGGACCTTTCAGACAAGATTTCA 667
Db      212 AlaLeuPheSerGIuLeuAlaGIuLeuArgGIuLeuAspLeuSerArgAsnAlaLeuArg 231
QY      668 AGTATTTATTTGACAGACTTGGCGGTTTACATCAATGCCCCCTACTCAATCTCTCTTTA 727
Db      232 AlaIle-----LysAlaAsnValPheAlaGIuLeuProArgLeuGIu--LysLeu 247
QY      728 GACCTGCTCCGTATGCTATGAACCTTATTCACACGAGTGCATTTTAAAGAAATTAGG--- 784
Db      248 TyrLeuAspArgAsnLeuIleAlaValAlaPheProGIuAlaPheLeuGIuLeuLysAla 267
QY      785 CTTTCATAGCTGACTTTAAGAAATTAATTTGATAGTTAATGAAATGAAACTTGTATT 844
Db      268 LeuArgTrpLeuAspLeuSerHisAsn--ArgValAlaGIuLeuGIuAspTrpPhe 286
QY      845 CAAGCTCTGCTGCTTTAAGAGTCATCGTTGGTCTGGAGAATTTAGAAATGAAAGA 904
Db      287 ProGIuLeuLeuGIuLeuArgValLeuArgLeu----- 297
QY      905 AACTTGGAAAAGTTTGACAAATCGCTCTAGAGGCGCTGCAATTTGACATTGAGAGAA 964
Db      298 -----SerHisAsnAlaIleAlaSerLeuArgProArgTrpPheGIuAsp 312
QY      965 TTCCGATTAGCATTTAGACTACTACCTGATGATATTATTGACTTATTTAATTTGTTG 1024
Db      313 Leu-----HisPheLeuGIuGIuLeu----- 319
QY      1025 ACAAAATGTTTCTTCATTTTCCCTGGTAGAGTGAATTTGAAAGGTAAGAACTTTCT 1084
Db      320 -----GlnLeuGIuHisAsnArgTrpLeuArgGIuLeuAlaGIuArgSer 333
QY      1085 TATATTTTGGATGGCAACATTTAGATTTGATTAACGTGAAATTTGGACAGTTTCCACA 1144
Db      334 PheGIu--GlyLeuGIuGlnLeuGIuValLeuThrLeuAspHisAsnGlnLeuGln 352
QY      1145 TTGAACCTCAAACTCTCAAAAGGCTTACTTTCACCTTC-----AACAAAGGTGGGAAT 1198
Db      353 ValLysValGIuAlaPheLeuGIuLeuThrAsnValAlaValMethAsnLeuSerGIuAsn 372
QY      1199 GCTTTTTCAGAGTTGATCTTACCAAGCCTTAGTTCTAGATCTCAGTAGA--AATGGC 1255
Db      373 CysLeuArg-----AsnLeuProGIuGlnValPheArgGIuLeuGIuLysLeuHisSer 390
QY      1256 TTGAGTTTCAAAAGGTTCTGT-----TCTCAAGTGATTTTGGGACAAAC 1300
Db      391 LeuHisLeuGIuGIuSerCysLeuGIuArgTrpProHisThrPheAlaGIuLeuSer 410
QY      1301 AGCCTAAAGTATTTAGATCTGAGCTTCATGCTGTATTTACATGAGTTCAAACTTCTTG 1360
Db      411 GlyLeuArgArgLeuPheLeuLysAspAsnGIuLeuValGIuLeuGIuGlnSerLeu 430
QY      1361 ---GCTTACAAACAATGAAACTGTGATTTCCAGACTTTCACATTTGAAACAAATGAGT 1417
Db      431 TrpGIuLeuAlaGIuLeuLeuGIuLeuAspLeuThrSerAsnGlnLeu----- 446

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QY      1418 GAGTTTTCAGTATTCCTATCTACAGAAAACCTCATTTACCTTGACATTTCTCATCTCAC 1477
Db      447 ----- 448
QY      1478 ACCAGAGTTGCTTTCAATGCAATCTTCAATGGCTTTGCAAGTCTGAAAGTGAATG 1537
Db      449 LeuPro-----HisLeuPheGlnGIuGIuLeuGIuYrLeuGIuYrLeuLeuLeu 465
QY      1538 GCTGGCAATTTCTTCCAGAAAACCTTCTTCA-----GATATCTTACAGAGCTGGAAC 1594
Db      466 SerHisAsnArgLeuAlaGIu-----LeuProAlaAspAlaLeuGIuProLeuGIuArg 483
QY      1595 TTGACCTTCCAGCTCTCTCAGTGTCAACTGAGAGAGTTGTCTTCAACAGCATTTAAC 1654
Db      484 AlaPheTrpLeuAspValSerHisAsnArgLeuGIuAlaLeuProGIuSerLeuLeuAla 503
QY      1655 TCACCTTCCAGTCTTCCAGCTACTAAATATGAGCCACAAACAATCTTTTCAATTGATACG 1714
Db      504 SerLeuGIuArgLeuArgTrpLeuAsnLeuArgAsnAsn-----SerLeuArgThr 520
QY      1715 TTTCTTAAAGTGTGTGAACTCCCTCCAGTTCTTGATTACAGTCTCATGATTAAG 1774
Db      521 PheThrProGln----- 524
QY      1775 ACTTCAAAAACAGGAAGTACAGCATTTTCCAGTATGCTTACTTTCTTAATCTTACT 1834
Db      525 -----ProProGIuLeuGIuArgLeuArgLeuGIu 534
QY      1835 CAGATGACTTGTCTTGATCTTGTGAACCAAGCT----- 1870
Db      535 GlyAsnProTrpAspCysSerCysProLeuLysAlaLeuArgAspPheAlaLeuGlnAsn 554
QY      1871 -----TTCCTGCAATGATC-----AAGGACCAAGGCGAGCTC 1903
Db      555 ProSerAlaValProArgPheValGlnAlaIleCysGIuGIuAspAspCysGlnProPro 574
QY      1904 TTGCTGGAAGTTGAAACAATGGAATGTGCAACACCTTTCATAGACGAGGCACTCTG 1963
Db      575 ValIYrThrTyrAsnAsnIleThrCysAlaSerProProGIuValAlaGIuLeuAspLeu 594
QY      1964 CTGAGTTTG 1972
Db      595 ArgAspLeu 597

RESULT 14
T42218
slit-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #seqquence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; PMID:98360089; PMID:9693030
A:Accession: T42218
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NA>
A:Cross-references: UNIPROT:088279; EMBL:AB011530; NID:93449289; PID:BA032460.1; PID:93
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF4
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

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```

Alignment Scores:
Pred. No.: 5,46e-15 Length: 1531
Score: 307.50 Matches: 173
Percent Similarity: 34.788 Conservative: 99
Best Local Similarity: 22.128 Mismatches: 271
Query Match: 3.588 Indels: 240
DB: 2 Gaps: 28

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US-09-396-985b-1 (1-4868) x T42218 (1-1531)
QY 83 ACCAGTGAAGATGATGTCGCGCTCGGCGCTGGAGCTGATCCCA 142
   ::: :
Db 264 SerGlyInclGluAlaAlaGlnValProIaCyThrIeuSerGlySerCySPro 283
QY 143 GCCATGGCCCTTCCTCTCTCGGTGAGACACAAAAGCTGGAGCCCTCGTGAAGTGT 202
   |||||
Db 284 AlMetCyS-----SerCyS----- 288
QY 203 CCAATATTAATTAATCAATGATGAGCTGAATTTCAAAAATCCCGACAACCTCCC 262
   |||||
Db 289 SerAsnIlyIleValIaerCySArgIlyeGlyIeuThrAlaIleProAlaSerIeuPro 308
QY 263 TTCTCAACCAAGAACCTGAGACCTGAAGCTTAATCCCTGAGGACTTTAGGACAGTAAGC 322
   :
Db 309 GluThrIeuThrGluIleArgIleuGluIleuAsnIlyIleuSerIleProGlyAla 338
QY 323 TTCTTCAGTTTCCAGACTGACAGGTGCTGGAATTTATCCAGTGTGAATCCAGACAACT 382
   ||| :
Db 329 PheSerProIytrArgIySleuArgIyIleAspIeuSerAsnGlnIleAlaGluIle 348
QY 383 GAAATGGGGCATATCAAGACCTTAAGCCACTCTCACTTAATATTGACAGAAACCC 442
   ||| :
Db 349 AlaProAspAlaPheGlnIlyIleuArgSerIeuAsnSerIeuValIeIuYrGlyAsnIlyS 368
QY 443 ATCCAGAGTTTACGCCCTGGAGCCTTTCTGACTATCAAGTTTACGAAGCTGTGGCT 502
   ||| :
Db 369 IleThrAspIeuProArgIyValPheGlyIleuYrThrIeuGlnIleuIeuLeu 387
QY 503 GTGAGACAAATCTAGCATCTTAGAGAACTTCCCATTTGGACATCTCAAAACTTTGAA 562
   387
Db 563 GAACTTAATGTGGCTCAATCTTATTCATCTTTCAAAATTAACCTGAGTATTTCTAAT 622
   |||||
Db 388 ---LeuAsnAla-----AsnIlySleAsnCySerIleArg---ProAspAlaPheGlnAsp 403
QY 623 CTGACCAATCTTAAGACCTTGACCTTTCAGACACAAAGATTCAAGATTT----- 673
   |||||
Db 404 LeuGlnAsnIeuSerIeuLeuSerIeuYrAspAsnIlySleGlnSerIeuAlaIySgly 423
QY 674 TATTGCACAGACTTGGCGGTTTCTACATCAATGCGCCCTACTCATCTCTTTAGACCTG 723
   |||
Db 424 ThrPheThrSerIeuArgAlaIleGln-----ThrIeuHISleu 436
QY 734 TCCCTGAATCCTATGAACCTTATTCACAAGTGCATTTAAAGAAATTAGGCTTCATTAAG 793
   :
Db 437 AlaGlnAsnPro-----PheIleCyAspCyAsnIeuIyStrIeuAla----- 451
QY 794 CTGACTTTAAGAAATATTTGATAGTTTAAATGTAATGAATACTGTATTCAGAGCTG 853
   :
Db 452 -----AspPheIeuArgThrAsnProIleGlnIy-----ThrGlyAla 464
QY 854 GCTGTTTAGAAGTCATGTTGGTT-----CTGGAGAGATTTAGAATGAAGA 904
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Db 465 ArgCyAsnIaSerProArgIyGleuAlaAsnIyAspIyIleGlyGlnIleIySer----- 482
QY 905 AACCTGAAAAGTTTGAACAATCTGCTCTAGAGGCGCTGTGCAATTGACCATTTGAAGAA 964
   :
Db 483 -----LysIySphearGySerAlaIyGln-----GlnIy 493
QY 965 TTCGATTAAGCATTAAGCTACTACTGAT-----GATATTATTGAC 1009
   :
Db 494 PheIleProGlyThrGluAspIyRHSleuAsnSerGlnCySerThrSerAspValaIaCyS 513
QY 1010 TTAATTATTTGTTGACAAATGTTTCTTCAATTTTCCCTGTGAGTGAAGTATTGAAG 1069
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Db 514 ProHISlyCySArgCySgluAlaSerValaIgluCySerGlyIeuIySleuSerIyS 533
QY 1070 GTAAAGACTTTTCTTAATAATTCGAGTGGCAACATTTAGAAATTAGTTAACTGTAAATTT 1129
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Db 534 IleProGlu---ArgIleProGlnSerThrThrGluIleuArgIleuAsnGlnIle 552
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Db 553 SerIleuGlnAlaThrGlyIleuPheIyS-----LysIeuSerHISleuIySlySle 570
QY 1172 ACTTTCACCTTCAACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATTCACCAAGCTTGAAG 1231
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Db 571 AsnIeuSerAsnIeuS-----ValSerGlnIleGlnAspGlyThrPheGln 586
QY 1232 TTTCTAGATCTCAGTGAATAGGCTTGAGTTTCAAGGTTGCTTCTCAAAAGTATTT 1291
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Db 586 ----- 586
QY 1292 GGGACAAACAGCTAAGATTTAGATCTGAGCTCAATGAGTGTATTAACATGAGTTCA 1351
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QY 1352 AAC---TTCCTGGGCTTGAACAACCTAGAACATCTGGAATTTCCAGCATTCCAATTTGAA 1408
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QY 1409 CAATGAGTGAGTTTTCAGTATTTCTATCACTCAGAAACCTCAATTACCTTGACATTTCT 1468
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Db 627 CySleIleHISAsnAspSer---PheThrGlyIleuArgAsnValaArgIeuIeuSerIeuYr 645
QY 1469 CATACTCACACCAAGATTTGCTTCATGGCATCTCAATGAGCTTCAATGAGCTTCCGAAGTC 1528
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Db 646 AspAsnHISleIleThrThrIleSerProGlyAlaPheAspThrIeuGlnAlaIeuSerThr 665
QY 1529 TTGAAATGGCTGGCAATCTTTCCAGAAACTTC----- 1564
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Db 666 LeuAsnIleuAlaAsnProPheAsnCySAsnCySglnIleuAlaIyStrIeuGlyAspTrp 685
QY 1564 ----- 1564
Db 686 LeuArgIyAspIySleValaThrGlyAsnProArgCySglnAsnProAspPheIeuArg 705
QY 1564 ----- 1564
Db 706 GlnIleProIeuGlnAspValaIaPheProAspPheArgCySglnIyGlnIyGln 725
QY 1564 ----- 1564
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QY 1565 -----CTTCCAGATATCTTCACAGAG 1585
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Db 746 ArgCySerAsnIySHISleuGlnAlaIeuProIyGlyIleProIySAsnValaThrGln 765
QY 1586 CTG-----AGAAC 1594
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QY 1655 TCACCTCCAGTCTTCCAGTACTTAATATGAGCCACAAACAATCTTTTCATTGATGATAG 1714
   :
Db 806 AsnMetSerGlnIeuThrThrIeuIleuSerIyAsnAlaIeuGlnIyCySleProPro 825
QY 1715 TTTCTTAATAAGTGTGAACCTCCCTCCAGGTTCTTGATTAAGTCTCATCAATCAATAAG 1774
   :
Db 826 LeuAlaPheGlnIyIleuArgSerIeuArgIleuSerIeuHISglnIyAsnAspValaSer 845
QY 1775 ACTTCAAAAACAGAGAACTACAGCATTTTCCAGTGAAGTCTAGCTTTCTTAATCTTACT 1834
   |||
Db 846 ThrIeuGlnIyGlyIlePheAlaSepVal---ThrSerIeuSerIleuAlaIleGly 864
QY 1835 CAGAAATGACTTGTGTTGACTTGTGAACACAGAGTTTCTGCAATGATCAAGACAG 1894
   |||
Db 865 AlaAsnProIeuYrCySAspCySHISleuArgTrpIeuSerSerTrpValIySThrGly 884

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 263.083 Seconds
(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaataactccctgcctcaaa.....caaaaaaaaaaaaaaaaaaa 4868

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US0939685/Runatc.28032005_155743_21146/app_query.fasta.1.85098
-DB=uniprot_03 -QFMT=faetan -SUFFIX=rup -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=bloum62 -TRANS=human40.cdd -LIST=45
-DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US0939685.@CCN.1.1.5213.@Runatc.28032005_155743_21146 -NCPU=6 -IFPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4355	50.8	839	1	TLR4_HUMAN
2	4341	50.6	839	1	TLR4_PANPA
3	4310	50.2	837	2	Q8SPB8
4	4182	48.7	828	1	TLR4_PONPY
5	4043	47.1	826	1	TLR4_PAPAN
6	3342	39.0	843	1	TLR4_HORSE
7	3321.5	38.7	841	1	TLR4_BOVIN
8	3316.5	38.7	841	2	Q8SQS5
9	3316.5	38.7	841	2	Q6WCDS
10	3313.5	38.6	833	1	TLR4_FELCA
11	3307.5	38.6	841	2	Q6WC44
12	3197.5	37.3	841	1	TLR4_PIG
13	3102.5	36.2	839	2	Q8MI02
14	3017	35.2	838	1	TLR4_CRIGR
15	2860.5	33.3	835	1	TLR4_RAT
16	2852	33.2	835	2	Q8K2T5

17	2847	33.2	835	1	TLR4_MOUSE	Q9qk6 mus musculu
18	2206	25.7	636	2	Q8SQH3	Q8sqh3 canis fami1
19	1847	21.5	843	2	Q7ZRG5	Q7zrg5 gallus galli
20	1285.5	15.0	819	2	Q6TS41	Q6ts41 brachydanio
21	1274.5	14.9	817	2	Q6NV08	Q6nv08 brachydanio
22	834.5	9.7	258	2	Q70EK4	Q70ek4 sus scrofa
23	690	8.0	945	2	Q801F9	Q801f9 carassius a
24	685	8.0	961	2	Q76CT9	Q76ct9 paraliichthy
25	678.5	7.9	940	2	Q8RT53	Q8rt53 brachiosto
26	677	7.9	960	2	Q76CT7	Q76ct7 paraliichthy
27	668.5	7.8	991	2	Q6RSN8	Q6rsn8 mus musculu
28	663	7.7	661	1	C180_MOUSE	Q6212 mus musculu
29	645	7.5	661	2	Q8C251	Q8c251 mus musculu
30	641.5	7.5	784	2	Q6YU2	Q6y92 rattus norv
31	633.5	7.4	973	2	Q6KCC7	Q6kcc7 oncochynch
32	629.5	7.3	661	1	C180_HUMAN	Q9q97 homo sapien
33	617.5	7.2	784	1	TLR2_MOUSE	Q9q97 mus musculu
34	616.5	7.2	784	2	Q8K3D9	Q8k3d9 mus musculu
35	613.5	7.2	784	2	Q811T5	Q811t5 mus musculu
36	610.5	7.1	661	2	Q7YRL4	Q7yrl4 sus scrofa
37	602.5	7.0	784	1	TLR2_HUMAN	Q60603 homo sapien
38	601.5	7.0	785	2	Q76LZ4	Q76l24 sus scrofa
39	600.5	7.0	785	2	Q6TN21	Q6tn21 sus scrofa
40	597	7.0	784	2	Q6T752	Q6t752 equus cabal
41	595.5	6.9	784	1	TLR2_MACFA	Q95m53 macaca fasc
42	591.5	6.9	784	1	TLR2_CRIGR	Q9rl8 cricetus
43	580.5	6.8	793	1	TL21_CHICK	Q9dd78 gallus galli
44	580.5	6.8	1032	1	TLR8_MOUSE	P58682 mus musculu
45	580	6.8	781	1	TL22_CHICK	Q9dgb6 gallus galli

ALIGNMENTS

RESULT 1
TLR4_HUMAN STANDARD; PRT; 839 AA.
ID O00206; Q9UK78; Q9UM57;
AC O00206; Q9UK78; Q9UM57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll-like receptor 4 precursor (tr011).
GN Name=TLR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlburt P., Janeway C.A. Jr.;
RT "A human homologue of the Drosophila Toll protein signals activation
of adaptive immunity.";
RT Nature 388:394-397(1997).
RN [2]
RP SEQUENCE OF 41-839 FROM N.A.
RC TISSUE=Retal liver, lung, and Placenta;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.586;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
Toll.";
RT Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
locus (TLR4).";
RT Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10635634; DOI=10.1038/76048;
RA Aebour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,

RA Frees K, Watt J.L., Schwartz D.A.;
RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in
LN humans."; *Nat. Genet.* 25:187-191(2000).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hengst W.J.,
RT "Signal peptide prediction based on analysis of experimentally
RN verified cleavage sites."; *Protein Sci.* 13:2819-2824(2004).
RP [6]
RX MUTAGENESIS OF GLU-697; ARG-710; ASP-711 AND PRO-714.
RA MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RT Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.,
RN "Structural basis for signal transduction by the Toll/interleukin-1
RL receptor domains."; *Nature* 408:111-115(2000).
RP [7]
RX CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
RA MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
RT da Silva Correia J., Ulevitch R.J.,
RN "MD-2 and TLR4 N-linked glycosylations are important for a functional
RL lipopolysaccharide receptor."; *J. Biol. Chem.* 277:1845-1854(2002).
RP [8]
RX VARIANTS ARG-188; SER-246; GLY-299; SER-329; ILE-399; LEU-443;
RN IYS-474; HIS-510; ARG-694; HIS-763 AND HIS-834.
RP MEDLINE=21405531; PubMed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.,
RT "Expression of rare amino acid polymorphisms in the Toll-like receptor 4
RN in humans."; *Genetics* 158:1657-1664(2001).
RL [9]
RX FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response.
CC -1 SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC their respective TIR domains.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 TISSUE SPECIFICITY: Highly expressed in placenta, spleen and
CC peripheral blood leukocytes. Detected in monocytes, macrophages,
CC dendritic cells and several types of T-cells.
CC -1 PTM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to
CC be necessary for the expression of TLR4 on the cell surface and
CC the LPS-response. Likewise, mutants lacking two or more of the
CC other N-glycosylation sites were deficient in interaction with
CC LPS.
CC -1 POLYMORPHISM: Allele TLR4*8 (Gly-299, Ile-399) is associated with
CC a blunted response to inhaled LPS.
CC -1 SIMILARITY: Belongs to the Toll-like receptor family.
CC -1 SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
CC -1 SIMILARITY: Contains 1 TIR domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U93091; AAC60227.1; -;
DR EMBL; U88880; AAC34135.1; -;
DR EMBL; AF177765; AAFO5316.1; -;
DR EMBL; AF177766; AAFO7823.1; -;
DR EMBL; AF172171; AAF89753.1; -;
DR EMBL; AF172163; AAF89753.1; JOINED.
DR EMBL; AF172170; AAF89753.1; JOINED.
DR HSSP; O60603; 1FYW.
DR Genew; HGNC:11850; TLR4.

DR	MM: 603030; -	C: integral to plasma membrane; TAs.
DR	GO: 00050867; C: lipopolysaccharide receptor complex; NAS.	
DR	GO: 00046866; F: lipopolysaccharide binding; NAS.	
DR	GO: 00015130; F: transmembrane receptor activity; NAS.	
DR	GO: 0004888; P: activation of NF-kappaB-inducing kinase; ISS.	
DR	GO: 0007260; P: detection of fungi; NAS.	
DR	GO: 0016046; P: detection of pathogenic bacteria; NAS.	
DR	GO: 0009598; P: immune response; TAs.	
DR	GO: 0006955; P: macrophage activation; IMP.	
DR	GO: 0042116; P: mast cell activation; ISS.	
DR	GO: 0004576; P: negative regulation of osteoclast different. . . ; NAS.	
DR	GO: 00045671; P: positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO: 00045384; P: positive regulation of interleukin-12 biosyn. . . ; NAS.	
DR	GO: 00045368; P: positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO: 00045410; P: positive regulation of interleukin-6 biosyn. . . ; ISS.	
DR	GO: 0007165; P: signal transduction; TAs.	
DR	GO: 0042088; P: T-helper 1 type immune response; NAS.	
DR	InterPro: IPR001611; LRR.	
DR	InterPro: IPR000483; LRR_Cterm.	
DR	InterPro: IPR003591; LRR_Typ.	
DR	InterPro: IPR001571; LRR_Typ.	
DR	Pfam: PF00560; LRR: 12.	
DR	Pfam: PF01463; LRRCT: 1.	
DR	Pfam: PF01582; TIR: 1.	
DR	PRINTS: PR00019; LEBRICRPT.	
DR	SMART: SM00369; LRR_Typ: 2.	
DR	SMART: SM00082; LRRCT: 1.	
DR	SMART: SM00255; TIR: 1.	
DR	PROSITE: PS50104; TIR: 1.	
KW	Direct protein sequencing; Glycoprotein; Immune response;	
KW	Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;	
KW	Repeat; Signal; Transmembrane.	
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FT	DOMAIN	24 631
FT	TRANSMEM	632 652
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FT	C -> S.	

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/FtId=VAR_018731.
FT VARIANT 399 399 T -> I (in allele TUR4*B; reduced LPS-
response; dbSNP:4986791).
/FtId=VAR_012740.
FT VARIANT 443 443 F -> L.
/FtId=VAR_018732.
FT VARIANT 474 474 E -> K.
/FtId=VAR_018733.
FT VARIANT 510 510 Q -> H.
/FtId=VAR_018734.
FT VARIANT 694 694 K -> R.

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4355.00 Matches: 839
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.76% Indels: 0
DB: 1 Gaps: 0

US-09-396-985b-1 (1-4868) x TUR4_HUMAN (1-839)

QY 104 ATATATGTGCTCGCGGCTGCGGACTCTGATCCAGCCATGCGCTCTCTCTGCTGC 163
DB 1 MetMetSerLaserLaserLagLylThleuIlleProLametrLapheLaserCys 20

QY 164 GTGAGCCGAAGCGGAGGCGCTGCGGAGTGCTTCTATATTAATTACTTCAATGC 223
DB 21 ValAlrProGlnSerThrGlnProCysValGluValAlProAsnIleMrIyrglnCys 40

QY 224 ATGAGCTGAATTTCTCAAAATCCCGCAACCTCCCTTCAACCAAGAACTTGAC 283
DB 41 MetGluLeuAsnheThyrlsIleProAspAsnLeuProPheSerThrIyAsnLeuAsp 60

QY 284 CTGAGCTTAAATCCCTGAGGCACTTAAAGCACTTAAGCTTCTTCAAGTTCCAGAACTG 343
DB 61 LeuSerPheAsnProLeuArghIleuGlySerIySerPhePheSerPheProGlnLeu 80

QY 344 CAGGCTGCTGATTTATCCAGGTGGAATCCAGCAATTGAAGTGGGCACTATCAAGC 403
DB 81 GlnValLeuAspLeuSerArghCysGlnIleGlnThrIleGlnAspGlnAlaIyrglnSer 100

QY 404 CTAAAGCCACTCTCTAATTAATTTGACAGAAACCCCATCCAGAGTTTAAAGCCTGGCA 463
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120

QY 464 GCGTTTCTGAGACTATCAAGTTTACAGAGCTGCGCTGAGACAAATCTTACGATCT 523
DB 121 AlaPheSerClyLeuSerSerLeuGlnIyLeuValAlaValGlnThrAsnLeuAlaSer 140

QY 524 CTAGAGAACTTCCCGCACTTGGACATCTCAAACTTTGAAGAAATTAAATGGGCTCAAT 583
DB 141 LeuGlnAsnheProIleGlyHisLeuIySerThrLeuIySerIyLeuAsnValAlaHisAsn 160

QY 584 CTATCAATCTTTCAAAATTAATCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTG 643
DB 161 LeuIleGlnSerheThyLeuProGlnIyPheSerAsnLeuThrAsnLeuGlnHisLeu 180

QY 644 GACCTTTCCAGACAAAGATTCAAGATTATTTGACAGACTTGGCGGCTTCTTACATCA 703
DB 181 AspLeuSerSerAsnIySerIleGlnSerIleTyrcyThrAspLeuArghValIleuHisGln 200

QY 704 ATGCCCTACTCATCTCTTTTAAAGCTTCCCTGAATTCCTTGAACCTTATCCAACTCA 763
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220

QY 764 GTGCAATTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATATTTGATAGTTTA 823
DB 764 GTGCAATTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATATTTGATAGTTTA 823

DB 221 GlyAlaPheLeuGlnIleArghLeuHisIySerLeuThrLeuArghAsnAspSerLeu 240
QY 824 AATGTAATGAAAACCTGATTTCAAGGCTCGGCGGTTTGAAGTCCATGCTGTTGCTTCG 883
DB 241 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArghLeuValLeu 260
QY 884 GGAGATTTTGAAGAAATGAGAAAACCTTGGAAAAGTTTGAACAAATCTGCTAGAGGCGCTG 943
DB 261 GlyGlnPheArghAsnIleGlnIyAsnLeuGlnIySerPheAspIySerIleGlnIyGlyLeu 280
QY 944 TGCATTTGACCACTTGAAGAAATTCGATTTAGCACTTACTGACTTCACTCCATGATAT 1003
DB 281 CysAsnLeuThrIleGlnIyPheArghLeuAlaIyIyLeuAspIyTyrcyThrLeuAspArghIle 300
QY 1004 ATTTGATTTTAAATTTGTTTGAACAAATGTTTCTCAATTTCCCTGCGGAGTGAGCTAT 1063
DB 301 IleAspLeuPheAsnIySerLeuThrAsnValSerSerPheSerLeuValSerValIle 320
QY 1064 GAAAGGGTAAAAAGACTTTTCTTAATTAATTCGAGTGGCAACATTTAGAAATTAGTTAACTG 1123
DB 321 GlnArghValIyAspPheSerIyArghAsnPheGlyIyTrpGlnHisLeuGlnLeuValAsnIy 340
QY 1124 AATTTGACAGTTTCCACATTTGAATCAAAATCTTCAAAAGCTTACTTCACTTCC 1183
DB 341 IyPheGlyGlnPheProThrLeuIySerLeuIySerLeuIyArghLeuThrPheThrSer 360
QY 1184 AACAAAGGTGGGAATGCTTTTTCAGAACTTGATCTACCAAGCTTGATTTCTAGATCTTC 1243
DB 361 AsnIyGlyGlyAsnAlaPheSerGlnValAlaPheProSerLeuGlnPheLeuAspLeu 380
QY 1244 AGTAGAAATGCTGAGTTTCAAAAGTTCTGTTTCAAGAGTAAATTTGGGCAACACAGC 1303
DB 381 SerArghAsnGlyLeuSerPheIySerGlyCysSerGlnSerAspPheGlyThrThrSer 400
QY 1304 CTAAAGTATTAATGATCTGAGCTTCAATGCGTGTATTAATTCAGATGATTCAAACTTTCTGGGC 1363
DB 401 LeuIyTyIyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1364 TTAGAACACTGAAACATCTGATTTCCAGCACTTCCAAATTTGAAAACAAATGAGTGAGTT 1423
DB 421 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuIyGlnMetSerGlnPhe 440
QY 1424 TCAGTATCTTCACTCAGAAACCTCATTTACCTTGAATTTCTGATCTCAGACACAG 1483
DB 441 SerValPheLeuSerLeuArghAsnLeuIleTyIyLeuAspIleSerHisThrHisArgh 460
QY 1484 GTTGCTTTCAATGCACTTTCATATGCTTGTCCAGTCTGAAATCTTGAATGAGCTGCG 1543
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIySmetAlaGly 480
QY 1544 AATTTCTTCCAGAAAACCTTCTTCCAGATATCTTCAAGAGCTGAGAACTTGAACCTTC 1603
DB 481 AsnSerPheGlnGlnAsnheLeuProArghIlePheThrGlnLeuArghAsnLeuThrPhe 500
QY 1604 CTGGAACCTCTCAGGTCGCACTGAGGAGCTGTCTCCAAACGCAATTAACTCACTCTCC 1663
DB 501 LeuAspLeuSerGlnIySerGlnLeuGlnIyGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1664 AGCTTTCAGGTAATAATATGAGCCACAAACCTTCTTTTCAATGGATACGTTTCTCTAT 1723
DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 540
QY 1724 AAGTCTGTAATCTCCTCCAGGTTCTTGATTTACAGTCTCAATCACTTAATGACTTCCAA 1783
DB 541 IySAsnLeuAsnSerLeuGlnValLeuAspIySerLeuAsnHisIleIleMetThrSerIyS 560
QY 1784 AAACAGAGACTCAGCAATTTCCAGTAGCTTCTTCAATTTCTTCAATTTCTCAGATGAC 1843
DB 561 IySglnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGTACTTGTGAACACAGATTTCTGCAATGGATCAAGACCAAGGAGCTC 1903
DB 581 PheAlaCysThrCysGlnIySerPheLeuGlnIyTrpIleIyAspGlnArghGlnLeu 600

OY	1904	TTGGGGAAGATTGAAAGAAATGGAAATGGTCAACACCTTCAGATTAAGACAGGATGCGTGTG	1963
Db	601	LeuValGluValGlnArgMetGluCysAlaIatmrProSerAspLysGlnGlyMetCysProVal	620
OY	1964	CTGAGTTTGAATATCATCCCTGTCAATGGAATAGACCATCATGTGGTGTGTGCGTCTCAGT	20233
Db	621	LeuSerLeuAlanIleThrCysGlnMetCysAsnLysThrIleIleGlyValSerValLeuSer	640
OY	2024	GTGCTTTAGATGATCTGTGTGTGAGCACTTTCGGTCTTAAGTTCTATATTTTACCTGATGCTT	20833
Db	641	ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu	660
OY	2084	CTTGCTGGCTGCATTAAGATGATGGTATGAGAGTGAAGAAACATCTAATAGCCTTTGGTATATAC	21434
Db	661	LeuAlaGlyCysLileLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyr	680
OY	2144	TCAAGCCACGAGATGAGAGCTGGGTTAAGGAATGACGTATGAAGAAATTTAGAAAGAGGGGTG	22033
Db	681	SerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal	700
OY	2204	CCTGCATTTACAGCTTGCCTTCATACAGACACTTATTCGGGTGTGGCCATTTGCTGCC	22633
Db	701	ProProPheGlnLeuCysLeuHisIleTyrArgAspPheIleProGlyValAlaIleAla	720
OY	2264	AACATCATCATGAAGGTTTCCATTAAGACCGGAAGGTGATGGTGTGGTCCACAGAC	23233
Db	721	AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHis	740
OY	2324	TTTCATCCAGACCGCGTGGTGTATCTTTGAATATAGATTTGCTCAGACCTGGCAGTTTCTG	23833
Db	741	PheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeu	760
OY	2384	AGCAGTCCGTGGTGGATATATCTTATTCCTCCGGAAGGTGGAAGAAACCTGCTCCAG	24433
Db	761	SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysGthrLeuLeuArg	780
OY	2444	CAGCAGGTGAGACTTACCGCTTTCAGCAGAAACACTTACCTGGATGGGAGGACAGT	25033
Db	781	GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLysSer	800
OY	2504	GTCTCGGCGGCACATCTTTCTGGAGACGACTCAGAAAGACCTGCTGGATGGTAAATCA	25633
Db	801	ValLeuGlyArgHisIleIlePheTyrArgArgLeuArgLysValAlaLeuLysGlyLysSer	820
OY	2564	TGGAATCCAGAAAGAAACAGTGGGTTCAGATGCCATTTGGCAGAAACATCTATC	2620
Db	821	TyrAsnProGlnGlyThrValGlyThrGlyCysAsnTyrGlnGlnAlaThrSerIle	839
RESULT 2			
TLR4_PANPA			
ID	TLR4_PANPA	STANDARD;	PRT; 839 AA.
AC	OQTTN0;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Toll-like receptor 4 precursor.		
GN	Name=TLR4;		
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.		
OX	NCBI_Taxid=9597;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RX	MEDLINE=20558910; PubMed=11104518;		
RA	Smithova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;		
RT	"Phylogenetic variation and polymorphism at the Toll-like receptor 4		
RT	locus (TLR4)".		
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).		
CC	-I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (By similarity).		

CC	-1	STBUNIT	Belongs to the lipopolysaccharide (LPS) receptor, a	
CC	-1	MULTI-protein complex containing at least CD14, LY96 and TLR4.		
CC	-1	Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via		
CC	-1	their respective TIR domains (By similarity).		
CC	-1	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).		
CC	-1	SMILARITY: Belongs to the Toll-like receptor family.		
CC	-1	SMILARITY: Contains 21 leucine-rich (LRR) repeats.		
CC	-1	SMILARITY: Contains 1 TIR domain.		
CC	-1	-----		
CC	-1	This SWISS-PROT entry is copyrighted. It is produced through a collaboration		
CC	-1	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	-1	the European Bioinformatics Institute. There are no restrictions on its		
CC	-1	use by non-profit institutions as long as its content is in no way		
CC	-1	modified and this statement is not removed. Usage by and for commercial		
CC	-1	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	-1	or send an email to license@isb-sib.ch).		
CC	-1	-----		
DR	EMBL	AF179220	AAFO5320.1; JOINED.	
DR	EMBL	AF179218	AAFO5320.1; JOINED.	
DR	EMBL	AF179219	AAFO5320.1; JOINED.	
DR	HSSP	Q15399	1FVY.	
DR	GO	GO:0046666	C:lipopolysaccharide receptor complex; ISS.	
DR	GO	GO:0001530	F:lipopolysaccharide binding; ISS.	
DR	GO	GO:0004888	F:transmembrane receptor activity; ISS.	
DR	GO	GO:0007250	P:activation of NF-kappa-inducing kinase; ISS.	
DR	GO	GO:0016046	P:detection of fungi; ISS.	
DR	GO	GO:0009598	P:detection of pathogenic bacteria; ISS.	
DR	GO	GO:0042116	P:macrophage activation; ISS.	
DR	GO	GO:0045671	P:negative regulation of osteoclast different. . . ; ISS.	
DR	GO	GO:0045084	P:positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO	GO:0045368	P:positive regulation of interleukin-12 biosyn. . . ; ISS.	
DR	GO	GO:0045410	P:positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO	GO:0042088	P:T-helper 1 type immune response; ISS.	
DR	InterPro	IPR001611	LRR.	
DR	InterPro	IPR000483	LRR_Cterm.	
DR	InterPro	IPR003591	LRR_Cyp.	
DR	InterPro	IPR001571	TIR.	
DR	Pfam	PF00560	LRR_12.	
DR	Pfam	PF01463	LRRCT_1.	
DR	Pfam	PF01582	TIR_1.	
DR	PRINTS	PR00019	LEURICRPT.	
DR	SMART	SM00369	LRR_TYP_2.	
DR	SMART	SM00082	LRRCT_1.	
DR	SMART	SM00255	TIR_1.	
DR	PROSITE	PS50104	TIR_1.	
KW	Glycoprotein		Immune response; Inflammatory response;	
KW	Leucine-rich repeat		Receptor; Repeat; Signal; Transmembrane.	
KW	SIGNAL	1	Potential.	
FT	CHAIN	24	839	Toll-like receptor 4.
FT	DOMAIN	24	631	Extracellular (Potential).
FT	TRANSMEM	632	652	Potential.
FT	DOMAIN	653	839	Cytoplasmic (Potential).
FT	REPEAT	52	76	LRR 1.
FT	REPEAT	77	100	LRR 2.
FT	REPEAT	101	124	LRR 3.
FT	REPEAT	128	149	LRR 4.
FT	REPEAT	150	173	LRR 5.
FT	REPEAT	174	197	LRR 6.
FT	REPEAT	203	225	LRR 7.
FT	REPEAT	228	252	LRR 8.
FT	REPEAT	277	303	LRR 9.
FT	REPEAT	307	330	LRR 10.
FT	REPEAT	332	350	LRR 11.
FT	REPEAT	351	372	LRR 12.
FT	REPEAT	373	398	LRR 13.
FT	REPEAT	400	421	LRR 14.
FT	REPEAT	422	445	LRR 15.
FT	REPEAT	447	469	LRR 16.
FT	REPEAT	470	494	LRR 17.
FT	REPEAT	495	518	LRR 18.
FT	REPEAT	520	541	LRR 19.

FT REPEAT 543 566 LRR 20.
FT REPEAT 568 592 LRR 21.
FT DOMAIN 672 818 TIR.
FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 282 282 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 497 497 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 526 526 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 630 630 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 839
Score: 4341.00 Matches: 836
Percent Similarity: 99.88% Conservative: 2
Best Local Similarity: 99.64% Mismatches: 1
Query Match: 50.60% Indels: 0
DB: 1 Gaps: 0

US-09-396-985b-1 (1-4868) x TLR4_PANPA (1-839)

QY 104 ATGATGCTCTGCGCTGCGCTGCGGAGCTGTGATCCAGCCAGTGGCTTCTCTCTG 163
DB 1 MetMetSerHisLeuSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 164 GTGAGACCCAGAAAGCTGGAGGCCCTGCGTGGAGGTGCTTCTAATATTACTTATCAATGC 223
DB 21 ValArgProGluSerThrGluProCysValGluValAlaProAlaIleThrTrpGlnCys 40
QY 224 ATGAGCTGTAATTTTCAAAATCCCGAGAACTCCCTTCCACCAAGAACTTGGAC 283
DB 41 MetGluLeuAsnMetPheTrpLysIleProAlaPheLeuProPheSerThrLysAsnLeuAsp 60
QY 284 CTGAGCTTATCCCTCGAGGAGCTTTAGGAGCTATGCTTCTTCAAGTTCCCGAAGCTG 343
DB 61 LeuSerPheAsnProLeuAlaGlnIleGlnThrIleGluLeuSerPhePheSerPheProGluLeu 80
QY 344 CAGTGTCTGATTTATTCAGGTGTGAATCCAGAACTTGAAGATGGGAGCATACAGAC 403
DB 81 GlnValLeuAsnProLeuSerArgCysGluIleGlnThrIleGluLeuSerPheGlnSer 100
QY 404 CTAGACCACTCTCTACCTTAATATTGACGAGAAACCCCATCCAGAGTTTACCTGGGA 463
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 464 GCCTTTCTGAGCTATCAAGTTTACAGAGCTGTGGCTGTGAGCAAAATCTAGCATCT 523
DB 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaGluThrAsnLeuAlaSer 140
QY 524 CTAGAGAACTTCCCATTTGAGACATCTCAAACTTTGAAGAACTTATGTGCTCAAT 583
DB 141 LeuGluAsnMetProIleGlnHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
QY 584 CTATTCATCTTTCAAAATTAATCTGAGTATTTTCTAATCTGACCAATCTAGGACCTTG 643
DB 161 LeuIleGlnSerPheLysLeuProGluTrpPheSerAsnLeuThrAsnLeuGluHisLeu 180
QY 644 GACCTTTCCAGAAACAAGATTCAAAAGTATTATTTGACAGACTTGGGGGTCTTACATCA 703
DB 181 AsnSerSerSerAsnLysIleGlnSerIleTrpCysThrAsnLeuAlaLeuHisGln 200
QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGATCTTATGAATCTTATCAACCA 763
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 764 GGTGCAATTAAGAAATTAAGCTTCAATAGCTGATCTTAAAGAAATTAATTTGATAGTTTA 823
DB 221 GlyAlaPheLysGluIleArgLeuHisIleLysLeuThrLeuArgAsnAsnPheAspSerLeu 240

QY 824 AATGTATGAAAACTTGATATCAAGGTCTGGCTGTTTAGAAGCTCATGCTTGTCTG 883
DB 241 AsnValIleMetLysThrCysIleGlnGlnLysLeuAlaGlyLeuGlnValHisArgLeuValLeu 260
QY 884 GGAATATTGAAATTAAGAAACTTGGAAAAAGTTTGAACAATTCCTCTAGAGGGCTG 943
DB 261 GlyGluPheArgAsnGlnGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 280
QY 944 TGGCAATTTGACCACTTGAAGAAATTCGATTAGCATTAATGACTACCTGATGATATT 1003
DB 281 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTrpLeuAspTrpTrpLeuAspPheIle 300
QY 1004 ATGACTTATTTAATGTTTGAACAATGTTTCTTCAATTTCCCTGAGTGTGACTATT 1063
DB 301 IleAspLeuPheAsnMetCysLeuThrAsnValIleSerSerPheSerLeuValSerValThrIle 320
QY 1064 GAAAGGTTAAAGACTTTTCTTATTAATTTCCGATGGCAACATTTAGAAATTAATCTGT 1123
DB 321 LysSerValLysAspPheSerTrpAsnPheGlyTrpGlnHisLeuGluLeuValAsnCys 340
QY 1124 AAATTTGACAGTTTCCCATTTGAAATCAAAATCTCTCAAAAGGCTTACTTCACTTCC 1183
DB 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
QY 1184 AACAAAGTGGGAATCTTTTTCAGAACTGATCTACCAAGCTTGAATTTCTAGATCTC 1243
DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1244 AGTGAATATGGCTTGAGTTTCAAAAGTGTCTGTCTCAAAAGTATTTGGAGACACACG 1303
DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1304 CTAAATATTTGATGATGCTTCAATGAGTTTATTAACATGATGTTCAAACTTCTGGGC 1363
DB 401 LeuLysTrpLeuAsnProLeuSerPheAsnGlyValIleThrMetSerAsnPheLeuGly 420
QY 1364 TTAGAACAACTAGAACATCTGATTTTCAGCAATTTCCAAATTTGAACAAATGAGTGAATT 1423
DB 421 LeuGluGlnLeuGlnHisLeuAsnPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
QY 1424 TCAGTATTCCTATCACTCAAGAAACCTCATTTACCTTGACATTTCTCATCTACACACGA 1483
DB 441 SerValPheLeuSerLeuArgAsnLeuIleTrpLeuAspIleSerHisThrHisArg 460
QY 1484 GTTGCTTGAATGGCACTTTCAATGAGCTGTGTCAGCTGGAAGTCTTGAAGAAATGGCTGGC 1543
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 480
QY 1544 AATTCTTCCAGGAAACTTCTCTCCAGATATCTTCAAGAGCTGAGAAACTTGACCTTC 1603
DB 481 AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1604 CTGAGCTTCTTCAGTGTCACTGAGCAAGTGTCTTCAACAGCAATTTAACTCATCTTCC 1663
DB 501 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1664 AGCTTCAAGTACTAATTAATGAGCCCAACAACCTTTTCAATGGAATGCTTCTCTTAT 1723
DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsnProTrpPheProTrp 540
QY 1724 AAGTGTCAACTCTCCCTCCAGGTTCTTGATTACAGTCTCAATCACTAATGACTTCAAA 1783
DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTrpSerLeuAsnHisIleIleThrSerLys 560
QY 1784 AAACAGAACTACAGCAATTTTCCAGTACTGACTTCTTAAATCTTAACTCAAGAAATGAC 1843
DB 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGAATCTTGAACAACAAGATTCCGCGCATGATGATGACAGGAGGCGAGCTC 1903
DB 581 PheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 600
QY 1904 TTGCTGAAGTTGAACGAATGGAATGTGCAACCTTCAGATTAAGCAGGAGCTGCTGTG 1963

OY	584	CTTATCCCATCTTTCAAATTCATCTGAGATATTTTCTTATCTGACCAACTTCAGACACTGG	643
Db	159	LeuIleGlnSerPheLysLeuProGluYrPheSerAsnLeuThrAsnLeuGluYrYrLeu	178
OY	644	GACCTTTCAGACAAAGATTCAAAGTATTTTATTCACAGACTTCGGGGTTCTACATCA	703
Db	179	AspLeuSerSerAsnLysIleGlnSerIleYrCyStrHisAspLeuArgValLeuHisSerGln	198
OY	704	ATGCCCTTACTCATCTCTCTTTAGACCTGTCCCTGAATCCTATGAACTTTATCCACCA	763
Db	199	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetThrPheIleGlnPro	218
OY	764	GGTGCAATTTAAAGAAATTAAGCTTCATTAAGCGACTTTTAAGAAATAATTTGATGTGTT	823
Db	219	GlyAlaPheLysGluIleArgLeuHisLysLysLeuThrLeuLeuArgAsnAspPheSerLeu	238
OY	824	AATGTAAATGAAAACTTGATTCACAGTCTGGCTGGCTTTTAAAGATCATCGTTGGTTCTG	883
Db	239	AsnValMetLysThrCysIleGlnIleLeuHisAspGluLeuGluValAlaArgArgLeuValLeu	258
OY	884	GGAGCAATTTAGAAATGAAAGAACTTGGAAAAATTGACAAATCTGCTCTAGAGGGCTGTG	943
Db	259	GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGluYeu	278
OY	944	TGCAATTTGACCATTTGAGAAATTCGGATTAGCATCTTACGACTACTACCTGATGATATT	1003
Db	279	CysAsnLeuThrIleGlnGluPheArgLeuAlaYrLeuAspYrYrYrLeuAspAspIle	298
OY	1004	ATTGACTATTTTAAATTTGTTTGACAAATGTTTCTTCAATTTCCCTGGTAGTGCTATTT	1063
Db	299	IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	318
OY	1064	GAAGGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTTAGATTAGTAACGT	1123
Db	319	GluArgValLysAspPheSerYrAsnPheGlyTrpGlnHisLeuGluLeuValAsnCys	338
OY	1124	AAATTTGGACAGTTTCCACATTCGAATCTCAATTTCTCAAAAGGCTTACTTCACTTCC	1183
Db	339	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer	358
OY	1184	AACAAAGGTGGGAATGCTTTTTCAGAGTGAATTCACCAAGGCTTGAATTTCTGATCTC	1243
Db	359	AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeu	378
OY	1244	AGTAGAAATGGCTTGAGTTTCAAGAGTTGCTGTTCTCAAGTGAATTTTGGACCAACGAC	1303
Db	379	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	398
OY	1304	CTTAAAGTATTTAGATCTGAGCTTCATAGTGTTATTCACATGAGTTCAAATCTTTGGGC	1363
Db	399	LeuYrYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly	418
OY	1364	TTAGAACAACTRAGAACATCTGGAATTTCCAGACTTCCAATTTGAAACAAATAGAGATTT	1423
Db	419	LeuGluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe	438
OY	1424	TCAGTATTCATCACTCAGAAACCTCATTTATACCTTGACATTTTTCATATCACAACAGA	1483
Db	439	SerValPheLeuSerLeuArgHisLeuLeuIleYrLeuAspIleSerHisThrHisThrArg	458
OY	1484	GTTGCTTTCAATGCGATCTTCAATAGGCTTGTCAGTCTTGAAAGTCTTGAATAAGGCTGGC	1543
Db	459	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly	478
OY	1544	AATCTTTCCAGGAAAACTTCCTTCACATATTCCTCAAGAGCTGAGAACTTGAACCTTC	1603
Db	479	AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuLeuArgAsnLeuThrPhe	498
OY	1604	CTGACACTCTCTCACTGATGTCAACTGAGACAGTTGTTCCAAAGCAATTTAACTCACTCC	1663
Db	499	LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer	518
OY	1664	AGTCTTCAAGGTATTAATATAGACCAACAATCTTTTCAATTTGAGATGACTTCTTAT	1723

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21405531; PubMed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans."; 1657-1664(2001).
RL Genetics 158:1657-1664(2001).
CC -!- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
immune response to bacterial lipopolysaccharide (LPS). Acts via
Myd88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
secretion and the inflammatory response (By similarity).
CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds Myd88 and TIRAP via
their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL: AF497562; AAM18616.1; -;
DR EMBL: AF497560; AAM18616.1; JOINED.
DR EMBL: AF497561; AAM18616.1; JOINED.
DR HSSP: O60603; IFYM.
DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO: GO:0001530; P:lipopolysaccharide binding; ISS.
DR GO: GO:0004889; F:transmembrane receptor activity; ISS.
DR GO: GO:0007240; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO: GO:0016046; P:detection of fungi; ISS.
DR GO: GO:0009398; P:detection of pathogenic bacteria; ISS.
DR GO: GO:0042116; P:macrophage activation; ISS.
DR GO: GO:0045576; P:mac cell activation; ISS.
DR GO: GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_Cyp.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_12.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00369; LRR_TYR; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 828 Toll-like receptor 4.
FT DOMAIN 24 629 Extracellular (Potential).
FT TRANSMEM 630 650 Cytoplasmic (Potential).
FT DOMAIN 651 828 LRR 1.
FT REPEAT 50 74 LRR 1.
FT REPEAT 75 98 LRR 2.
FT REPEAT 99 122 LRR 3.
FT REPEAT 126 147 LRR 4.
FT REPEAT 148 171 LRR 5.

FT REPEAT 172 195 LRR 6.
FT REPEAT 201 223 LRR 7.
FT REPEAT 226 250 LRR 8.
FT REPEAT 275 301 LRR 9.
FT REPEAT 325 348 LRR 10.
FT REPEAT 371 396 LRR 11.
FT REPEAT 420 443 LRR 12.
FT REPEAT 445 467 LRR 13.
FT REPEAT 468 492 LRR 14.
FT REPEAT 493 516 LRR 15.
FT REPEAT 518 539 LRR 16.
FT REPEAT 541 564 LRR 17.
FT REPEAT 566 590 LRR 18.
FT REPEAT 628 652 LRR 19.
FT DOMAIN 670 816 LRR 20.
FT CARBOHYD 33 33 TIR.
FT CARBOHYD 171 171 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 203 203 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 280 280 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 307 307 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 495 495 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 524 524 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 573 573 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 622 622 N-1-linked (GlcNAc. . .) (potential).
FT CARBOHYD 628 628 N-1-linked (GlcNAc. . .) (potential).
SQ SEQUENCE 828 AA, 94340 MW, 51AC0984E5970FDF CRC64;

Alignment Scores:

Pred. No.: 3, 24e-304 Length: 828
Score: 4182.00 Matches: 808
Percent Similarity: 98.31% Conservative: 8
Best Local Similarity: 97.35% Mismatches: 12
Query Match: 48.75% Indels: 2
DB: 1 Gaps: 1

US-09-396-985B-1 (1-4868) x TLR4_PONPY (1-828)

QY 104 ATGAGTCTGCGCTGGCGCTGGCTGGACTGATCCGACGATGCGCTTCCTGCTGCG
DB 1 MetMetSerLaserArgLeuAlaGlyThrLeuLeuProAlaMetAlaLeuSerCys 20
QY 164 GTGAGCAGGAAGCTGGAGCGCTGGAGGTGCTTCTAATTTACTTATCAATGC 223
DB 21 ValArgProGluSerTyrProIleProCys-----ValValProAsnIleThrTyrGlnCys 38
QY 224 ATGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACCAAGACTGAGC 283
DB 39 MetGluLeuAsnPhenTyrIleProAsnLeuProPheSerThrIleAsnLeuAsp 58
QY 284 CTGAGCTTAAATCCCTGAGGATTTAGGCACCTATAGCTTCTTCACTTCCAGAACG 343
DB 59 LeuSerPheAsnProLeuArgIleLeuGlySerTyrSerPhePheSerPheProGluLeu 78
QY 344 CAGGTGCTGATTTATCCAGGTGTAATCCAGCAATGAAGATGGGCATATCAGAC 403
DB 79 GlnValLeuAspLeuSerIleGlyGlnThrIleGluAspIleTyrGlnSer 98
QY 404 CTAGCCACCTTCTACCTTAATATTGACAGAAACCCATCCAGATTAGCCCTGGGA 463
DB 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
QY 464 GCTTTTCTGAGCTATCAGTTTACGAGAGCTGGCGCTGGTGGAGCAATCTAGCATCT 523
DB 119 AlaPheSerGlyLeuSerSerLeuGlnValAlaValGluThrAsnLeuAlaSer 138
QY 524 CTAGAGACTTCCCATTCGACATCTCAAACTTTGAAGAATTAATGCTGCTCACAAT 583
DB 139 LeuGluAsnPhenProIleGlyHisLeuGlySerThrLeuGlyLeuAsnValAlaHisAsn 158
QY 584 CTATTCGAATCTTTCAATTAATCTGAGATTTTCTAATCTGACCAATCTGAGCACTTG 643
DB 159 LeuIleGlnSerPheLeuSerProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 178

QY 644 GACCTTCCAGAACAGATTTCAGAGCTTGGCGGTTCTACATCAA 703
 DB 179 AspLeuSerSerLeuSylIeGlnSerIleTyCybysAspLeuGlnValIeHnIeGln 198
 QY 704 ATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAATCTTAACTTATTCACCA 763
 DB 199 MetProIeuLeuSbnLeuSerLeuAspLeuSerIeuSbnAlIeMetAsnPhelIeGlnPro 218
 QY 764 GGTGCAATTTAAATAATTTAGCTTCATACCTTAAGAAATAATTTGATAGTTA 823
 DB 219 GlyAlaPheLeuSylIeAlaGlnLeuHsLysLeuThrIeuArgAsnSerPheAspSerLeu 238
 QY 824 AATGTAATGAAAATCTGTATTCAGAGCTGTGGTGTGTTAGAGTCCATCTTGGTCTTG 883
 DB 239 AsnValMetLysThrCySylIeGlnGlyLeuAlaGlyLeuGlnValHsLsLeuValLeu 258
 QY 884 GAGAAATTTAGAAATGAGGAAAATTTGAAAAGTTTGACAAATCTGCTTGAAGGGCTG 943
 DB 259 GlyGluPheArgAsnGlnLysAsnLeuGlnLysPheAspThrSerAlaLeuGlnGlyLeu 278
 QY 944 TGCATTTGACCATTTGAAGAAATCCGATTGACATCTTACATCTACCTCGATGATATT 1003
 DB 279 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyIeLeuAspTyTyIeLeuAspAspIle 298
 QY 1004 ATGACCTTATTTAATTTGACAAATGTTCTTCAATTTTCCGTGGAGTGGACATTT 1063
 DB 299 IleAspLeuPheSbnCysLeuAlaAsnValSerSerPheSerLeuValSerValIle 318
 QY 1064 GAAAGGGTAAAGACCTTTCTTAAATTTGAGTGGCAATTTAGAAATTTAACTGT 1123
 DB 319 LysSerValLysAspPheSerTyArgAsnPhelTyIleGlnHsIleuGlnLeuValAsnCys 338
 QY 1124 AATTTGGACATTTCCCATTTGAACCTCAATCTCTCAAAAGGCTTACTTTCACTTCC 1183
 DB 339 LysPheGlyGlnPheThrIleuGlnLysLeuSylSerLeuSylArgLeuThrPheIleAla 358
 QY 1184 AACAAAGTGGGAAATGCTTTTTCAGAAATGATCTCAAAAGCTTGGAGTTCTAGATCTC 1243
 DB 359 AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu 378
 QY 1244 AGTAGAAATGGCTTGAATTTCAAGGTGCTGTCTCAAGATTTTGGAGAACACAGC 1303
 DB 379 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrIleSer 398
 QY 1304 CTAAATGATTTAGATCTGAGCTTCAATGCTGTATTATTCATGAGTTCAAACTTTGGGC 1363
 DB 399 LeuLysTyIeLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly 418
 QY 1364 TTAGAACAACTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGAATT 1423
 DB 419 LeuGlnIleuGlnIleuHsLeuAspPheGlnHsSerAsnLeuSylGlnMetSerGlnPhe 438
 QY 1424 TCAGATTTCTATCACTAGAAACCTCATTTACTTACATTTCTCATATCTCACACAGC 1483
 DB 439 SerValPheLeuSerIeuArgAsnLeuIleTyIeLeuAspIleSerHsIleThrHsIleThrArg 458
 QY 1484 GTTGTCTTCAATGCAATCTTCAATGCTGTGCTGCAAGTCTTGAATGAGCTGGC 1543
 DB 459 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuSylValIleuSylMetAlaGly 478
 QY 1544 AATTTCTTCCAGGAAAATCTTCCATGATATCTTCCAGAGCTGGAAGAACTGACCTTC 1603
 DB 479 AsnSerPheGlnIleuSbnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 498
 QY 1604 CTGACCTCTCTCAAGTGTCAACTGAGAGCTGTCTCAACAGCATTTTAACTCACTTCC 1663
 DB 499 LeuAspLeuSerIleCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 518
 QY 1664 AGTCTTCAGGTACTTAAATATGAGCCACACAACTTTCTTCAATGATGATGCTTCTTAT 1723
 DB 519 SerLeuGlnValIleuSbnMetSerHsAsnAsnPhePheSerLeuAspThrPheProTy 538

QY 1724 AAGTGTCTGAACCTCCCTCAAGGTTCTTGATTCAGTCTCAATCACAATGACTTCCAA 1783
 DB 539 LysCysLeuAsnSerIeuGlnValIleuAspTyIeSerLeuAsnHsIleMetThrSerLys 558
 QY 1784 AAAACAGAACTACAGCATTTTCCAACTAGCTTACGCTTTTAAATCTTACTGCAATGAC 1843
 DB 559 LysGlnGlnLeuGlnHsIlePheProSerSerLeuAlaPheLeuSbnLeuThrGlnAsnAsp 578
 QY 1844 TTTGCTTGTACTGTGAACACCGAGATTCTCCGATGGATGCAAGGACGAGGACGCTC 1903
 DB 579 PheAlaCysThrCysGlnHsIleGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 598
 QY 1904 TTGGTGAAGTTGACGAAATGGAATGTGCAACACTTTCAGATTAAGACGAGGACGCTGTG 1963
 DB 599 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 618
 QY 1964 CTGAGTTTGAATATCACTGTCAAGATGAATTAAGACCATCATTTGGTGTGCTTCAGT 2023
 DB 619 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrValIleGlyValSerValPheSer 638
 QY 2024 GTGCTTGTAGTATCTGTTGAGACGTTCTGCTATTAAGTTCATTTTCACTGATGCTT 2083
 DB 639 ValLeuValValSerValAlaValAlaValLeuValTyLysPheTyIeHsIleuMetLeu 658
 QY 2084 CTGTGCTGCTGCAATAAGTATGAGTGAAGGAGGAAAACATCATGATGCTTGTATCTAC 2143
 DB 659 LeuAlaGlyCysAlaIleLysTyIeGlyArgGlyGlnAsnThrTyIeAspAlaPheValIleTy 678
 QY 2144 TCAAGCCAGATGAGAGCTGGTAAAGAAATGAGCTTGAAGAAATTTGAAGAGGGGTG 2203
 DB 679 SerSerGlnAspGluAspIleArgAsnGlnLeuValLysAsnLeuGlnGlyVal 698
 QY 2204 CCTCATTTCAAGTCTGCTTCACTACAGACCTTATTCGCCGCTGGCATTTGCTGCC 2263
 DB 699 ProThrPheGlnLeuSylLeuHsIleTyIeArgAspPheIleProGlyValAlaIleAlaAla 718
 QY 2264 AACATCATCAGAAAGTTCATTAATAAGCCGAAAGGATGTTGTGTGTCCTCCAGCAC 2323
 DB 719 AsnIleIleIleGlnGlyPheHsIleSylSerAspGlyValIleValValLysSerGlnHs 738
 QY 2324 TTCATCCAGAGCCGCTGTGTATCTTTGAATATGAGATTTGCTCAGCTGGCAGTTCTG 2383
 DB 739 PheIleGlnSerArgTyIePheGlyIlePheIleValIleuGlnLysValGlnTyIeThrLeuAsp 758
 QY 2384 AGCAGTCGCTGCTGATCATCTTCAATTCCTCGACAGAAAGTGGAGAAAGCCGCTCAGG 2443
 DB 759 SerSerArgAlaGlyIleIlePheIleValIleuGlnLysValGlnTyIeThrLeuAsp 778
 QY 2444 CAGCAGGTGAGCTGTAACGCCCTTCTCAGCAGGAAACATTAACCTGAGTGGAGAGCAGT 2503
 DB 779 GlnGlnValGlnLeuTyIeArgLeuLeuSerArgAsnThrTyIeGlnIleTrpGlnAspSer 798
 QY 2504 GTTCTGGGGCGGCACATCTTCTGAGACGACTCAGAAAAGCCCTGTGATGGTAAATCA 2563
 DB 799 ValLeuGlyArgHsIleIlePheThrParGArgLeuArgValIleuLeuAspGlyLysSer 818
 QY 2564 TGGATTCGAAAGAAACAGTGGGTACAGCA 2593
 DB 819 TrpAsnProGlnGlyThrValGlyThrGly 828

RESULT 5
 ID TIR4_PAPAN STANDARD; PRT; 826 AA.
 AC Q9TSE2;
 DT 28-FEB-2003 (rel. 41, Created)
 DT 28-FEB-2003 (rel. 41, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE TOLL-like receptor 4 precursor.
 GN Name-TIR4;
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.

NCBI_TaxId=9555;
[1]
SEQUENCE FROM N.A.
MEDLINE:20558910; PubMed:11104518;
RA Smirnova I.; Poltorak A.; Chan E.K.L.; McBride C.; Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
CC -!- IMMUNE: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AF180964; AAF07059.1; -.
CC EMBL; AF180962; AAF07059.1; JOINED.
CC EMBL; AF180963; AAF07059.1; JOINED.
CC HSSP; 015399; 1FVY.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; F:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:macrophage activation; ISS.
DR GO; GO:0045571; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_13.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT CHAIN 1 23
FT SIGNAL 24 826
FT DOMAIN 24 631 Extracellular (Potential).
FT TRANSMEM 632 652 Potential.
FT DOMAIN 653 826 Cytoplasmic (Potential).
FT REPEAT 53 76 LRR 1.
FT REPEAT 77 100 LRR 2.
FT REPEAT 101 124 LRR 3.
FT REPEAT 128 149 LRR 4.
FT REPEAT 150 173 LRR 5.
FT REPEAT 174 197 LRR 6.
FT REPEAT 203 225 LRR 7.

FT REPEAT 228 252 LRR 8.
FT REPEAT 277 303 LRR 9.
FT REPEAT 327 350 LRR 10.
FT REPEAT 351 372 LRR 11.
FT REPEAT 373 398 LRR 12.
FT REPEAT 400 421 LRR 13.
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FT REPEAT 470 494 LRR 16.
FT REPEAT 495 518 LRR 17.
FT REPEAT 520 541 LRR 18.
FT REPEAT 543 569 LRR 19.
FT REPEAT 571 592 LRR 20.
FT DOMAIN 672 818 TIR.
FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
SQ SEQUENCE 826 AA; 94678 MW; 422777318B5F1769 CRC64;

Alignment Scores:
Pred. No.: 8, 35e-294 Length: 826
Score: 4043.00 Matches: 776
Percent Similarity: 96.97% Conservative: 23
Best Local Similarity: 94.17% Mismatches: 25
Query Match: 47.13% Indels: 0
DB: 1 Gaps: 0

US-09-396-985b-1 (1-4868) x TLR4_PAPAN (1-826)
QY 104 ATGATGCTGCTGCTGGCGCTGGCTGGAGCTGATCCAGACGAGCTTCTCTCTG 163
DB 1 MetThrSerAlaLeuArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 164 GTGAGACCGAAGAGCTGGAGCGCTGCGTGGAGGTGCTCTTAATTTACTTATCAATGC 223
DB 21 ValArgProGluSerTyrPheIleProCysValAlaGluValAlaProAsnIleThrTyrGlnCys 40
QY 224 ATGGAGCTGAATTTTACAAAATCCCGGACCACTCCCTTCTCAACCAAGACCTGGAG 283
DB 41 MetGluLeuAspPheThrLysIleLeuProAspAsnIleProPheSerThrLysAsnLeuAsp 60
QY 284 CTGAGCTTAAATCCCTGAGGAGCATTTAGGACGCTTCTTCAAGTTTCCAGAACTG 343
DB 61 LeuSerPheAsnProLeuArgHisLeuGlnSerTyrSerPheLeuArgPheProGluLeu 80
QY 344 CAGGTCTGATTTATTCACGGTGTGAATTCAGACAACTTGAAGATGGGCAATTCAGAGC 403
DB 81 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY 404 CTAAAGCACTCTCACTTAATATTTAGCAGAAACCCGATCCAGGTTTGGCCCTGGGA 463
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlnAspProIleLeuSerLeuAlaLeuGln 120
QY 464 GCGTTTCTGACATACGATTACGAGAGCTGTGGCTGTGGAGCAAAATCTAGCATCT 523
DB 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 140
QY 524 CTAGAGAACTTCCCATTTGAGACATCTCAAACTTTGAAGAACTTATGTGCTCAAT 583
DB 141 LeuGluAsnPheProIleGlnHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
QY 584 CTTATCGAATCTTTCAATTTACCTGAGTATTTTCTTAATCTAGCAATCTAGAGCACTTG 643
DB 161 LeuIleGlnSerPheLysLeuProGlnTyrPheSerPheAsnLeuThrAsnLeuGlnHisLeu 180
QY 644 GACCTTCCAGAACAAAGATTCAAAGTATTTATTCAGACAGACTTGGGGTTCATCAATCA 703

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|||||.....
Db 181 AspreuserSerAenlysiLegInAnliIetyrCyseLysAspleuGInValIeunHiEgIn 200
Qy 704 ATGCCCTACTCAATCTCTCTTAGACCTGCTCCGTAATCTTAACTTATCAACCA 763
Db 201 MetProleuProAsnSerLeuAspleuSerLeuAsnProIleAsnPhelIeGInPro 220
Qy 764 GGTCATTTAAAGAAATTAGGCTCATAGCTGACTTAAAGAAATAATTTTGTAGTTTA 823
Db 221 G1yAlaIheLysGInIleArgLeuHLeuLysLeuThrLeuArgSerAsnPhAspleu 240
Qy 824 AATGTAAAGAAAATTGTATTCAGAGCTGGCTGGTTAGAGTCCATCGTTGGTCTG 883
Db 241 AsnValMetLysThrCySIIeGInGlyLeuAlaGlyLeuGInValHIsArgLeuValLeu 260
Qy 884 GGAGATTTTGAATTAAGAGAACTTGGAAAAAGTTTGACAATTCGCTCTAGAGGGCTG 943
Db 261 G1yGluIheArgAsnGluArgAsnLeuGInGluIheAspLysSerAlaLeuGInGlyLeu 280
Qy 944 TGCAATTTGACCAATTGAAGAAATTCGATTAAGCTACTAGCTACTGATATTT 1003
Db 281 CyAsnLeuThrIleGInGluIheArgLeuThrTyLeuAspTyTyTyLeuAspAsnIle 300
Qy 1004 ATTGACTTATTTAATTGTTGAACAATGTTTCTTCAATTTCCCTGAGTGTGACTATT 1063
Db 301 IIsAspleuHeanCyseLueAlaAsnAlaSerSerPheSerLeuValSerValAsnIle 320
Qy 1064 GAAAGGTTAAAGACTTTTCTTATATTTGGATGGACAATTGAATTAAGTTACTGT 1123
Db 321 LysArgValGInAspPheSerTyArgAsnPhArgTrpGInHIsLeuGInLeuValAsnCyS 340
Qy 1124 AAATTTGGACAGTTCCCACTTGAAGAACTCAATCTCCAAAGGCTTACTTCACTTC 1183
Db 341 LysPheGInGluIheProThrLeuGInLeuGInLysLeuLysArgLeuThrPheThrAla 360
Qy 1184 AACAAAGGTGGAGATGCTTTTTCAGAGTTGATCTACCAAGCCTTGAATTCTAGATCTC 1243
Db 361 AsnLysG1yGInAsnAlaPheSerG1yValAspleuProSerLeuGInPheLeuAspleu 380
Qy 1244 AGTGAATAGCTTGAATTCAAAAGTTGCTGTTCTCAAAAGTATTTTGGACACCAAGC 1303
Db 381 SerArgAsnG1yLeuSerPheLysG1yCyseLysSerInSerAspPheG1yThrThrSer 400
Qy 1304 CTAAAGATTTAGATCGAGGTTCAATGAGTATTAACAAGTCAAGCTTCTTGAGG 1363
Db 401 LeuLysTyLeuAspleuSerPheAsnAspValIleThrMetG1ySerAsnPhLeuG1y 420
Qy 1364 TTAGAACACTAGAACATCTGATTTCCAGATTTCCAAATTTGAAAACAATGAGTGAATT 1423
Db 421 LeuGInGInLeuGInHIsLeuAspPheGInHIsSerAsnLeuLysGInMetSerGInPhe 440
Qy 1424 TCAGTATTTCTATCACTCAGAAACCTCATTTTACCTTGAATTTCTCATCTACACAGA 1483
Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAspLysIleSerIleThrIleThr 460
Qy 1484 GTTGCTTTCAATGGCATCTTCAATGAGCTTGGCCAGTCCAGTCCGTAAGAGTGGCTGC 1543
Db 461 ValAlaPheAsnG1yIlePheAspG1yLeuLeuSerLeuLysValLeuLysMetAlaG1y 480
Qy 1544 AATTTCTTCCAGAAAACCTTCCAGATATTTCCAGATTTCCAGAGTGAAGAACTTGACCTTC 1603
Db 481 AsnSerPheGInGluAsnPhLeuPheLeuProAspLysPheThrAspleuLysAsnLeuThrPhe 500
Qy 1604 CTGAGACTTCTCTCAGTCTCAACTGAGACAGTTGTCTCCAAACAGATTTAACTCACTCC 1663
Db 501 LeuAspLeuSerGInCySInLeuGInGInLeuSerProThrAlaPheAspThrLeuAsn 520
Qy 1664 AGCTTGAAGTAAATATAGACCAACAACATCTTTTCAATGATGATAGTTTCCATT 1723
Db 521 LysLeuGInValIleuAsnMetSerHIsAsnAsnPhPheSerLeuAspValPheProTyTr 540
Qy 1724 AAGTGTGAACCTCCCTCAGGTTCTTGAATTAAGTCTCAATCAATAGACTTCCAAA 1783
|||||.....

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Db 541 LysCyseLeuProSerLeuGInValLeuAspTySerLeuAsnHIsIleMetThrSerLys 560
Qy 1784 AAACAGAAACTAAGACTTTTCCAGATAGCTAGCTTTCTTAAATCTTACTCAAGATGAC 1843
Db 561 AsnGInGluProGInHIsPheProSerSerLeuAlaPheLeuAsnLeuThrGInAsnAsp 580
Qy 1844 TTTGCTTGTACTTGTGAACACAGAGTTTCTGCAATGATCAAGACACAGAGCAGCTC 1903
Db 581 PheAlaCySerThrCySInHIsGInSerPheLeuGInThrIleLysAspGInArgGInLeu 600
Qy 1904 TTGGTGAAGTTGAACGAATGGAATGTGCAACACTTCAGATAGCAAGGAGGCTGTG 1963
Db 601 LeuValG1yValaG1yValaGmetG1yCySAlaThrProSerAspLysGInG1yMetProVal 620
Qy 1964 CTGAGTTTGAATATCACTGTCAGATGATTAAGACATCATCTTGGTGTGGCTCAGT 2023
Db 621 LeuSerValAsnIleThrCySInMetAsnLysThrIleLeuG1yAlaSerValPheSer 640
Qy 2024 GTGCTGTAGTATCTGTGTGAGCAATTCGTCATATAGTTCTATTTTCACTGATGCTT 2083
Db 641 ValLeuValValSerValValAlaValaValLeuValTyLysPheTyThrPheHIsLeuMetLeu 660
Qy 2084 CTGCTGCTGCTCATAAAGTATGAGTGAAGTGAAGAAACATCTATATGCTTTGTATCTAC 2143
Db 661 LeuAlaG1yCySIIeLysTyArgG1yArgG1yGluAsnIleTyArgAspAlaPheValIleTy 680
Qy 2144 TCAGGCGAGATAGAGACTGGCTGAAGAAATGAGCTGTAAAGATTTAAGAAAGGGCTG 2203
Db 681 SerSerG1yAspLysPheTrpValArgAsnG1yLeuValLysAsnLeuGInG1yVal 700
Qy 2204 CTTCAATTCAGCTGCTGCTTCACTACAGAGACTTATTCCTCGGTGTGGCACTTGCTGCC 2263
Db 701 ProPheGInLeuCySLeuHIsTyArgAspPheIleProG1yAlaAlaIleAla 720
Qy 2264 AACATCATCATGAAGTTTCCATAAAGCCGAAGGTGATTTGTGTGTGCTCCAGAC 2323
Db 721 AsnIleIleHIsGInG1yPheHIsLysSerArgLysValIleValValValSerGInHIs 740
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Db 741 PheIleGInSerArgTrpCySIIePheG1yTyGInIleAlaGInThrTrpGInPheLeu 760
Qy 2384 AGCAGTCGTCGTGATCATCTTCAATGTCCTCAGAGGTGAGAGAACCTGCTCAG 2443
Db 761 SerSerArgAlaG1yIleIlePheIleValLeuGInLysValGInLysThrLeuLeuArg 780
Qy 2444 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGGAACATTTACTGAGTGGAGAGCAGT 2503
Db 781 GInGInValG1yLeuTyArgLeuLeuSerArgAsnThrTyLeuGInTrpG1yAspSer 800
Qy 2504 GTCTTGGGGCGGCAATCTTTGAGAGACGACTCAGAAAAGCCTGCTGATGTTGAATCA 2563
Db 801 ValLeuG1yGInHIsIlePheTrpArgArgLeuArgLysAlaLeuLeuAspG1yArgSer 820
Qy 2564 TGGATTCAGAA 2575
Db 821 TrpAsnProGlu 824

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RESULT 6

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TIR4 HORSE STANDARD; PRT; 843 AA.
ID TIR4 HORSE
AC GMYN3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T011-like receptor 4 precursor.
GN Name=TIR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.

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QY 824 AATGTAATGAACTTGTATTCAGAGTCTGGCTGGTTTGAAGATCCATCGTTGGTCTG 883
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 QY 884 GGAGAAATTTGAATGAAAGAACTTGGAAAAGTTTGAACAAATGCTCTTGAAGAGCTG 943
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 Db 261 GlyIuPheLysAsnGlnArgGlyLeuGlnArgPheAspThrSerAlaLeuArgGlyLeu 280
 QY 944 TGCAATTTGACCATTTGAAGAATTCGGATTGACATCTACTCTACTCTCGAT---GAT 1000
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 Db 281 HisAsnLeuThrIleGlnGluPheArgLeuAlaTyrIleAspAsnTyrSerSerLysAsp 300
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 Db 301 SerIleAspLeuLeuAsnGlyLeuAlaAspIleSerLysIleSerLeuValSerLeuAsp 320
 QY 1061 ATTGAAGAAGGTAAAGAATTTTCTTATTAATTCGGATGGCAACATTTAGAATTAGTTAAC 1120
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 Db 321 LeuGlyAsnLeuLysAspPheProLysGlyPheGlyTyrGlnAspPheGlnLeuValAsn 340
 QY 1121 TGTAAATTTGGACAGCTTTCCACATTTGAACCTCAATCTCTCAAAAGGCTTACTTCACT 1180
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 Db 341 CysArgIleGlnGlyPheProThrLeuGlnLeuThrSerLeuLysArgLeuValPheThr 360
 QY 1181 TCCACAAGAGGTGGGAATGCTTTTTCAGAAAGTTGATGATCCCAAGCTTGAATTTCTAGAT 1240
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 Db 361 SerAsnLysAspMetLysSerPheAsnGlnValLysLeuProSerLeuGlnPheLeuAsp 380
 QY 1241 CTCAGTGAAGAATGCTTGAAGTTTCAAGGTTGCTGTTCTCAAAAGTGAATTTGGACAAAC 1300
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 Db 381 LeuSerArgAsnArgLeuSerPheLysSerCysSerGlnAlaAspLeuLysThrThr 400
 QY 1301 AGCTTAAGATTTAGATCTGAGCTTCAATGCTTATTCACAGATTTCAAACTTTCTTG 1360
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 Db 401 ArgLeuLysHisLeuAspLeuSerPheAsnAspValIleSerMetSerSerAspPheMet 420
 QY 1361 GGCTTAGAACAATGAGAACTGAGATTTTCCAGATTTCAATTTGAACAAATGAGTAGAG 1420
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 Db 421 GlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnAlaSerAsp 440
 QY 1421 TTTTCAGTATTCCTATCTACTCAGAAACCTCATTTACTTGAATTTCTACTACTCAGACC 1480
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 Db 441 PheProValIlePheLeuSerLeuLysAsnLeuArgTyrLeuAspIleSerTyrThrAsnThr 460
 QY 1481 AGAGTTCCTTCATGAGCATCTTCAATGAGCTTGCAGCTCTCGAAGCTTGAATAGTCT 1540
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 Db 461 ArgValAlaPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuLysMetAla 480
 QY 1541 GGCAATCTTTCAGAGAAACCTTCTCCAGATATCTTTCACAGAGCTGAGAACTTGACC 1600
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 Db 481 GlyAsnSerPheLysAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThr 500
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 Db 541 TyrIleProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe 560
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 Db 561 LysTyrGlnGlnLeuGlnHisPheProSerSerLeuAlaSerLeuAsnLeuThrGlnAsn 580
 QY 1841 GACTTTCCTTGTACTTGTGAACACAGAGTTTCTGCAATGATCAAGACAGAGGAGAG 1900
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 Db 581 AspPheAlaCysValCysGlnTyrGlnSerPheLeuGlnTyrValLysAspGlnArgGln 600

QY 1901 CTCTTGAGAACTTGAACGAATGAGATGCAACACTTCAGATTAAGACAGGCAATGCT 1960
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 Db 601 LeuLeuValGlnValGlnHisLeuValCysAlaIleProLeuGlnMetArgGlyMetPro 620
 QY 1961 GTGCTGAGTTG---AATATCACCTGTCCAGATGAATTAAGCCATTCATGCTGTGCTG 2017
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 Db 621 ValLeuGlyPheAsnAsnAlaThrCysGlnIleSerLysThrIleValGlyLysVal 640
 QY 2018 CTCAGTGGCTGTAGATCTGTGTGAGCAGTCTGCTCATTAAGTTCTATTTTCACTG 2077
 :::
 Db 641 PheSerIleLeuMetValSerValIleAlaValLeuValTyrLysPheThrPheHisLeu 660
 QY 2078 ATGCTTCTGCTGCTGCTGCAATTAAGTAGTAGAGTGAAGAAACATCTATGATGCTTGT 2137
 :::
 Db 661 MetLeuLeuAlaGlyCysLysLysTyrGlnArgGlyGlnSerIleTyrAspAlaPheVal 680
 QY 2138 ATTACTCAAGCCAGATGAGAGCTGAGTGAAGATGAGCTAGTAAAGAAATTTAGAGAA 2197
 :::
 Db 681 IleTyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGln 700
 QY 2198 GGGTGCCCTCCATTTTCAAGCTGCTGCTTCACTAGAGACTTTATCCCGGTGGCCAT 2257
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 Db 701 GlyValProProPheGlnLeuLysCysLeuHisTyrArgAspPheIleProGlyValAlaIle 720
 QY 2258 GCTGCCAAGATCATCCATGAGGTTTCCATTAAGCCGAAGGTGATGTTGTGTGTGCTCC 2317
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 Db 721 AlaAlaAsnIleIleGlnGlnGlnGlyPheHisLysSerArgLysValIleValValSer 740
 QY 2318 CAGCACTTCATCCAGAGCCGCTGTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAG 2377
 :::
 Db 741 GlnHisPheIleGlnSerArgLysArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGln 760
 QY 2378 TTTCTGAGAGCTGCTGCTGATCATCTTCATCTGCTGCTGAGAGGTGAGAGAGCCCTG 2437
 :::
 Db 761 PheLeuSerSerArgAlaGlyIleIlePheIleValLeuHisLysLeuGlnLysSerLeu 780
 QY 2438 CTCAGCAGCAGAGGTGAGGCTGTACCGCTTCTCAGAGCAACATTAAGCTGAGTGGAGAG 2497
 :::
 Db 781 LeuArgGlnGlnValGlnLeuLysTyrArgLeuLeuAsnArgAsnThrTyrLeuGlnTyrGln 800
 QY 2498 GACAGTGTCTCTGGGGCGGACATCTTCTGAGAGCGATCAAGAAAGCCCTGCTGATGCT 2557
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 Db 801 AspSerValLeuGlnLysArgHisIlePheTyrArgArgLeuArgLysAlaLeuLeuAspGly 820
 QY 2558 AATATCATGAATCCAGAGGAAACA 2581
 :::
 Db 821 LysProTyrSerProAlaGlyThr 828

RESULT 7
 TLR4_BOVIN STANDARD; PRT; 841 AA.
 AC Q9GL5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name-TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guionaud C.T., Dubey C., Jungi T.W.;
 RT "Bovine Toll-like receptor 4 (TLR4)."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 immune response to bacterial lipopolysaccharide (LPS). Acts via
 MyD88, TIRAP and TRAM6, leading to NF-kappa-B activation, cytokine
 secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 multi-protein complex containing at least CD14, LY96 and TLR4.

CC Binds IY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, AF10952, MAG32061.2, -.
 DR HSP, O6603, LFYX.
 DR GO, GO:0046696, C:lipopolysaccharide receptor complex; ISS.
 DR GO, GO:0001530, F:lipopolysaccharide binding; ISS.
 DR GO, GO:0004888, F:transmembrane receptor activity; ISS.
 DR GO, GO:0007250, P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO, GO:0016046, P:detection of fungi; ISS.
 DR GO, GO:0009598, P:detection of pathogenic bacteria; ISS.
 DR GO, GO:0045576, P:macrophage activation; ISS.
 DR GO, GO:0045571, P:negative regulation of osteoclast different. . . ; ISS.
 DR GO, GO:0045562, P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO, GO:0045084, P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO, GO:0045368, P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO, GO:0045410, P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO, GO:0020288, P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611, LRR.
 DR InterPro: IPR000483, LRR_Cterm.
 DR InterPro: IPR003591, LRR_Cterm.
 DR InterPro: IPR00157, TIR.
 DR Pfam: PF00560, LRR_13.
 DR Pfam: PF01463, LRRCT_1.
 DR Pfam: PF01582, TIR_1.
 DR PRINTS, PRO0019, LEURICHRPT.
 DR SMART, SM00369, LRR_TYP_1.
 DR SMART, SM00082, LRRCT_1.
 DR SMART, SM00255, TIR_1.
 DR PROSITE, PS50104, TIR_1.
 KM Glycoprotein; Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 841 Toll-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 841 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 102 124 LRR 3.
 FT REPEAT 149 173 LRR 4.
 FT REPEAT 174 197 LRR 5.
 FT REPEAT 203 225 LRR 6.
 FT REPEAT 277 300 LRR 7.
 FT REPEAT 310 334 LRR 8.
 FT REPEAT 350 372 LRR 9.
 FT REPEAT 373 398 LRR 10.
 FT REPEAT 400 421 LRR 11.
 FT REPEAT 422 445 LRR 12.
 FT REPEAT 446 469 LRR 13.
 FT REPEAT 471 494 LRR 14.
 FT REPEAT 495 518 LRR 15.
 FT REPEAT 520 542 LRR 16.
 FT REPEAT 544 566 LRR 17.
 FT REPEAT 568 592 LRR 18.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 73 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 73 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc . . .) (Potential).

FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 841 AA; 96026 MW; C5B17CB9C798CD16 CR64;
 Alignment Scores:
 Pred. No.: 9, 21e-240 Length: 841
 Score: 3321.50 Matches: 639
 Percent Similarity: 86.41% Conservative: 86
 Best Local Similarity: 76.16% Mismatches: 113
 Query Match: 38.72% Indels: 1
 DB: 1 Gaps: 1
 US-09-396-985B-1 (1-4868) x TIR4_BOVIN (1-841)
 QY 104 ATGATGTCGCTGCGGCTGGGCTGATCCAGCCATGCGCTTCCTGCTGCG 163
 |||||::: |||||
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaLeuIleProAlaIleLeuSerCys 20
 QY 164 GTGAGACCAAAAGCTGGAGCCCTGCGTGAAGTGTCTTATTTACTATCAATG 223
 ::|||
 Db 21 LeuArgThrGluSerThrAspProCysValGlnValProAsnIleSerThrGlnCys 40
 QY 224 ATGAGACGTAATTTCTACAAATCCCGCAACCTCCCTTCAACCAAGACCTGAG 283
 |||||
 Db 41 MetGlnLeuAsnLeuThrGlnIleProAsnIleProIleSerThrIleLeuAsp 60
 QY 284 CTGAGCTTTAATCCCTGAGGACATTAGGACGTATAGCTTTCAGTTTCAGAGACTG 343
 |||||
 Db 61 LeuSerPheAsnThrLeuArgIleGlnIleGlnIleAsnPheSerThrProGluLeu 80
 QY 344 CAGTCTGCTGATTTATTCAGGTGTGAATCCAGACATTTGAAGTGGGCAATTCAGAC 403
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 Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnIleGlnIleAspThrPheGlnGly 100
 QY 404 CTAGAGCACTCTCTACCTTATATTTAGACAGAAACCCATCAGAGTTAGCGCTGAG 463
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 Db 101 LeuAsnIleLeuSerThrLeuIleLeuThrGlnAspProIleIleSerLeuAlaTrpGly 120
 QY 464 GCCTTTTCTGACTATCAAGTTTACAGAGCTGTGCTGTGGAGCAAAATCTAGCATCT 523
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 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThrAsnLeuValSer 140
 QY 524 CTAGAGACTTCCCATTTGAGACTTCGAAATCTTGAAGAACTTATGTGCTCATCAAT 583
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 Db 141 LeuAsnAspPheProIleGlyIleLeuIleValGlnIleValAlaIleAsn 160
 QY 584 CTATCCAACTTTTCAATTAACCTGAGTATTTCTAATCTGACCAATCTAGAGCACTTG 643
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 Db 161 PheIleIleSerPheLeuProGlnIlePheSerAsnLeuProAsnLeuGlnIleVal 180
 QY 644 GACCTTTCAGACCAAGATTCAAGATTTATTTAGCAAGACTTGGCGGTTCTACATCAA 703
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 Db 181 AspLeuSerAsnAsnIleGlnAsnIleThrGlnAspValIleValLeuIleGln 200
 QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGATCTTATGAACTTTATCCACCA 763
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 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 764 GGTGACATTTAAAGAAATTTAGGCTTCAAGCTTGAAGCTTTAAAGAAATTTGATAGTTTA 823
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 Db 221 GlyThrPheLeuGlnIleLeuLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSer 240
 QY 824 AATGTAATGAAATCTGTATTCAGGCTGTGCTGTTAGAGTCCATGCTTGTGTTCTG 883
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 Db 241 HisValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuIleThrAsnArgLeuValLeu 260
 QY 884 GAGAAATTTAGAAATGAGAAATCTTGAAGAAATTTGACAAATCTGCTCTAGAGGCGCTG 943
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 Db 261 GlyGlnPheLeuAsnGlnArgIleGlnArgPheAspArgSerPheLeuGlnGlyLeu 280

QY 944 TCGAATTGACATTTGAGAAATTCGATTAAGTACTTACCTGATGATATT 1003
 Db 281 Cysahneuthrliegluglnphearglilealatyrlneuspyspheserlglyaspa 300
 QY 1004 ATTGACTTATTATTGTTTGAACAATGTTTTCATTTTCCCTGGAGGTGACTATT 1063
 Db 301 Thraspneupheancysleuallaaenvalservallieserleuenserlleseu 320
 QY 1064 GAAAGGTAAGAAGCTTTCTTAATTGCGANTGCAACTTTAGAAATAGTTAATGTT 1123
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 QY 1124 AATTTGACAGTGTCCCATTTGAAATCTCAAACTCTCAAAAGCTTACTTCACTTCC 1183
 Db 341 AspneaplyspheroalaleulyseuserleuylsyphevalphethrAsp 360
 QY 1184 AACAAAGTGGGAAGCTTTTTCAGAAATGATTCACAAAGCTTGAGTTTCTAGATCTC 1243
 Db 361 AsnlyasprlleserThrphethrGluPheglneuproserleuglnlyrleuAspLeu 380
 QY 1244 AGTAAAGTGGCTGATTCGAAAGTGTCTGTTCTCAAGTATTTGGGACAAACGAC 1303
 Db 381 LysArgshnhi sleuserPheulysglyCysCysserthsthraspphegllythrAsn 400
 QY 1304 CTAAGTATTTAGATCTGAGCTTCAATGATGTTATTATTCAGATGAGTTCAACTTCTGGGC 1363
 Db 401 LeuLyhhi sleuaspseuserPhehnaapvalillethrleugllyserhnaPheMetGly 420
 QY 1364 TTGAACAACATAGAACATCTGATTTTCACATTCACAAATTTGAACAATGATGATTT 1423
 Db 421 LeuGlInleuglnhlsleuaspheglnhlseserThrleuylsnglnleaaalape 440
 QY 1424 TCAGTATTCCTATCACTCAACAACTCTATTACTTACATTTCTCATCTACACACAGA 1483
 Db 441 SerAlapheuserleuArgnaenleuArglyrleuaspilleserlyThrAsnillearg 460
 QY 1484 GTTGCTTTCAATGGACCTTCAATGGCTTTCAGAGTCTGCAAGTCTTGAANAATGGCTGC 1543
 Db 461 IlevalPhehlselglyllephethrGlyleuvalSerleuendlnhrleuulyshealagly 480
 QY 1544 AATTTCTTCAGAGAAATCTTCTTCAGATATCTTTCACAGAGTGAACAACTTGACCTTC 1603
 Db 481 AsnserPheglnaenleuLeuProaspillephethrGluLeuThrAsnleuThrVal 500
 QY 1604 CTGAGACTCTCTCAGTGTCACTGAGACATGTTCTTCAACAGCATTTAACTCACTCTCC 1663
 Db 501 LeuaspLeuserlyscysGlnleuGlnvalalaglnhrAlaphehlseserleuser 520
 QY 1664 AGTCTTCAGGTACTAAATATAGCCCAACAACACTTCTTTCATGATGATGTTCTCTTAT 1723
 Db 521 SerleuglnvalleuasnmetSerhlsanlyleuLeuSerleuaspnrPheLeuYr 540
 QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTGATTACAGTCTCAATGACATTAATGACTTCCAA 1783
 Db 541 GluProleuhlseserleuArglileuaspCysSerPhehnaarglleMetAlaserly 560
 QY 1784 AAACAGGAATACAGCATTTTCCAGTAGTCTGCTTTTAACTTACTTCAAGATGAC 1843
 Db 561 GluGlnGlnleuGlnleuasnProargserleuThrTrpLeuasnleuThrGlnAaAla 580
 QY 1844 TTTGCTGTGTAAGTGTGAACACGAGATTTCTGCAATGATGATGACGACGAGGCGCTC 1903
 Db 581 PheAlaCysValaCysgluhslnseuserPheleuglntrpAllyasapglinaGlnleu 600
 QY 1904 TTGGTGAAGTGAACGAATGATGTCAACACTTCAGATTAAGCAGGCGATGCTGTG 1963
 Db 601 LeuValaGlyalaglnGlnmetMetCysAlaGluProleuaspmetGluaspMetProval 620
 QY 1964 CTGAGTTTG---AATATCACTGTCAAGATTAAGAACCATCACTGTGTGTGCTGCTC 2020
 Db 621 LeuSerPheargnaenlathrCysGlnleuSerlyThrIleleSerValserValval 640

QY 2021 AGTGTCTGTAGTACTATCTGTTGAGCAGTCTGCTCTAATAAGTTCTATTATTCACCTGATG 2080
 Db 641 ThrValleuLeuValserValvalGlyValleuValTyrlyserheryrPhehlsleuMet 660
 QY 2081 CTTCTTGCTGGCTGTCATTAAGTATGTTAGAGTGAAGCAATCTATGATGCTTTGTTATC 2140
 Db 661 LeuLeuAlaglyCyslyserlyrGlyArgGlyGlnserllelyrAspAlaphevalille 680
 QY 2141 TACTCAAGCAGATGAGACCTGGGTAAAGAAAGTACTGTAAGAATTTAAGAAGAAGG 2200
 Db 681 TyrSerSerGlnaspGlnaspnrIpaValArgshnleuVallyasnleuGlnGly 700
 QY 2201 GTGCTTCATTTGAGCTCTGCTTCACTACAGAGACTTTATTCGCGGTGGCATTGCT 2260
 Db 701 ValProProPhehlnleuCyseuwhlseryrArgAspPhehlerProGlyValAlaIleAla 720
 QY 2261 GCCAATCATTCATGAAAGTTTCCATTAAGCCGAAGGTGATTTGTTGTGCTCCAG 2320
 Db 721 AlaasnilleleGlnleuglnPhehlsyserArglyeValilleValValserGln 740
 QY 2321 CACTCATCAAGACCGCTGGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTT 2380
 Db 741 HisPheillelnserArgtrpCysllephelGlyrGlnleuAlaglnhrtrpGlnPhe 760
 QY 2381 CTGAGCAGTGTGCTGTTATCATCTTCATTGTCTTCAGAGAGTGAAGACCTGCTC 2440
 Db 761 LeuSerSerArgAlaelylillellePheillevalleuglnhlyseuulysserleuLeu 780
 QY 2441 AGGACGACGTGAGCTGTACCGCTTCTCAAGCAGAAACATTTACCTGAGTGGAGAGAC 2500
 Db 781 ArgGlnGlnValaGlnleuTyrArgleuLeuSerArgAsnthrlyrleuGlntrpGluasp 800
 QY 2501 AGTGTCTGTGGGGGAGACATCTTCTGAGACACATCAAGAAAGCCCTGCTGATGCTTAA 2560
 Db 801 SerValleuglnArgghlsvalPheItrpArgArgleuArglyvalaleuLeuAlaglylys 820
 QY 2561 TCATGGAATTCAGAAAGAACAGTGGGTACAGATGCAATTTGAGAGAACACATCT 2617
 Db 821 ProGlnSerProGlnGlyThrAlaapAlaGlnThrAsnProGlnlnuAlathrThr 839

RESULT 8
 Q88055 PRELIMINARY; PRT; 841 AA.
 AC Q88055;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 AC Ito T., Morimatsu M.,
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056444; BAB86840.1; -.
 DR HSSP; 060603; 1077.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0003958; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macr cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.

QY 1904 TTGGTGAAGTTGAACCAATGATGCAACCTTCAGATTAAGCAGGCGATCCTGTG 1963
 Db 601 LeuValGlyValGluGlnMetMetCysAlaGlnProLeuaspMetGluAspMetProVal 620
 QY 1964 CTGAGTTG--AATATCACCTGTGCAGATGAATTAAGCAATCATTTGGTGTGCGCTC 2020
 Db 621 LeuSerPheArgAsnAlaThrCysGlnLeuSerCysThrIleIleSerValSerValVal 640
 QY 2021 AGTGTGCTTGAATGATGTTGTGAGCATTCCTGCTATAGTCTTATTTTTCCTGATG 2080
 Db 641 ThrValLeuLeuValSerValValGlyValLeuValIlyrCysPheIlyrPheHisLeuMet 660
 QY 2081 CTTCTTGCTGCTGCATATAAGTATGATGAGTGTAAGAAACATCTATGATGCTTGTATATC 2140
 Db 661 LeuLeuValIleCysIlyrCysIlyrGlyIlyrGlyIlyrSerIleIlyrAspAlaPheValIle 680
 QY 2141 TACTCAAGCCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2200
 Db 681 TysSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValIlyrAsnLeuGlnGlnGly 700
 QY 2201 GTGCTTCATTTTCAAGCTCTGCTCTCTCACTACAGAGACTTTATCCCGGTGCGCATTTGCT 2260
 Db 701 ValProProPheGlnLeuCysLeuHisIlyrArgAspPheIleProGlyValAlaIleAla 720
 QY 2261 GCCAATCATTCATGAAAGTTTCCATTAAGCCGAAAGGATGTTGTGTGCTGCCAG 2320
 Db 721 AlaAsnIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 740
 QY 2321 CACTTCATCCAGAGCCGCTGCTGATCTTGAATATGATGATGCTCAACCTGCGAGTTT 2380
 Db 741 HisPheIleGlnSerArgIlyrCysIlePheGlnIlyrGlnIleAlaGlnIlyrTrpGlnPhe 760
 QY 2381 CTGAGAGTGTGTGTGTATCATCTTATGTTCTCTGAGAGAGTGAGAGAGAGAGAGAGAG 2440
 Db 761 LeuSerSerArgIlyrIleIlePheIleValLeuGlnIlyrSerLeuLeu 780
 QY 2441 AGCAGAGAGTGAGCTGTACCGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2500
 Db 781 ArgGlnGlnValGlnLeuIlyrArgLeuLeuSerArgAsnThrIlyrLeuGlnIlyrGlnAsp 800
 QY 2501 AGTGTCTGAGCGGAGCATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2560
 Db 801 SerValLeuGlnIlyrArgHisValPheTrpArgArgLeuArgIlyrAlaLeuValIleGlyLys 820
 QY 2561 TCATGCAATCCAG 2617
 Db 821 ProGlnSerProGlnIlyrThrAlaAspAlaGlnIlyrAsnProGlnIlyrAlaThrThr 839

RESULT 9
 O6WCD5 PRELIMINARY; PRT; 841 AA.
 AC O6WCD5; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2833971; PubMed=12915733; DOI=10.1073/pnas.13339571100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.B.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 RT prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL; AY297040; AA062700.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_CysC.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 12.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00365; LRR_SD2; 6.
 DR SMART; SM00369; LRR_TYP; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;

Alignment Scores:
 Pred. No.: 2,18e-239 Length: 841
 Score: 3316.50 Matches: 638
 Percent Similarity: 86.29% Conservative: 86
 Best Local Similarity: 76.04% Mismatches: 114
 Query Match: 38.66% Indels: 1
 DB: 2 Gaps: 1

US-09-396-985b-1 (1-4868) x O6WCD5 (1-841)

QY 104 ATATGTCGCTCGCGGCTGAGCTGTATCCAGCCATGCGCTTCTCTCTG 163
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
 QY 164 GTGAGACCAAGAGCTGGAGCGCTGAGAGAGTGTCTTATTTACTTATCAATGC 223
 Db 21 LeuArgThrGlnSerThrPheProCysValGlnValAlaProAsnIleSerIlyrGlnCys 40
 QY 224 ATGAGAGTGAATTTCTACAAATCCCGACCAACCTCCCTTCAACCAAGAGCTGAG 283
 Db 41 MetGlnLeuAsnLeuIlyrIlyrIleProAspAsnIleProIleSerThrIlyrMetLeuAsp 60
 QY 284 CTGAGCTTATATCCCTGAGAGCATTTAGAGAGATTAAGCTTCTTCAAGTTCAGAGACTG 343
 Db 61 LeuSerPheAsnIlyrLeuArgIlyrIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 QY 344 CAGTGTGATTTATCCAGGTGTGAATCCAGAGCAATGAAGATGGGATATCAAGAGC 403
 Db 81 GlnValLeuAspLeuSerIlyrCysGlnIlyrIleIleLeuIlyrAspThrPheGlnGly 100
 QY 404 CTAGCCACCTCTCTCACTTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
 Db 101 LeuAsnHisLeuSerThrIleuIleuThrGlnAspProIleIleSerIleuAlaIlyrGly 120
 QY 464 GCCTTTTGTGACTATCAAGATTTACAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAG 523
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIlyrLeuValAlaValGlnThrAsnLeuValSer 140
 QY 524 CTGAGAGACTCCCATTTGAG 583
 Db 141 LeuAsnAspPheProIleGlyHisLeuIlyrAsnLeuIlyrSerLeuValAlaHisAsn 160
 QY 584 CTATCAATCACTTTCAATTAATCTGAGTATTTTCTAATCTGAGAGAGAGAGAGAGAG 643
 Db 161 PheIleHisSerPheIlyrLeuProGlnIlyrPheSerAsnLeuProAsnLeuGlnHisLeu 180
 QY 644 GACCTTTCAG 703
 Db 181 AspLeuSerAsnAsnIlyrIleGlnAsnIleIlyrGlyAlaAspAlaIlyrValLeuHisGln 200
 QY 704 ATGCGCTCTCAATCTCTTATGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 764 GGTGATTTAAAGAAATTAGAGCTTCAAGCTGATTAAGAAATTAATTTGATAGTTTA 823

Db 221 GlyThrPheIysGluIleuIeysIleuAsnGlyLeuThrIleuArgSerAsnPheAsnSerSer 240
 QY 824 AATGTAATGAAGAACTGTATTCAGAGCTGGCTGGTTAGAACTCATCGTTTGGCTTCG 883
 Db 241 HisValMetLeuThrCysIleGlnGlyLeuValagIleuIysThrAsnArgLeuValLeu 260
 QY 884 GGAGAAATTTAGAAATGAAGAACTTGAAGAACTTGAACAATCTCTCTAGAGGCTTCG 943
 Db 261 GlyGluPheIysAsnGluArgIysIleuGlnArgPheAsnArgSerPheIleuGlnGlyLeu 280
 QY 944 TGCATATTGACCAATTGAGAAATTCGATTCATCTAGACTACTACTCGATGATATT 1003
 Db 281 CysAsnLeuThrIleGlnGlnPheArgIleAlaTyrIleuAsnArgIysPheSerGlyAspAsp 300
 QY 1004 ATTGACTTATTTATGTTTGAACAATGTTTCTTCATTTTCCCTGGAGAGTGCATATT 1063
 Db 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerIleuSerIleSerLeu 320
 QY 1064 GAAAGGGTAAAGACTTTTCTTATTAATTTGCGATGCGAACATTTAGAACTTAACTGT 1123
 Db 321 GlySerIleuGlnAlaIleuLeuIysAspPheArgTrpGlnHisIleuGlnIleIleAsnCys 340
 QY 1124 AAATTTGACAGTTTCCCATTCATGAACTGCAAACTCTCAAAAGCTTACTTCACTTCC 1183
 Db 341 AspPheAsnArgIysPheProAlaIleuIysLeuSerSerIleuIysPheValPheThrAsp 360
 QY 1184 AAGAAAGTGGGAATGCTTTTTCAGAAAGTGAATCTACCAAGCTTGAATTTCTAGATCTC 1243
 Db 361 AsnIlyAsnArgIleSerThrPheThrGlnPheGlnLeuProSerIleuGlnIlyIleAsnArg 380
 QY 1244 AGTAGAAATGGCTTGAGTTTCAAGGCTGCTGTTCTCAAGATTTTGGAGCAACAGC 1303
 Db 381 LysArgAsnHisIleuSerPheIysGlyCysCysSerHisThrAsnArgPheGlyThrThrAsn 400
 QY 1304 CTAACTATTATGATCTGAGCTTCAATGCTGTTATTCATCAATGAGTTCAAACTTCTGGGC 1363
 Db 401 LeuIlyHisIleuAsnArgPheAsnArgValIleThrIleuGlySerAsnPheMetGly 420
 QY 1364 TTGGAACAATAGAACCTCGATTTCCAGACTTCCCAATTCGAAAGAAAGATGAGTTT 1423
 Db 421 LeuGlnGlnIleuGlnHisIleuAsnArgPheGlnHisSerThrIleuIysGlnIleAsnAlaPhe 440
 QY 1424 TCAGATTTCTTATCTACCTCAGAAACCTCATTTACCTTGACATTTCTCATCTACACACGA 1483
 Db 441 SerAlaPheIleuSerIleuArgAsnLeuArgTyrIleuAsnArgIleSerTyrThrAsnIleArg 460
 QY 1484 GTTGCTTTCAATGAGCATCTTCAATGCTTTCAGAGTCTGCAAGCTTTGAAATGGCTGAC 1543
 Db 461 IleValPheHisGlyIlePheThrGlyLeuValSerIleuGlnThrIleuIysMetAlaGly 480
 QY 1544 AATTTCTTCCAGGAAAACTTCCCTCCAGATTCCTTCACAGAGCTGAGAAACTTGACCTTC 1603
 Db 481 AsnSerPheGlnHisAsnHisIleuLeuProAspIlePheThrGlnLeuThrAsnLeuThrVal 500
 QY 1604 CTGAGACTCTCTCAGTGTCAATGAGCAGTGTTCACAGATTTAACTCACTCTCC 1663
 Db 501 LeuAsnLeuSerIysCysGlnIleuGlnValAlaGlnThrAlaPheHisSerLeuSer 520
 QY 1664 AGTCTTCAAGTACTAATATAGACCAACAACACTTCTTTTCATGTGATGAGTTTCTTAT 1723
 Db 521 SerIleuGlnValIleuAsnMetSerHisAsnIlyLeuIleuSerIleuAsnArgPheLeuTyr 540
 QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTCAGTCTCAATCACAATAGACTTCCAA 1783
 Db 541 GluProIleuHisSerIleuArgIleLeuAspCysSerPheAsnArgIleMetAlaSerLys 560
 QY 1784 AAACAGGAATCAGACATTTTCCAAAGTACGTGACTTCTTAATCTTACTCAGAAATGAC 1843
 Db 561 GlnGlnGlnIleuGlnHisIleuLeuProArgSerIleuThrTrpIleuAsnIleuThrGlnHisAla 580
 QY 1844 TTGGCTTGTACTTGTGAACCAAGATTTCTTCGAATGATCAAGCAACAGAGCAGCTC 1903
 Db 581 PheAlaCysValCysGlnHisGlnSerPheIleuGlnTrpValIysAsnArgIleGlnIleu 600

QY 1904 TTGGTGAAGTGAACGAATGGAATGTGCAACACCTTCAGATTAAGCAGGCGATGCTGTG 1963
 Db 601 LeuValGlyAlaGlnIleuMetCysAlaGluProLeuAsnMetGlnAsnMetProVal 620
 QY 1964 CTGAGTTTG---AATATCACCTGTGAGATGAATGAACCATTCATTTGGTGTGCTCTC 2020
 Db 621 LeuSerPheArgAsnAlaThrCysGlnIleuSerLysThrIleIleSerValSerValVal 640
 QY 2021 AGTGTGCTGTAGTATCTGTGTAGCAGCTTCGTGCTTAATACTTCATTTTCACTGAG 2080
 Db 641 ThrValLeuLeuValSerValAlaGlyValLeuValTyrLysPheTyrPheHisIleuMet 660
 QY 2081 CTTCCTGCTGCTGTCATAAAGTATGAGTGAAGGTAAGAAACATCATGATGCTTGTATTC 2140
 Db 661 LeuIleuAlaGlyCysAlaYelYsTyrGlyArgIysGlyIleuSerThrTyrAsnAlaPheValIle 680
 QY 2141 TACTCAAGCCAGATGAGGACTGGTAAAGAAATGAGCTAGTAAAGATTTAGAAAGAGG 2200
 Db 681 TyrSerSerGlnAsnArgIleuArgValAlaArgAsnGlnIleuValIysAsnIleuGlnGly 700
 QY 2201 GTGCTTCATTTCACTGCTGCTCTCACTACAGAGACTTATTCCTCGGTGTGCGCATTTGT 2260
 Db 701 ValProPheGlnIleuCysIleuHisTyrArgAsnArgPheIleProGlyValAlaIleAla 720
 QY 2261 GCCAATCATCATGAAGGTTTCCATTAAGACCCGAAAGGATGTTGTGGGTGCCAG 2320
 Db 721 AlaAsnIleIleGlnIleuGlyPheHisIlySerAsnArgValIleValValIleSerGln 740
 QY 2321 CACTTCATCAGAGCCGCTGTGTATCTTGAATATGAGATTTGCTCAGACTGCGAGTTT 2380
 Db 741 HisPheIleGlnSerArgTrpCysIlePheGlnIlyTyrGlnIleAlaGlnThrTrpGlnPhe 760
 QY 2381 CTGAGCAGTCTGCTGTGATCATCTTCATTTGCTTCGAGAAAGTGAAGAACCTCTGCTC 2440
 Db 761 LeuSerSerArgAlaGlyIleIlePheIleValIleuGlnIlySerIleuIysSerIleuLeu 780
 QY 2441 AGCAGCAGATGAGGAGCTGTACCGCTTCCAGAGAGAAACATTAACCTGAGTGGAGAGAC 2500
 Db 781 ArgGlnGlnValGlnIleuTyrArgIleuLeuSerHisAsnThrTyrIleuGlnTrpGlnAsp 800
 QY 2501 AGTGTCTGCGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCCTGTGATGCTGATAA 2560
 Db 801 SerValIleuGlyArgHisValPheTrpArgArgLeuArgValAlaIleuLeuAlaGlyLys 820
 QY 2561 TCATGGAATCCAGAAAGAAACAGTGGGTACAGATGCATTTGGCAGGAACAACATCT 2617
 Db 821 ProGlnSerProGlnGlyThrAlaAsnArgIleuThrAsnProGlnGlnIleuAlaThrThr 839
 RESULT 10
 TIR4_FELCA STANDARD; PRT; 833 AA.
 ID TIR4_FELCA
 AC P58727;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TIR4;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN NCBI_TaxID=9685;
 RP SEQUENCE FROM N.A.
 RA Yoshioka N., Kano R.;
 RT "Felis catus Toll like receptor 4.",
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -i- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -i- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIR4.

CC Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
 CC -- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/announce/](http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB060687; BAB3947.1; -.
 DR HSP; O60603; 1PYX.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0045576; P:macrophage activation; ISS.
 DR GO; GO:0045571; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR InterPro: IPR001577; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYF; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KM Glycoprotein; Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT CHAIN 1 833 Potential.
 FT DOMAIN 24 632 Toll-like receptor 4.
 FT TRANSMEM 633 653 Extracellular (Potential).
 FT DOMAIN 654 833 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.
 FT REPEAT 310 334 LRR 9.
 FT REPEAT 350 372 LRR 10.
 FT REPEAT 373 398 LRR 11.
 FT REPEAT 399 421 LRR 12.
 FT REPEAT 422 445 LRR 13.
 FT REPEAT 447 469 LRR 14.
 FT REPEAT 470 494 LRR 15.
 FT REPEAT 495 518 LRR 16.
 FT REPEAT 520 542 LRR 17.
 FT REPEAT 544 566 LRR 18.
 FT REPEAT 568 592 LRR 19.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 570 570 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 833 AA; 95592 MW; 3E3A84F2BB8A55EA CRC64;
 Alignment Scores:
 Pred. No.: 3,65e-239 Length: 833
 Score: 3313.50 Matches: 637
 Percent Similarity: 87.53% Conservative: 86
 Best Local Similarity: 77.12% Mismatches: 102
 Query Match: 38.62% Indels: 1
 DB: 1 Gaps: 1
 US-09-396-985B-1 (1-4868) x TLR4_FELCA (1-833)
 QY 104 ATGATGTCGCTCGGCGCTGGGAGCTGTGATCCAGCATGGCCCTTCCTCTG 163
 Db 1 MetMetProProThrArgLeuAlaGlyThrLeuLeuLeuProAlaMetAlaPheLeuSerCys 20
 QY 164 GTGAGACGAGAAAGCTGGAGCCCTGCTGGAGGTGCTTCAATATTAATCAATGC 223
 Db 21 LeuArgProGluSerThrPaspProCysValGluValAlaProbeniLeThrTyGlnGly 40
 QY 224 ATGAGACTGAATTTCTACAAAATCCCGGACACCTCCCTTCACACCAAGACCTGAC 283
 Db 41 MetAspLeuAsnLeuMetIleCysIleProAspAsnIleProSerSerThrIysAspLeuAsp 60
 QY 284 CTGAGCTTAATCCCTGAGGAGCTTAGGAGGATGATGCTTCAATTCAGATTCGAGAACTG 343
 Db 61 MetSerPheAsnProLeuArgPheLeuGlnGlySerHisSerPheSerAsnPheProGluLeu 80
 QY 344 CAGGTGCTGATTTATTCAGGTGTGAATTCAGACAAATTGAAGTGGGCAATTCAGAGC 403
 Db 81 GluValLeuAspPheLeuSerArgCysGluIleGlnIleIleGluAspAspAlaTyGlnGly 100
 QY 404 CTAGACCACTCTCTACCTTAATATTCAGACGAAACCCATCCAGATTAGCCCTGGGA 463
 Db 101 LeuAsnHisLeuSerIleLeuIleLeuThrGlyAsnProIleGlnArgLeuPheProGly 120
 QY 464 GCCTTTTCGAGCTATCAAGTTATGACAGAGCTGTGCTGTGGAGCAATCTAGACATCT 523
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGluThrAsnIleAlaSer 140
 QY 524 CTAGAGCACTCCCAATGAGATCTCAAACTTTGAAGAACTTAATGCTGCTCAAT 583
 Db 141 LeuGluAspPheProIleGlyHisLeuGlyThrLeuGlyGluLeuAsnValAlaHisAsn 160
 QY 584 CTATTCGAATCTTCAATTAATCTGAGTATTTTCTCAATCTGACCAATCTAGACACTG 643
 Db 161 LeuIleHisSerPheLeuSerProGlyIlyPheSerAsnMetSerAsnLeuGlyTyLeu 180
 QY 644 GACCTTCGAGCAAGAGATTCAGAAATTAATTTGACAGAGCTGTGGGGTTCACATCA 703
 Db 181 AspLeuSerAsnAsnIleGlnAsnIleTyHisLeuAspLeuGlnValLeuHisGln 200
 QY 704 ATGCCCTACTCAATCTCTTTAGACTGTCCCTGATCTGAATCTTAATCTTATCAACCA 763
 Db 201 LysProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAsnPheIleGlnPro 220
 QY 764 GGTGCACTTTAAGAATTAAGCTTCAAGCTGACCTTTAAGAATTAATTTGATAGTTTA 823
 Db 221 GlyAlaPheLeuGluValIysLeuArgGluLeuThrLeuArgSerAsnPheAsnSerThr 240
 QY 824 AATGTAATGAAGAACTGTATTAAGGTCTGGCTGTGATGAAGTCATGATGTTGGTTCG 883
 Db 241 AspValMetCysLeuAlaSerIleGlnGlyLeuAlaGlyLeuGlnIleHisGlnLeuValIleu 260
 QY 884 GGAGATTTTGAAGATGAAGAACTTGAAAAGTTTGACAAATCTGCTAGAGGCTTG 943
 Db 884 |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||

Db 261 GYGLVPhelysAngluArgAsnLeuGlyArgPheAspIysSerIleLeuGluGlyLeu 280
 QY 944 TGGAAATTGACATTCAGAAATTCGAGATTAGCACTAGTACACTACCGATGATATT 1003
 Db 281 CysAsnLeuIleIleGluYsPheArgIleAlaTyPheAspYsPheSerGluAspAla 300
 QY 1004 ATTGACTTATTTAATTGTTGACAAATGTTCTTCATTTTCCCTGGAGTGTACTATT 1063
 Db 301 IleAspSerPheAsnCysLeuAlaAsnValSerThrIleSerLeuValHisLeuTyPhe 320
 QY 1064 GAAAGGCTAAAGACTTTTCTTATTTGCGATGGCAGACTTTAGATTAGTTAACTGT 1123
 Db 321 TySGlyLeuYsGlnLeuProYsAsnLeuGlyTyTrpGlnArgLeuGlnLeuValAsnCys 340
 QY 1124 AAATTTGGACAGTTTCCACATTCGAAATCTCTCAAAAGGGCTTACTTCACTGTC 1183
 Db 341 GluPheGluGlnPheProIleTrpYsLeuAspProLeuYsGlnLeuValPheSerAla 360
 QY 1184 AACAAAGTGGGAATGCTTTTTCAGAAATGATCTCAACAGCTTGATTTCTAGATCTC 1243
 Db 361 AsnGluValArgAsnAlaPheThrGlnValTyLeuGlnSerLeuGlnPheLeuAspLeu 380
 QY 1244 AGTAGAAATGGCTTGAGTTCAAAGGTGCTGTTCTCAAGATGATTTGGAGACACCAGC 1303
 Db 381 SerArgAsnAspPheSerLeuYsSerCysSerGlnArgAspLeuGlyTyThrTrpArg 400
 QY 1304 CTAAAGATTTAGATGCTGAGCTTCAATGCTGATTAACATGATGATTTCAAACTTCTGGGC 1363
 Db 401 LeuYsHisIleuAspLeuSerPheAsnAlaIleThrIleSerSerAsnPheLeuGly 420
 QY 1364 TTGAACAATGACATGATCTGATTTCCAGACTTCCAAATTTGAAACAATGATGATTT 1423
 Db 421 LeuGlnGlnLeuGlnTyLeuAspPheGlnHisSerSerLeuYsGlnValSerAspPhe 440
 QY 1424 TCGATATCTTATCACTGACAAACCTCATTTACCTTGACATTTCTCATCTACACACCA 1483
 Db 441 SerValPheLeuProLeuYsAsnLeuArgTyLeuAspIleSerTyThrHisIleTrpGln 460
 QY 1484 GTTGCTTTCAATGAGCATCTTCAATGGCTTGTCCAGTGTGAGAGCTTGAAATGGCTGGC 1543
 Db 461 ValAlaPheHisGlyIlePheAsnGlyLeuIleSerLeuGlnIleLeuYsMetAlaGly 480
 QY 1544 AATTTCTTCCAGAAAACTTCTCCAGATATCTTCCAGAGCTGAGAAACTTGACCTTC 1603
 Db 481 AsnSerPheGlnAspAsnPheLeuProAsnIlePheMetGluLeuThrAsnLeuThrIle 500
 QY 1604 CTGGACCTCTCTCACTGATCACTGAGACAGTTGTCTCAACAGACTTTAACTCACTCTCC 1663
 Db 501 LeuAspLeuSerAspCysGlnLeuGlnValSerGlnValAlaPheAsnSerLeuPro 520
 QY 1664 AGTCTTCAAGTACTAATATAGACACACAACTTTCTTCAATGATGATGATGATGCTTAT 1723
 Db 521 TyLeuGlnIleuLeuAsnMetSerHisAsnHisIleuLeuSerLeuAspTrpLeuProTy 540
 QY 1724 AAGTGTGGAATCCCTCCAGGTTCTTGATTAACAGTCAATCAATCAATGACTTCCAA 1783
 Db 541 GluProLeuHisSerLeuGlnIleThrLeuAspCysSerPheAsnArgIleValAlaSerTy 560
 QY 1784 AAACAGGAATCAGCACTTTTCCAGATGATCTGACTTTTAACTTACTCAGATGAC 1843
 Db 561 GlnGlnGlnLeuArgHisPheProSerAsnLeuSerSerLeuAsnLeuThrArgAsnAsp 580
 QY 1844 TTGGCTTGATCTTGAGAACACAGAGTTTCTGCAATGATGATGATGATGATGATGATG 1903
 Db 581 PheAlaCysValCysGlnHisGlnSerPheLeuGlnIleTrpValYsAspGlnHisGlnLeu 600
 QY 1904 TTGGTGAAGTTGAACGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1963
 Db 601 LeuValGlnValGlnGlnMetValCysAlaTyPheProLeuAspMetGlnGlyMetPromet 620
 QY 1964 CTGAGTTTG---AATATCACTGTGATGATGATGATGATGATGATGATGATGATGATG 2020
 Db 621 LeuAsnPheArgAsnAlaThrCysGlnValArgYsThrIleIleThrGlySerValPhe 640

QY 2021 AGTGTGCTGTAGTATCTGTTGTAGACAGTTCTGTCTTAAGTTCTATTTTCACTGATG 2080
 Db 641 ThrValLeuLeuValPheLeuValValValLeuValTyTyLeuPheTyPheHisLeuMet 660
 QY 2081 CTTTCTTGTGCTGCTGCAATAAGATGATGATGATGATGATGATGATGATGATGATGATG 2140
 Db 661 LeuLeuAlaGlyCysTyLeuSerTySerArgGlyGlnSerThrTyTrpAspAlaPheValIle 680
 QY 2141 TACTAAGCAGAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2200
 Db 681 TySerSerGlnAspGlnAspTrpValArgAsnGlnLeuValTyAsnLeuGlnGly 700
 QY 2201 GTGGCTTCATTTCACTGCTGCTTCACTACAGAGACTTTATTCGCGTGTGCGCATGCT 2260
 Db 701 ValProProPheGlnLeuCysLeuHisIleTyArgAspPheIleProGlyAlaIleAla 720
 QY 2261 GCCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2320
 Db 721 AlaAsnIleIleGlnGlnGlnTyPheHisTySerArgTyValIleValValSerGln 740
 QY 2321 CACTTCATGACAGCGCGTGTGATCTTGAATATGAGATTGCTCAGACCTGAGAGTTT 2380
 Db 741 HisPheIleGlnSerArgTrpCysIlePheGlnTyGlyIleAlaGlnThrTrpGlnPhe 760
 QY 2381 CTGAGCAGTGTGCTGTATCATCTTCAATTTGCTGCGAGAGATGATGATGATGATGATG 2440
 Db 761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnTyLeuGlnTySerLeuLeu 780
 QY 2441 AGCAGCAGGTGAGTGTGATCGCTTCTCAGCAGGAGACATTTACTGAGTGGAGGAC 2500
 Db 781 ArgGlnGlnValGlnLeuTyArgTyArgLeuAsnAlaArgAsnThrTyLeuGlnTyTrpGlnAsp 800
 QY 2501 AGTGTGCTGTGCGGAGACATCTTCTGAGAGACGACTCAGAAAGCCCTGATGATGATA 2560
 Db 801 SerValLeuGlyArgHisIlePheTrpArgArgLeuArgValAlaLeuLeuAspGlyYs 820
 QY 2561 TCATGGAATCCAGAAAGA 2578
 Db 821 ProArgCysProGlnGly 826

RESULT 11
 Q6MCD4 PRELIMINARY; PRT; 841 AA.
 ID Q6MCD4;
 AC Q6MCD4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369 (2003).
 DR EMBL: AY297043; AAO62701.1; -;
 DR EMBL: AY297041; AAO62701.1; JOINED.
 DR EMBL: AY297042; AAO62701.1; JOINED.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003885; LRR_Cyst.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR00157; TIR.
 DR Pfam: PF01463; LRRCT; 1.


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|||||
Db      621 LeuSerPheArgSerAlaThrCysGlnLeuSerIleThrIleLeuSerValSerVal 640
|||
Qy      2021 AGAGTGGTGTAGATGATGTTGTTAGACAGTTCGTGCTATAGTTCATTTTCCCGG 2080
|||
Db      641 ThrValLeuLeuValSerValValGlyValLeuValTyrIleGlySerPheHisLeuMet 660
|||
Qy      2081 CTCTTGTGCTGCATGATTAAGTATGAGTGAAGTGAACATCTATGATGCTTGTATTC 2140
|||
Db      661 LeuLeuAlaGlyCysIleValTyrGlyArgGlyGlnSerIleTyrAspAlaPheValIle 680
|||
Qy      2141 TACTCAAGCCAGATGAGAGCTGGGTAAAGATGAGTCTATGAATTAAGAAAGAGG 2200
|||
Db      681 TyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValIleAsnLeuGlnGly 700
|||
Qy      2201 GTGCTCCATTTAGAGCTGCTGCTCTCTAGAGAGCTTTATCCCGTGGGCACTTGC 2260
|||
Db      701 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
|||
Qy      2261 GCCAATCATCATGATGAGGTTTCCATTAAGCCGAAGGATGATGTTGTTGTTGCCAG 2320
|||
Db      721 AlaAsnIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 740
|||
Qy      2321 CACTTCATCCAGAGCGCTGTGTATCTTGAATGATGATGATGATGATGATGATGATG 2380
|||
Db      741 HisPheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPhe 760
|||
Qy      2381 CTGAGAGCTGCTGCTGATCATCTTCATGCTGCTGAGAGAGGATGAGAGAGCCCTGC 2440
|||
Db      761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValLeuGlnIleValLeu 780
|||
Qy      2441 AGGACAGAGGTGAGCTGTACCGCTTCTCAGAGAGAACTTAACTGAGTGGAGAGAC 2500
|||
Db      781 ArgGlnGlnAlaGlnLeuTyrArgGlnLeuSerArgAsnThrTyrLeuGlnTyrGlnLeu 800
|||
Qy      2501 AGTGTCTGGGGGCGCATCTTCTGAGAGAGCTCAGAAAGCCCTGCTGATGTTAA 2560
|||
Db      801 SerValLeuGlyArgIleValPheTyrArgGlnLeuArgIleValLeuAlaGlyIle 820
|||
Qy      2561 TCATGGAATCCAGAGAGAGAGGAGTGCATGATGAGAGAGAGAGAGAGATCT 2617
|||
Db      821 ProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnAlaThrThr 839
|||
RESULT 12
TLR4_PIG STANDARD; PRT; 841 AA.
ID TLR4_PIG
AC Q68Y56;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Alveolus;
RA Shinkai H.; Uemishi H.;
RL "The function of porcine TLR4 gene."
RT Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.

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CC -1- SIMILARITY: Contains 1 TIR domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL, AB188301, BMD36843.1, -.
DR PROSITE, PS50104, TIR, 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 841
FT DOMAIN 24 632
FT TRANSMEM 633 653
FT DOMAIN 654 841
FT REPEAT 53 76
FT REPEAT 77 100
FT REPEAT 102 124
FT REPEAT 149 173
FT REPEAT 174 197
FT REPEAT 203 225
FT REPEAT 277 300
FT REPEAT 310 334
FT REPEAT 350 372
FT REPEAT 373 398
FT REPEAT 400 421
FT REPEAT 422 445
FT REPEAT 446 469
FT REPEAT 471 494
FT REPEAT 495 518
FT REPEAT 520 542
FT REPEAT 544 566
FT REPEAT 568 592
FT DOMAIN 673 819
FT CARBOHYD 35 35
FT CARBOHYD 205 205
FT CARBOHYD 238 238
FT CARBOHYD 282 282
FT CARBOHYD 309 309
FT CARBOHYD 526 526
FT CARBOHYD 575 575
FT CARBOHYD 625 625
SQ SEQUENCE 841 AA; 96308 MW; C52B2622D1C0E253 CRC64;

Alignment Scores:
Pred. No.: 1,79e-230
Score: 3197.50
Percent Similarity: 84.03%
Best Local Similarity: 73.06%
Query Match: 37.27%
DB: 1
Gaps: 1

US-09-396-985b-1 (1-4868) x TLR4_PIG (1-841)
Qy 104 ATGATGTCGCTCGCGCTGCGCTGAGCTGATCCAGCACTGCGCTTCTCTGCG 163
|||
Db 1 MetIleProArgIleArgLeuAlaValAlaThrIleProAlaMetValaPheLeuSerCys 20
|||
Qy 164 GTGAGACGAGAAAGCTGGAGCCCGTGGAGGGTCCATATATTCTATCAATGCG 223
|||
Db 21 LeuArgSerGlnSerTyrAspProCysValGlnValValProAsnIleSerTyrGlnCys 40
|||
Qy 224 ATGAGAGCTGAATTTCTACAAATCCCGCAACTCCCTTCTCAGCAACCAAGACTGAG 283
|||
Db 41 MetGlnLeuAsnPheTyrIleProAspAsnIleProThrSerValIleLeuAsp 60
|||
Qy 284 CTGAGCTTTAATCCCTGAGCAATTTAGGACGCTATAGCTTTTCCAGTTCCAGACTG 343
|||
Db 61 LeuSerPheAsnTyrLeuSerHisLeuAspSerAsnSerPheSerPheProGlnLeu 80

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Db      801 SerValleuGlYrghIstIlePheTPrGArgLeuYsAlaleuLeuAbpGlyLys 820
QY      2561 TCATGGAATCCAGAAAGAACAGTGGTACAGATGCAATTTGGACAGAGAACATCT 2617
Db      821 ProTrpSerProGluGlyThrGluAepSerGluSerAsnGlnHisAspThrThrAla 839

RESULT 13
Q8MIQ2 PRELIMINARY; PRT; 839 AA.
ID      Q8MIQ2
AC      Q8MIQ2;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Toll-like receptor 4.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SQUENCE FROM N.A.
RA      Kajikawa O., Frevert C.W., Goodman R.B., Wong V.A., Martin T.R.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ101394; AAM50060.1; -.
DR      HSSP; O60603; 1077.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR      InterPro; IPR001611; IRR.
DR      InterPro; IPR000483; IRR_Cterm.
DR      InterPro; IPR003591; IRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF00560; LRR_1; 11.
DR      Pfam; PF01582; TIR_1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRCT_1.
DR      SMART; SM00369; LRR_Typ; 1.
DR      SMART; SM00255; TIR_1.
DR      PROSITE; PSS0104; TIR; 1.
KM      Receptor.
SQ      SEQUENCE 839 AA; 96338 MW; 09F7D401ECC1456A CRC64;

Alignment Scores:
Pred. No.: 2,336-223 Length: 839
Score: 3102.50 Matches: 611
Percent Similarity: 82.64% Conservative: 84
Best Local Similarity: 72.65% Mismatches: 141
Query Match: 36.16% Indels: 5
DB: 2 Gaps: 3

US-09-396-985b-1 (1-4868) x Q8MIQ2 (1-839)
QY      104 ATATATGTGCTCCGCGCCCTGGGTGGACCTGTATCCACGACATGGCTTCTCTCTGC 163
Db      1 MetMeProArgLeuArgLeuAlaGlyThrLeuValProAlaMetAlaPheLeuSerTyr 20
QY      164 GTGAGACCAAGAAAGCTGGAGCCCTGGGTGGAGTGTCTTAATATTACTTATCATGCG 223
Db      21 LeuArgProGluIleTrpGluProCysValGluValAlaProAsnIleThrTyrGlnCys 40
QY      224 ATGAGCTGAATTTTCAAAATATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 283
Db      41 MetGluLysAsnLeuTyrLysIleProAspAsnIleProPheSerThrLysAsnLeuAsp 60
QY      284 CTGAGCTTTAATCCCTGAGGACATTTAGGACCTATAGCTTCTTCAAGTTCCAGAACTG 343
Db      61 LeuSerPheAsnLeuLeuGlnHisLeuGlySerHisSerPheLeuHisValSerGluLeu 80
QY      344 CAGGTGTGATTTATTCAGGTGGAATCAGACATTCAGCAATTAAGATGGGATATTCAGAGC 403
Db      81 HisPheLeuAspPheLeuSerArgCysLysIleHisThrIleGluAspAlaTyrGlnGly 100
QY      404 CTAAAGCACTCTCTAATCTTAATATTGACAGAAACCCATCCAGAGTTTAAAGCTTGGAG 463

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Db      101 LeuLysAsnLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuSerProGln 120
QY      464 GCCTTTTTCGACTATCAAGTTTATACAGAGCTGGGCTGGAGCAAAATCTTACATCT 523
Db      121 AlaPheSerGlyLeuSerAsnLeuGlnLysLeuValAlaGluThrHisLeuThrSer 140
QY      524 CTAGAGAACTTCCCATTCGACATCTCAAACTTTGAAAGAACTTAATGTGCTCACAAT 583
Db      141 LeuGlyAspPheProIleGlyHisLeuSerThrLeuLysGluLeuAsnValHisAsn 160
QY      584 CTATTCCAATCTTTCAATATACCTGAGATTTTCTAATCTGACCAATATAGACACTTG 643
Db      161 LeuIleHisSerPheSerIleProAspTyrPheSerAsnLeuSerSerLeuGlnHisLeu 180
QY      644 GACCTTCCAGCAACAAAGTTCAAGTATTTATTCAGACAGACTCGGGGTCTTACATCA 703
Db      181 AspLeuSerAsnAsnLysIleGlnSerIleTyrHisLysAspLeuArgValLeuHisGln 200
QY      704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAACTCTTGAACCTTTATCCAAACA 763
Db      201 MetProLeuGlyThrLeuSerLeuAspLeuAlaLeuAsnProIleAspPheIleProPro 220
QY      764 GGTGCAATTAAGAAATTTAGCTTCAATAGCTGACTTTAAGAAATATTTGATAGTTTA 823
Db      221 GlyAlaPheGluAlaIleArgLeuHisGluLeuIleLeuLysSerAsnPheLysSerThr 240
QY      824 AATGTAATGAAACTGTGTTCAGGTCTGGCTGTTTGAAGTCCATGCTTGTGGTGTG 883
Db      241 AsnIleMetLysIleLysGlnIleGlnLysSerGlyLeuGluValHisArgLeuValLeu 260
QY      884 GGAGAAATTTAGAAATGAAAGAACTTGGAAAGTTTGAACAACTGCTCTAGAGGCGCTG 943
Db      261 GlyGluPheLysAsnGluAsnGluAsnMetLysAsnPheAspLysSerAlaLeuGluGlyLeu 280
QY      944 TGCATTTTACCATTTGAGAAATTCGATTTGCAATCTTACTGACTTACTCTCATGATAT 1003
Db      281 CysAsnLeuAlaIleGluGluIlePheArgLeuAlaTyrIleAspAspLeuGluLysAsnIle 300
QY      1004 ATTTGACTTATTAATGTTTGAACAATGTTTCTTCAATTTCCCTGGTGGAGTACTATT 1063
Db      301 ThrAspLeuPheAspLysLeuGluLysAsnValSerValMetAlaLeuValHisMetTyrIle 320
QY      1064 GAAAGGTTAAGAAAGCTTTCTTAATATTTGAGTGGACATTTGAATTAATTAATCTG 1123
Db      321 AspAsnGlnGluIlePheProLysAspPheSerTrpLysSerLeuGluPheIleAsnCys 340
QY      1124 AAATTTGACAG---TTTCCCACTTGAACCTCAAACTCTTCAAAAAGCTTACTTCACT 1180
Db      341 GluPheSerGluAsnIlePhePheLeuLysLeuSerSerLeuArgArgLeuIlePheThr 360
QY      1181 TCCAAACAAAGTGGGAATGCTTTTCAAGAGTTGATCTCAAGCTTGAAGCTTGTAGAT 1240
Db      361 AlaAsnLysGlyValArgThrPheProGluLeuAsnThrProSerLeuGluPheLeuAsp 380
QY      1241 CTCAGTAGAAATGCTTGAAGTTTCAAGGTTCTGTTCTCAAGATATTTGGACAAAC 1300
Db      381 IleSerAsnAsnGlyLeuSerLeuGlnSerCysCysSerValAsnSerLeuArgLeuThr 400
QY      1301 AGCTTAAGTATTTAGATTTGAGCTTCAATGGTGTATTAACATGAGTTCAAACTTTCTG 1360
Db      401 GlnLeuLysHisIleLeuAsnLeuSerPheAsnGlyValIleThrMetThrSerAsnPheVal 420
QY      1361 GGTTTGAACAACCTGAATCTGATTTCCAGCAATTCGAATTTGAACAAATGAAGATGAG 1420
Db      421 GlyLeuGlnGluLeuGlnHisLeuTyrPheGlnHisSerAsnLeuArgAsnIleAsnGln 440
QY      1421 TTTTCAGTATCTTCACTCACTCAAAACCTCAATTTACTTGAATTTCTCATCTCAACC 1480
Db      441 PheSerIlePheLeuSerLeuAsnAsnLeuLeuTyrLeuAspIleSerTyrThrHisIle 460
QY      1481 AGAGTTGCTTTCAATGACATCTTCAATGGCTTGTCCAGTCTGGAAGTCTTGAATGGCT 1540
Db      461 ArgValAlaPheArgGlyIlePheAspGlyLeuTyrSerLeuArgValLeuLysMetAla 480

```

OY	1541	GGCAATCTTTTCAGGAAAACTCTTCTTCAGATATCTTCACAGAGCTGAAAGATCGAC	1600
Db	481	GIYsEnAlaPhEGInAsPhAsnArgLeuEuaEnIlePhEThrGluMetThrSerLeuThr	500
OY	1601	TTCTGACCTCTCTCAGCTGTCAACTGGAGCAGTTGTCTCCAAACGACATTTAACTCACTC	1660
Db	501	ThrLeuAspLeuSerSerCysGlnIleuGluGlnValTyrGlnGlnAlaPhGlnIleuSerLeu	520
OY	1661	TCGAGCTTCAGAGTACTAAATATATAGCGCAAAACAATCTTTTCAATTGGAATACGTTTCT	1720
Db	521	ProArgLeuGluSerLeuAsnMetSerHisAsnAsnLeuLeuValLeuAspThrLeuThr	540
OY	1721	TATAAGTCTCGAACTCCCTCCAGGTTCTTTATTAACCTCAATTCACATPATGACTTCC	1780
Db	541	TyrIleCysLeuTyrIleSerLeuGlnValLeuAspLeuSerPheAsnHisIleGlyAsnIle	560
OY	1781	AAAAAACAGGAACCTACAGACTTTTCCAGATAGCTACGTTTCTTAAATCTTACTCAGAAAT	1840
Db	561	ThrGluProGlyGlnGlnHisPheProSerAsnLeuThrLeuLeuHisIleLeuThrIleSerLeu	580
OY	1841	GACTTTGCTGTACTGTGGAACACCAAGATTCTCGCAATGAGATCAAGACCAAGAGAG	1900
Db	581	AlaPheValCysAspCysGlnHisGlnIlePheMetGlnTrpIleLeuAspGlnThrArg	600
OY	1901	CTTTGTGTGAAGTTGAACGAGATGGAAATGTGCACACCTTCAGATTAAGCAGGACGATGCT	1960
Db	601	LeuLeuValIleGluValIleGluIleMetValCysIleThrProProAsn-----MetPro	617
OY	1961	GTGCTGAGTTGG---AATATCACCTGTGAGATGAATAAGACCATCTGGTGTGCTGGCT	2017
Db	618	ValLeuSerPheThrAsnAlaThrCysGlnIleSerIleSerIleIleSerValSerVal	637
OY	2018	CTCAGTGTCTGTAGTATCTGTTGTGACACTTCGAGCTTAAGTTCTATTTTACCTGT	2077
Db	638	PheSerValLeuValValSerPheAlaValValLeuValTyrIlePheThrProLeu	657
OY	2078	ATGCTTCTTGCTGGCTGCATAAAGTATGGTGAAGGTGAACCATCTATGATGCTTGT	2137
Db	658	MetLeuLeuValIleGlyArgArgIleTyrIleGlyGluSerValTyrAspAlaPheVal	677
OY	2138	ATTAAGTCAACCCAGAGATGAGAGACCTGGTGAAGATGACATGAATTAAGAAAGA	2197
Db	678	IleTyrSerSerGlnAspGlnAspTrpValAlaArgAsnGluLeuValIleAsnIleGluIle	697
OY	2198	GGGGTGCTCCATTTCAAGCTCTGCTTACTACACAGACTTATTTCCGGGTGGCCATT	2257
Db	698	GlyAlaProProPheArgLeuCysLeuHisIleTyrIleArgPheIleProGlyValAlaIle	717
OY	2258	GCTGGCAATCATTCATGAAGGTTTCCATAAAGCCGAAGGATGTTGTGTGTCTC	2317
Db	718	AlaIleAsnIleIleGlnGlnIlePheHisIleCysSerAlaGlyValIleValIleValSer	737
OY	2318	CAGACATTCATCCAGAGCCGCTGGTGATCTTTGAATATGAGATTGTCCAGACCTGGAG	2377
Db	738	GlnHisPheIleGlnIleSerIleArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGln	757
OY	2378	TTTCTGACAGCTGCTGTGTATCATCTTCAATGTCTTCAGAAAGTGAGAAACCTG	2437
Db	758	PheLeuSerSerHisAlaGlnIleIlePheIleValLeuGlnIleValIleGluIleSerLeu	777
OY	2438	CTCAGGCAAGAGGTGAGAGCTGTACCGCTTCTCAGAGGAAACAATTACCTGTGAGGAG	2497
Db	778	LeuArgGlnAspValGlnLeuTyrArgLeuLeuSerHisArgAsnTrpTyrLeuGlnTrpIle	797
OY	2498	GACAGTGTCTGGGGCGGACACATCTTTCGAGAGCAGCTCAGAAAAACCTGTGATGT	2557
Db	798	AspThrValLeuGlnAlaArgHisIleIlePheThrArgArgLeuArgIleAlaLeuLeuAspIle	817
OY	2558	AAATCATGGAATCCAGAGAAACAGTGGGTACAGATTCGCAATTTGGCAAGAGCAACATCT	2617
Db	818	LysThrIleuSerProGlnGlyMetAlaArgAlaGluAsnAsnGlnGlnGlnAlaMetThr	837

DB	2618	ATC	2620	OY
Db	838	Leu	838	---
RESULT 14				
TLR4_CRIGR	STANDARD;	PRT;	838 AA.	
AC	09w482.			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor.			
GN	Name=TLR4;			
OS	Cricetus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Cricetus.			
OX	NCB1_TaxID=10029;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Macrophage;			
RX	MEDLINE=20148868; PubMed=10683379;			
RA	Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukawa K.,			
RA	Fenton M.J., Oikawa M., Ourehli N., Monks B., Finberg R.W.,			
RA	Ingalls R.R., Goldenbock D.T.,			
RT	"Toll-like receptor 4 impacts ligand-specific recognition of bacterial			
RT	lipopolysaccharide.";			
RL	J. Clin. Invest. 105:497-504(2000).			
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate			
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via			
CC	MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine			
CC	secretion and the inflammatory response (By similarity).			
CC	-1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a			
CC	multi-protein complex containing at least CD14, LY96 and TLR4.			
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via			
CC	their respective TIR domains.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-1- TISSUE SPECIFICITY: Detected in macrophages and the Chinese			
CC	hamster ovary fibroblast cell line.			
CC	-1- SIMILARITY: Belongs to the Toll-like receptor family.			
CC	-1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.			
CC	-1- SIMILARITY: Contains 1 TIR domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF153676; AAD41891.1; -.			
DR	HSSP; A15399; 1PFV.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000483; LRR_Cterm.			
DR	InterPro; IPR003591; LRR_Cyp.			
DR	InterPro; IPR00157; TIR.			
DR	Pfam; PF00560; LRR; 8.			
DR	Pfam; PF01582; TIR; 1.			
DR	PRINTS; PR00019; LEORICHRPT.			
DR	SMART; SM00082; LRRCT; 1.			
DR	SMART; SM00369; LRR_TYP; 1.			
DR	SMART; SM00255; TIR; 1.			
DR	PROSITE; PS50104; TIR; 1.			
KM	Glycoprotein. Immune response; Inflammatory response;			
KM	Leucine-rich repeat; Receptor; Signal; Transmembrane.			
FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	838	Toll-like receptor 4.
FT	DOMAIN	26	629	Extracellular (Potential).
FT	TRANSMEM	630	650	Potential.
FT	DOMAIN	651	838	Cytoplasmic (Potential).
FT	REPEAT	31	52	LRR 1.
FT	REPEAT	53	75	LRR 2.


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FT REPEAT 76 99 LRR 3.
FT REPEAT 100 123 LRR 4.
FT REPEAT 127 148 LRR 5.
FT REPEAT 149 172 LRR 6.
FT REPEAT 173 196 LRR 7.
FT REPEAT 200 224 LRR 8.
FT REPEAT 227 251 LRR 9.
FT REPEAT 305 330 LRR 10.
FT REPEAT 351 370 LRR 11.
FT REPEAT 371 393 LRR 12.
FT REPEAT 396 419 LRR 13.
FT REPEAT 420 443 LRR 14.
FT REPEAT 468 492 LRR 15.
FT REPEAT 494 516 LRR 16.
FT REPEAT 517 538 LRR 17.
FT REPEAT 541 563 LRR 18.
FT REPEAT 565 589 LRR 19.
FT DOMAIN 670 816 TIR.
FT CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 237 237 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 838 AA; 96277 MW; 129B3596E908B48 CRC64;

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Alignment Scores:

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Pred. No.: 5,9e-217 Length: 838
Score: 3017.00 Matches: 581
Percent Similarity: 82.60% Conservative: 112
Best Local Similarity: 69.25% Mismatches: 142
Query Match: 35.17% Indels: 4
DB: 1 Gaps: 4

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US-09-396-985b-1 (1-4868) x TLR4_CRIGR (1-838)

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QY 104 ATGATGTGCGCTCGGCGCTGGCTGGAGCTCTGATCCAGCCAGTGGCTTCCTCTCTGC 163
   1 MetMetProSerPheCysIleuAlaGlyThrIleuMetMetAlaLeu---PheLeuSerSer 19
Db 164 GTAGAGCAAGAAAGCTGGAGAGCCCTGGCTGGAGGCTTCTATATATTACTTATCAATGC 223
   20 LeuArgProGlnSerIleuAspProCysValGluValAspSerAsnThrSerTyrglnCys 39
QY 224 ATGAGCTGAATTTCTCAAAATATCCCGCAACACTCCCTTCACACCAAGAACTGGAG 283
   40 MetAspArgAsnIleuAsnIleProAspAsnIleProSerSerValIysHisIleuAsp 59
Db 284 CTGAGCTTAAATCCCTGAGCAATTAGGCACTATAGCTTCTTCAAGTTTCCAGAACTG 343
   60 LeuSerPheAsnProIleuIysThrIleuGlySerHisSerPheAsnPheProGlnLeu 79
QY 344 CAGTGTGTGATTTATTCAGAGTGTGAATTCAGACATTTGAAGATGGGGCATATCAGAGC 403
   80 LysIleuAspIleuSerIleuAspIleuIleGlnThrIleuIleuAspIleuIleuGlnGly 99
Db 404 CTAGAGCACTCTCTCACTTAATATTGACAGAAACCCATCCAGAGTTTATGAGCTGGGA 463
   100 LeuHisGlnIleuThrIleuThrIleuThrIleuThrIleuThrIleuThrIleuThrIleu 119
QY 464 GCGTTTCTGAGTATCAAGTTTACAGAACCTGGTGGCTGGAGCAAAATCTGACATCT 523
   120 ThrPheSerGlyLeuAlaIleuGlnAsnLeuValAlaValGlnIleuIleuIleuIleuIleu 139
Db 524 CTAGAGCACTTCCCATTTGACATCTCAAAATTTGAAAGAACTTATTTGAGCTCACAAT 583
   140 LeuAspSerIleuProIleuGlyHisIleuValThrIleuIleuIleuIleuIleuIleuIleu 159

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QY 584 CTATATCAATCTTTCAATTAATTAATTAATTTTCTAATCTGACCAATCTAGAGCACTTG 643
   160 LeuIleHisSerPheIleuProGlnIleuThrPheSerAsnIleuThrAsnIleuGlnIleu 179
QY 644 GACCTTTCCAGACAAGATTGAAGATTTATTTGACACAGACTTGGCGTTCTTACTCA 703
   180 AspIleuSerAsnAsnIleuIleuGlnThrIleuIleuIleuIleuIleuIleuIleuIleu 199
QY 704 ATGCCCTCTCAATCTCTCTTGAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 763
   200 AsnProGlnIleuAsnIleuSerIleuIleuSerIleuAsnProIleuAsnIleuGlnPro 219
Db 764 GGTGCAATTTAAAGAAATTTAGGCTTCAAGCTGATCTTGAAGAAATTTGATAGTTTA 823
   220 GlyAlaPheGlnGlyIleuArgIleuHisGlnIleuThrIleuArgSerAsnIleuSerThr 239
QY 824 AATGTATGAAAACCTTGATTTCAAGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 883
   240 AsnValMetIleuThrCysIleuHisAsnIleuAspGlyLeuGlnValHisArgIleuIleu 259
Db 884 GGAGAAATTTAGAAAGAAAGAACTTGAAGAAAGTTTGAACAATCTGCTAGAGGCGCTG 943
   260 GlyIleuPheIleuAsnGlnIleuArgAsnValGluArgPheAspArgTyValIleuGlnIleu 279
QY 944 TGCATTTGACCATTTGAAGAAATTTCCGATTTAGCATTTAGACTTACTGCTGATGATATT 1003
   280 CysIleuValThrIleuGlnIleuPheArgPheThrTyValAsnGlnIleuSerGlnIleu 299
Db 1004 ATTTGACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTACTAT 1063
   300 ThrAsp---PheAspCysIleuAlaAsnValIleuSerIleuAlaAsnValTyIleu 318
QY 1064 GAAAGGCTAAAGACTTTTCTTATATATTTCCGATGGGCAACATTTGAATTTAGTTAATCTG 1123
   319 LysArgIleuGlnIleuAspIleuProIleuTyIleuIleuIleuIleuIleuIleuIleu 338
Db 1124 AATTTGACAGTTTCCCATTTGAAGAAATTTCAATCTTCAAGAAAGCTTACTTCACTTCC 1183
   339 GlnIleuIleuGlnIleuPheProIleuGlnIleuProPheIleuIleuIleuIleuIleu 358
QY 1184 AACAAAGTGGAAAGCTTTTTCAGAAAGTTGATCTTACCAAGCTTGAAGTTTCTGATCTTC 1243
   359 AsnIleuGlyAlaThrSerPheProGlnValAsnIleuProSerIleuThrPheIleuAspIleu 378
Db 1244 AGTAGAAATGAGCTGATTTCAAGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1303
   379 SerGlyAsnGlyMetSerPheArgGlyCysSerTyIleuAspIleuIleuIleuIleuIleu 398
QY 1304 CTAAAGTATTTAGATCTGACTTCAATGAGTGTATTAATCAATGATGTTTCTTGGGC 1363
   399 LeuIleuHisIleuAspIleuSerPheAsnGlyValIleuSerMetSerGlnIleuIleuMetGly 418
QY 1364 TTAGAACATTAACATCTGATTTCCAGCAATTTCCAAATTTGAAACAAATGAGTGAATT 1423
   419 LeuGlnIleuGlnIleuIleuAspPheGlnHisSerThrIleuIleuIleuIleuIleuIleu 438
Db 1424 TCAGATTTCTATCACTCAAGAAACCTTATTAATCTTGAATTTCTCACTTCCATCCACACA 1483
   439 SerMetPheIleuProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 458
QY 1484 GTTGCTTTCAATGAGCATTTCTCAATGCTTGTCCAGCTTCAAGATCTTGAAGAAATGAGCTGC 1543
   459 IleAspPheAsnGlyIleuPhePheGlyLeuThrIleuThrIleuAsnThrIleuIleuIleu 478
Db 1544 AATTTCTTCCAGAAAATCTTCTTCCAGATATCTTCAACAGACTGAGAAATTTGACCTTC 1603
   479 AsnSerPheIleuAspAsnIleuIleuSerAsnValIleuThrAsnThrIleuAsnIleuThrPhe 498
QY 1604 CTGAGACTCTCAAGTCAATCAATGAGAGCTTGTCCCAAGCAAGCAATTTAATCACTCTCC 1663
   499 LeuAspIleuSerIleuGlyGlnIleuGlnIleuIleuIleuIleuIleuIleuIleuIleu 518
QY 1664 AGTCTTCAAGTACTAAATATGAGCCACAACAATCTTCTTCAATGAGTACGTTTCTTAT 1723

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QY 1964 CTGAGTTTG---AATATCACCTGTGCAGATGAATAGACCATCATGTGTGCGGCTC 2020
Db 618 LeuAspPheThrAsnSerThrCysTrpIleTyrIleSerValSerValVal 637
QY 2021 AGTGTGCTTTAGTATCTGTGTGAGACGTTCTGCTATAAGTTCTATTTTCACCTGATG 2080
Db 638 SerValLeuValValAlaThrValAlaPheLeuIleTyrHisPheTyrPheHisLeuIle 657
QY 2081 CTTGTGCTGAGCTGATGAATAGTATGAGTGAACATCATATGATGACCTTTGTATC 2140
Db 658 LeuIleAlaGlyCysLysLysTyrSerArgLysIleTyrAspAlaPheValIle 677
QY 2141 TACTCAAGCCAGATGAGACCTGGGTAGAGATGAGTATGAAGATTAAGAAAGAGG 2200
Db 678 TyrSerSerGlnAsnGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 697
QY 2201 GTGCTTCATTTCAGCTGTGCTTCACTACAGAGACTTATTCCTGGGTGGCCATTGCT 2260
Db 698 ValProArgPheGlnLeuCyLeuHisTyrArgAspPheIleProGlyValAlaIleAla 717
QY 2261 GCCAACAATCATTCATGAAGTTTCCATTAAGCCGAAAGTGATGTTGTGTGCTGCCAG 2320
Db 718 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValSerArg 737
QY 2321 CACTTCATCCAGAGCCGCTGGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTTT 2380
Db 738 HisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPhe 757
QY 2381 CTGAGCAGTCGCTGTGTATCATTTGATGCTCTGCAGAAAGTGGAGAACCCCTGCTC 2440
Db 758 LeuSerSerArgSerGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeuLeu 777
QY 2441 AGGAGAGAGGTGAGCTGACCCGCTTCTCAGCAGAACACTTACTGAGTGGAGAGAC 2500
Db 778 ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAsp 797
QY 2501 AGTGTCTGGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCCTGTGATGTAA 2560
Db 798 AsnAlaLeuGlnArgHisIlePheTrpArgArgLeuLysLysAlaLeuLeuAspGlyLys 817
QY 2561 TCATGGAATCCAGAGAACAGTGGGTACAGGATGCATTTGGCAGAGCAACATCTATC 2620
Db 818 AlaLeuAsnProAsp-----GlnThrSerGlnGlnGlnGlnAlaThrThrLeu 834
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Search completed: March 29, 2005, 17:27:00
Job time : 350.083 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 163.22 Seconds
(without alignments)
18050.838 Million cell updates/sec

Title: US-09-396-985B-3
Perfect score: 6724
Sequence: 1 aacaggccaccctcgtcgtcac.....ttctactgcacagagagacta 3811

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=A.Geneseq.16Dec04 -QPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS-human40.cdi
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-USER=US09396985 -CCCN_1_1.4007@runat.28032005.155742.21135 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: A.Geneseq.16Dec04:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4325	64.3	839	6	ABU04773 Human exp
2	4325	64.3	839	6	ABU04774 Human exp
3	4325	64.3	839	6	ABU04775 Human exp
4	4325	64.3	839	7	ADCT8785 Human PRO
5	4325	64.3	839	7	ADCT8826 Human PRO
6	4315.5	64.2	837	2	AAW86361 Human DNA
7	4315.5	64.2	837	6	AAE16102 Human DNA
8	4308.5	64.1	837	6	ABU04776 Human exp
9	4308.5	64.1	837	5	AAE16116 Human DNA
10	4178	62.1	808	8	AD057782 Chimpanze

11	4167	62.0	808	8	AD057785 Gorilla t
12	4164	61.9	808	8	AD057803 Chimpanze
13	4141	61.6	799	2	AAW86352 Human DNA
14	4141	61.6	799	5	AAE16093 Human DNA
15	4141	61.6	799	5	ABE83162 Human TOL
16	4141	61.6	799	6	ABE84263 Human TOL
17	4141	61.6	799	7	ADB39121 Human TOL
18	4141	61.6	799	8	ADP56656 Human TOL
19	4141	61.6	799	8	ADP48597 Human TOL
20	4040	60.1	801	8	AD057788 Gibbon to
21	3918	58.3	795	8	AD057791 Rhesus mo
22	3892	57.9	805	8	AD057800 Hamadryas
23	3819	56.8	791	8	AD057797 Squirrel
24	3794	56.4	738	8	ADP29455 Human sec
25	3501	52.1	745	8	AD057794 White-fac
26	1090	16.2	208	3	AAW88059 Human TOL
27	919	13.7	178	8	ADN12270 IL-1R/TLR
28	785	11.7	179	7	ADCT42707 Murine To
29	619.5	9.2	661	2	AAW28510 Product o
30	619.5	9.2	661	2	AAW87556 B cell su
31	619.5	9.2	661	7	ADCT8652 Human sec
32	619.5	9.2	661	7	ADCT69098 Human MP5
33	618.5	9.2	650	3	AAW82527 Human RPI
34	605.5	9.0	661	2	AAW47274 Human B-c
35	603.5	9.0	784	2	AAW86350 Human DNA
36	603.5	9.0	784	5	AAE16091 Human DNA
37	603.5	9.0	784	5	ABE83161 Human TOL
38	603.5	9.0	784	8	ADN02005 Human inf
39	602.5	9.0	784	2	AAW05869 Human TOL
40	602.5	9.0	784	6	ABU61956 Human TOL
41	602.5	9.0	784	7	ADL15005 Human TOL
42	602.5	9.0	784	8	ADP56652 Human TOL
43	602.5	9.0	784	8	ADP48593 Human TOL
44	602.5	9.0	784	8	ADP23787 PRO poly
45	602.5	9.0	784	8	ADQ39727 Human myo

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
AC	ABU04773;	
XX		
XX	29-JAN-2003 (first entry)	
DT		
DE	Human expressed protein tag (EPT) #1439.	
XX		
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
KW	protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX		
PA	(ZYCO-) ZYCOS INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1439; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WPI at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 839 AA;

Alignment Scores:

Pred. No.:	0	Length:	839
Score:	4325.00	Matches:	839
Percent Similarity:	95.45%	Conservative:	0
Best Local Similarity:	95.45%	Mismatches:	0
Query Match:	64.32%	Indels:	40
DB:	6	Gaps:	1

US-09-396-985b-3 (1-3811) x ABU04773 (1-839)

QY 45 ATGATGTCGCTGCGCTGCGCTGCGAGACTTGATCCAGCAATGGCTTCTCTCTG 104
DB 1 MetMeSerIaSerAglLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 105 GTGACACAGAAAGCTGGAGCCCTGCGTGGAGACTTGCCCTAAACACACAGAAAGC 164
DB 21 ValArgProGluSerTrpGluProCysVal----- 30
QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCCTTCAACCCGATTCATTG 224
DB 30 ----- 30
QY 225 CTTCCTGCTAAATGCTGCGCTTTCATCAGAGGTGCTTCTTAATATTACTTATCAATGC 284
DB 31 -----GluValValProAlaIleThrIleCys 40
QY 285 ATGAGCTGAATTTCTACAAATCCCGACAACTCCCTTTCACACAGAACTGGAC 344
DB 41 MetGluLeuAsnProIleGlyProAspAsnLeuProPheSerThrIleAsnLeuAsp 60
QY 345 CTGAGCTTAAATCCCTGAGAGCAATTTAGAGCACTATAGCTTCTTCACTTCCAGAACTG 404
DB 61 LeuSerPheAsnProLeuAlaGlyIleuGlySerIlePhePheSerPheProGluLeu 80
QY 405 CAGGTGCTGAATTTATCAGAGTGTGAATCCAGAACTGAAGATGGGGCATATCAGAGC 464
DB 81 GluValLeuAspLeuSerAArgCysGluIleGlnThrIleGluAspGlyAlaIleArgIns 100
QY 465 CTAAAGCACTCTTACTTAAATTTAGACAGAAACCCCATCCAGAACTTAAAGCCTGGGA 524
DB 101 LeuSerIleLeuSerThrIleLeuThrGlyAsnProIleGlnSerIleuAlaLeuGly 120
QY 525 GCCTTTCTGAGACTATCAAGTTTACAGAGCTGGTGTGAGACAAATCTAGCATCT 584

DB 121 AlaPheSerGlyLeuSerSerIleuGlnIleuValAlaValGluThrAsnLeuAlaSer 140
QY 585 CTAGAGAACTTCCCATTTGAGACATCTCAAAATTTGAAAGAACTTAATGGCTCACAT 644
DB 141 LeuGluAsnProIleGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 160
QY 645 CTATTCGAATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 704
DB 161 LeuIleGlnSerPheIleuSerIleuProGluIleuIleuIleuIleuIleuIleuIleu 180
QY 705 GACCTTTCAGACAAAGTTCAGAAATTTATTCAGACAGACTTGGGCTTCAATCAA 764
DB 181 AspLeuSerSerAsnIleGlnSerIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
QY 765 ATGCCCTTCAATCTCTTAAACCTGTCCTGCAACCCCTAATGACTTTCACAAACA 824
DB 201 MetProLeuLeuAsnLeuSerIleuAspLeuSerIleuAsnProMetAsnPheIleGlnPro 220
QY 825 GGTGATTAAGAAATTAAGCTTCATTAAGTGAAGCTTAAAGAAATTAATTAATTAATTA 884
DB 221 GlyAlaPheLeuGluIleArgLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
QY 885 AATGTATGAAATCTTGAATTCAGAGTCTGGCTGTTGAAGTCCATGTTGTTCTG 944
DB 241 AsnValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValIleuArgLeuValLeu 260
QY 945 GAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1004
DB 261 GlyGluPheArgAsnGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 280
QY 1005 TGCATTTGACCATTTGAAGAAATTCGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1064
DB 281 CysAsnLeuThrIleGluGluIleuArgLeuAlaIleuIleuAspIleuIleuIleuIleu 300
QY 1065 ATGACTTATTAATTTGTTGAAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1124
DB 301 IleAspLeuPheAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 320
QY 1125 GAAAGGTAAAGACTTTCTTAATTAATTCGATTAAGTGAAGTGAAGTGAAGTGAAGTGA 1184
DB 321 GluArgValIleuAspPheSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 340
QY 1185 AAATTTGACAGTTTCCCATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1244
DB 341 LysPheGlyGlnPheProThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 360
QY 1245 AACAAAGTGGGAATGCTTTTCAGAGTGAATTCAGAGCTTGAAGTTCAGATCTC 1304
DB 361 AsnIleGlyGlyAsnAlaPheSerGluValAspLeuProSerIleuGluPheLeuAspLeu 380
QY 1305 AGTAGAAATGCTGATTCAGAAATGCTGCTTTCAGAAATGATTTGGGCAACACAC 1364
DB 381 SerArgAsnGlyLeuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAATTAATTAATGATGAGCTTCAATGAGTGAATTAATTAATTAATTAATTAATTAAT 1424
DB 401 LeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 420
QY 1425 TTAGAACAACTGAACATCTGATTTTCAGACTTCCAAATTTGAAACAAATGAAGTGA 1484
DB 421 LeuGluGlnLeuGlnIleuIleuAspPheGlnIleuIleuIleuIleuIleuIleuIleu 440
QY 1485 TCAGATTCCTATCATCTGAGAAACCTCATTTACCTTGAATTTCTCATCTCATCACACA 1544
DB 441 SerValPheLeuSerIleuArgAsnLeuIleuIleuIleuIleuIleuIleuIleuIleu 460
QY 1545 GTTGTCTTCAATGAGCACTTCAATGAGCTTGTGCTGCAAGTCTGAAGTCTTGAAGTCTG 1604
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerIleuGluValIleuIleuIleuIleu 480
QY 1605 AATTTCTTCAGAGAAATCTCTTCCAGATATCTTCAAGAGCTGAGAAATCTGACCTTC 1664

Db	481	AansrPhegIngluAAsnPhelLeuProaspIlePheThrGluLeuAArgAsnLeuThrPhe	500
QY	1665	CTGAACTCTCTCACTGTCACTGTGAGAGAGTTGTCTCAACAGCACTTTAACTCACTCTCC	1724
Db	501	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer	520
QY	1725	AGCTTCAGGATCTAAATATATGAGCCCAAACTCTTTGATTTGGATGAGCTTCCTAT	1784
Db	521	SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr	540
QY	1785	AAGTGTCTGAACCTCCCTCCAGAGTTCTTGATTTACAGTCTCAATTCACATATGACTTCCAA	1844
Db	541	LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys	560
QY	1845	AAACAGGAACCTACAGCACTTTTCCAAATAGTCTAGCTTTCTTAAATCTTACTCAGATGAC	1904
Db	561	LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	580
QY	1905	TTTGCTGTACTGTGGAAACAACAAGCTTCCGCAATGGATCAAGAGCAAGAGCAGCTC	1964
Db	581	PheAlaCysTrpCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu	600
QY	1965	TTGGTGAAGTGTGAACAGATGGAATGTGTCAACACCTTCAGATTAAGACAGCAGCATCTGTG	2024
Db	601	LeuValGluValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal	620
QY	2025	CTGAGTTTGAATATCACTGTCAAGTGAATTAAGACCATCATGTTGTGTGTGGTCTCCAGT	2084
Db	621	LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleGlyValSerValLeuSer	640
QY	2085	GTCGTTGAGATCTGTGTGTGAGAGTTGTGTCTATAGTTCTATTTTCACTGATGTT	2144
Db	641	ValLeuValValSerValAlaAlaValLeuValTyrLysPheHisLeuMetLeu	660
QY	2145	CTTGCTGGCTCATTAAGATATGTATGTAAGAGTAAACATCTATGATGCTTTGTTATCTAC	2204
Db	661	LeuAlaGlyCysIleLysTyrGlyArgGlyLeuAsnIleTyrAspAlaPheValIleTyr	680
QY	2205	TCAAGCCAGATGAAGGACTGGGTGAAGAATGAGCTAGTAAAGAAATTGAGAAAGGGGTG	2264
Db	681	SerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGluVal	700
QY	2265	CCTCATTTACGCTCTGCTTCATCAACAGACATTATCCCGGTGTGGCATTTGCTGCC	2324
Db	701	ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaIa	720
QY	2325	AACATCATCAATGAAGGTTTCCATTAAGCCGGAAGGATGTTGTGTGGTGTCCAGACAC	2384
Db	721	AsnIleIleHisGluGlyPheHisLysSerArgLysValIleValValValSerGlnHis	740
QY	2385	TTTCATCCAGACCGCTGTGTATCTTTGAAATATGAGATTTGCTCAGACCTGGCAGTTCTG	2444
Db	741	PheIleGlnSerArgTrpCysIlePheHisTyrGluIleAlaGlnThrTrpGlnPheLeu	760
QY	2445	AGCAGTGTGCTGTGATCATCTTCAATGTTCTTGCAGAAAGGTGAGAAAGACCTGTCTAAG	2504
Db	761	SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArg	780
QY	2505	CAGAGAGGTGAGCTGTACCGGCTTCTCAGAGAAACCTTACCTGAGGTGGAGAGACAGT	2564
Db	781	GlnGlnValGluLeuTyrArgLeuLeuSerArgAsnTrpTyrLeuGlnTrpGlnAspSer	800
QY	2565	GTCCTGGAGCGCACATCTTCTGAGAGACACTCAGAAAGCCCTGAGTGTATTAATCA	2624
Db	801	ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer	820
QY	2625	TGGAATCCAGAAAGAACAGTGGGTACAGAGATGCATTTGGCAGAAAGCAACATCTATC	2681
Db	821	TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle	839

AC ABU04774;
 XX
 XX
 DT 29-JAN-2003 (first entry)
 XX
 XX
 DE Human expressed protein tag (EPT) #1440.
 XX
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors) useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 XX
 PS Example 2; SEQ ID NO 1440; 134pp; English.
 XX
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 839 AA;
 XX
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 95.45% Mismatches: 0
 Query Match: 64.32% Indels: 40
 DB: Gaps: 1

Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 105 GTGAGACACGAAAGCTGGAGGCCCTGCTGTGAAGACTTGGCCCTTAACACACAGAAAGAGC 164
Db 21 ValArgProGlnSerThrGlnProCysVal----- 30
QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGGCTCAGCCCTTCAACCCCGATTCCATTG 224
Db 30 ----- 30
QY 225 CTTCCTGCTAAATGCTGCCGTTTATCAAGAGGTGGTTCCTAATAATTACTTATCAATGC 284
Db 31 -----GluValValProAsnIleThrTyrGlnCys 40
QY 285 ATGAGAGCTGAATTTCTACAAATATCCCGACAACTCCCTTCTCAACACGAAACCTGGAGC 344
Db 41 MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
QY 345 CTGAGCTTAAATCCCGTAGAGCAATTTAGCAGCTATGCTTCCAGTTTCCGAGACTG 404
Db 61 LeuSerPheAsnProLeuArgIleGlySerTyrSerPhePheSerPheProGlnLeu 80
QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATCCAGACAAATTGAGATGGGCGATATCAGAGC 464
Db 81 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY 465 CTAAAGCACTCTCTACCTTAATTTAGACGAAACCCCATCCAGAGTTTATGCCCTGGGA 524
Db 101 LeuSerThrIleuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 525 GCCTTTCTGACATCATCAATTAAACAGAGCTGTGGCTGTGGAGACAAATCTAGCATCT 584
Db 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 140
QY 585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAAATGTGCTCACAAT 644
Db 141 LeuGluAsnPheProIleGlyIleLeuLysThrLeuLysGluLeuAsnValAlaIleAsn 160
QY 645 CTATATCCAACTTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 704
Db 161 LeuIleGlnSerPheLysLeuProGlnLysPheSerAsnLeuThrAsnLeuGlnLysLeu 180
QY 705 GACCTTCCAGACAAAGATTCAAGATTAATTATTTGACAGACTTGGCGGTTTCAATCAA 764
Db 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValIleuIleGln 200
QY 765 ATGCCCTTACTCAATCTCTCTTTAGACTGTCCCTGAACCTTAAGACTTATTCACCA 824
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 825 GGTGCATTTAAAGAAATTAAGCTTCATTAAGCTGACTTAAGAAATATTTTGTATGTTTA 884
Db 221 GlyAlaPheLysGluIleArgLeuIleLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
QY 885 AATGTAATGAAAACCTGTATTCAGAGTCTGGCTGGTTTGAAGGTCATCGTTGGTCTTG 944
Db 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValIleAspGlyLeuVal 260
QY 945 GGAAGATTTAGAAATGAAAGAACTTGAAAGTTTGAACAAATCTGCTTAGAGAGGCTG 1004
Db 261 GlyGluPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
QY 1005 TGCATTTTGAACCATTTGAAGAAATTCGATTAAGCAATTAAGCAATCTACCTTCGATGAAT 1064
Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300
QY 1065 ATTAGACTTATTAATTTGTTGACAAATGTTTCTCATTTTCCCTGGAGAGTGATCAATT 1124
Db 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
QY 1125 GAAAGGTAAGAAAGCTTTTCTTAATATTTGCGATGGACAACTTGAATTAAGTAACTGT 1184
Db 321 GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnIleLeuGluLeuValAsnCys 340

QY 1185 AAATTTGACAGATTTCCCACTTGAAGCTCAAAATCTCAAAAGGCTTACTTCACTTCC 1244
Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheIleIleSer 360
QY 1245 AACAAAGGTGGAAATGCTTTTTCAGAAAGTGAATCTTACAAAGCTTGAAGTTTCTAGATCTC 1304
Db 361 AsnLysGlyGlyAsnAlaPheSerGluValaAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1305 AGTAGAAATGCTTGAATTTCAAAGTGTCTGTCTCAAAAGTATTTTGGGACACACAGC 1364
Db 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTAACATGATGTTCAAACTTCTTGGGC 1424
Db 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1425 TTGAAACAACTAGAACATCTGATTTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1484
Db 421 LeuGlnGlnLeuGlnIleLeuAspPheGlnIleSerAsnLeuLysGlnMetSerGlnPhe 440
QY 1485 TCAGTAATTCCTTACTCAGAAACCTCATTTACCTTGAATTTTCTCATACTACACACAGA 1544
Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerThrIleThrArg 460
QY 1545 GTTGCTTTCAATGGCACTTCAATGGCTGTGCAGTCTGAGAGTCTTGAATAATGGCTGGC 1604
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysPheAlaGly 480
QY 1605 AATTCCTTTCAGAGAAACTTCCCTCCAGATATCTTCAACAGACTGAGAAACTGACCTTC 1664
Db 481 AsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1665 CTGGACCTCTTCAAGTGTCACTGAGAGCAAGTTGTCTCAACAGCATTTAACTCACTCTCC 1724
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1725 AGTCTTCAAGTACTAAATATGAGCCACAACTTCTTCAATGAGTACGTTTCTTAT 1784
Db 521 SerLeuGlnValLeuAsnMetSerThrAsnAsnAsnPheSerLeuAspThrPheProTyr 540
QY 1785 AAGTGTCTGAATCTCCCTCCAGGTTCTTGATTAAGTCTCAATCACTAATGACTTCCAAA 1844
Db 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnIleIleMetThrSerLys 560
QY 1845 AAAACAGAACTTACAGATTTTCCAAAGTACTTGAAGTCTTAAATTTTCTAGAGATGC 1904
Db 561 LysGlnGlnLeuGlnIleAspPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1905 TTTGCTGTATCTTGTGAACACAGAGTTTCTGCAATGGATCAAGACACAGAGGACGCTC 1964
Db 581 PheAlaCysThrCysGlnIleIleGlnSerPheLeuGlnTrrIleLysAspGlnArgGlnLeu 600
QY 1965 TTGGTGAAGTTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGCGACTGTG 2024
Db 601 LeuValGluValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 620
QY 2025 CTGAGTTTGAATATCACTCTGTCAAGATGAATTAAGCAATGATGTGTGTCGCTCAAT 2084
Db 621 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 640
QY 2085 GTGCTGTATGATCTGTGTAGAGAGTTCTGCTATTAAGTCTAATTTTCACTGATGCTT 2144
Db 641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheIleLeuMetLeu 660
QY 2145 CTGTGCTGTCATTAAGTATGGTATGAGGTGAAACATCTATGATGCTTGTGTATCTAC 2204
Db 661 LeuAlaGlyCysIleLysTyrGlyArgGlyAsnIleTyrAspAlaPheValIleTyr 680
QY 2205 TCAAGCCAGATGAGAGCTGGGTAAAGAAATGAGCTATGTAAGAAATTTAAGAAAGGGGTG 2264
Db 681 SerSerGlnAspGluAspTrrValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 700

OY		2265	CCTCATTTACGCTGTGGCTTCACTAGACAGACTTTATTCGCCGGTGCGCATTGGCTGC	2324
Dd		701	ProPhePheGlnLeuCysLeuHisIstYrArgAspPheIleProGlyValAlaIleAla	720
OY		2335	AACATCATCCATGAAGGTTTTCCATTAAGCCGAAAGGTGATTGTGTGTGTGTCCAGCAC	2384
Dd		721	AsnIleIleHISGLUGLYPheHIElySerIstArgLysValIleValValSerGlnHis	740
OY		2385	TTCATCCAGAGCCGCTGGTGTATCTTTGAATATAGATGATTGCTCAGACCCTGGACGTTCTG	2444
Dd		741	PheIleGlnSerIstArgTrpCysIlePheGluTrpGluIleAlaGlnThrTrpGlnPheLeu	760
OY		2445	AGCAGTGTGTCGGTATCATCTTCATTTGCTCCTGCAGAAAGTGGAAGAAGCCCTGCAGC	2504
Dd		761	SerSerIstArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg	780
OY		2505	CAGCAGGTGAGACTGTACCGCCTTCTCAGCAGAAACAATTCACTCGAGGTGGAGAACAGT	2564
Dd		781	GlnGlnValIGluLeuTrpYrArgLeuLeuSerIstArgAsnThrTrpLeuGluTrpGluAspSer	800
OY		2565	GTCTCTGGGGCGGCACATCTTCTTGAGAGACACTCAGAAAAGCCCTGTGATGTAAATCA	2624
Dd		801	ValLeuGlyIstArgHISleIlePheThrArgIstArgLeuArgLysAlaLeuLeuAspGlyLysSer	820
OY		2625	TGGATTCAGAAAGAACAGCTGGGTTCAGAGATGCATTTGGCAGGAACCAACTCTATC	2681
Dd		821	TrpAsnProGlnGlyThrValGlyThrlGlyCysAsnTrpGlnAlaThrSerIle	839
RESULT 3				
ABU04775				
ID	ABU04775	standard; protein; 839 AA.		
XX				
AC	ABU04775;			
DT	29-JAN-2003	(first entry)		
DE		Human expressed protein tag (EPT) #1441.		
XX				
KW		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;		
KM		protease; protease inhibitor; transporter; cytoskeletal protein;		
KV		receptor; transcription factor; cancer; MHC;		
KW		major histocompatibility complex; myeloma; colon cancer; gastric cancer;		
XX		adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.		
OS	Homo sapiens.			
PN	MO200278524-A2.			
PD	10-OCT-2002.			
XX				
PF	28-MAR-2002; 2002WO-US009671.			
XX				
PR	28-MAR-2001; 2001US-0279495P.			
PR	21-MAY-2001; 2001US-0292544P.			
PR	08-AUG-2001; 2001US-0310801P.			
PR	01-OCT-2001; 2001US-0326370P.			
PR	04-DEC-2001; 2001US-0336780P.			
PR	20-FEB-2002; 2002US-0358985P.			
XX				
PA	(ZYCO-) ZYCOS INC.			
XX				
PI	Chicz RM, Tomlinson AJ, Urban RG;			
XX				
DR	WPI; 2003-040607/03.			
XX				
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,			
PT	cytoskeletal proteins, receptors or transcription factors), useful for			
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or			
XX	leukemia.			
PS	Example 2; SEQ ID NO 1441; 134dp; English.			
CC	The invention describes a purified polypeptide, which comprises a			

	fragment of a kinase, phosphatase, protease, protease inhibitor,						
CC	transporter, cytoskeletal protein, receptor or transcription factor. The						
CC	polypeptide is useful as an immunogenic composition for eliciting in a						
CC	mammal an immunogenic response directed against any of the purified						
CC	polypeptide. The purified polypeptide, or the antibody that binds to this						
CC	polypeptide, is useful for treating cancer. The polypeptide is also						
CC	useful for identifying compounds that binds to a naturally processed						
CC	class I or class II MHC-binding polypeptide. The polypeptides and						
CC	polynucleotides are particularly useful for treating or preventing						
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,						
CC	lymphoma or leukemia. These are also useful for screening agents for						
CC	treating the above mentioned diseases. This sequence represents an						
CC	expressed protein tag (EPT) isolated from human tissue for translational						
CC	profiling. Note: This sequence does not appear in the printed						
CC	specification but was obtained in electronic format directly from WIPO at						
CC	ftp.wipo.int/pub/published_pct_sequences						
XX							
SQ	Sequence 839 AA;						
Alignment Scores:							
Pred. No.:	0	Length:	839				
Score:	4325.00	Matches:	839				
Percent Similarity:	95.45%	Conservative:	0				
Best Local Similarity:	95.45%	Mismatches:	0				
Query Match:	64.32%	Indels:	40				
DG:	6	Gaps:	1				
US-09-396-985B-3 (1-3811) x ABU04775 (1-839)							
OY	45	ATGAGTCTCGCCTCGCGCGCTGGCTGGAGACTGTGATCCAGCCCATGGCCCTTCCTCTGC	104				
DB	1	MetwtSerAlaSerArgLeuAlaGlyThrIleuIleProIleMetAlaPheLeuSerCys	20				
OY	105	GTGAGACCAAGAAAGCTGGAGCGCTGCGTGAGAGACTTGCGCCCTTAACACACAAGAAGAGC	164				
DB	21	VallaGrProGIuSerTrpGluProCyVal-----	30				
OY	165	TGGCATGAACCACAGAGCTTTGAGACTCGGAGCCTGAGCCCTTACCCCGATTCCATTG	224				
DB	30	-----	30				
OY	225	CTTCTGTGCTAATGCTGCCGTTTTATCACGGAGGCGTCCATAATATTCATTATCATGC	284				
DB	31	-----GlutAlaValProAsnIleThrTyrgInCys	40				
OY	285	ATGAGAGTGAATTTCTACAAAATCCCCGACAACCTCCCCTTCTCAACCAAGAAGCTGGAC	344				
DB	41	MeGtIuLeuAsnPheTyrluSalleProAspAsnLeuProPheSerThiryluShenLeuAsp	60				
OY	345	CTGAGCTTTAATCCCCCTGAGGAGCATTTAAGGACAGCTATAGCTTTCATGTTTCCCAAGCTG	404				
DB	61	LeuSerPheAsnProLeuAlargHisLeuGlySerTyserPhePheSerPheProGluLeu	80				
OY	405	CAGGTGCTGATTTATCCAGGTGTGAATCCAGACAAATTGAAGATGGGGCATTCAGAGC	464				
DB	81	GlnValIleuAspLeuSerArgCysGluIleGlnThrIleGluAspIlyAlaTyrgInSer	100				
OY	465	CTAACCCACCTCTCACTTATATTTGACAGGAACCCCATCCAGGTTTAGCGCCGGGA	524				
DB	101	LeuSerHISLeuSerThrIleuIleuThrtyrGlyAsnProIleGlnSerIeualAlauGly	120				
OY	525	GCCCTTTTGTGACTATCAAGTTTACAGAAGCTGTGTGCTGTGGAGACAATCTAGCATCT	584				
DB	121	AlapheSerArgIyLeuSerSerIeuGlnIySerValAlaValGluThrshenLeuAlaser	140				
OY	585	CTAGAGAACTTCCCATTTGAGACATCTCAAACCTTTGAAGAACTTATGTGGCTCACAAT	644				
DB	141	LeuGluAsnPheProIleGlyHisIleuTystrIleuLysGluIleuAsnValAlaHisAsn	160				
OY	645	CTTATCCAACTCTTTCAAAATTACCTGAGATTTTCTTAATCTGACCAATCTAGAGCACTTG	704				
DB	161	LeuIIleGlnSerPheLysLeuProGluTyrrPheSerAsnIleuThrAsnLeuGluHisIleu	180				

QY	705	GACCTTTCCAGCAACAAGATTCAAAAGTATTATTTGACACAGCTCCGGGTTCTACATCA	764
Db	181	AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln	200
QY	765	ATGCCCTTACATCAATCTCTTTAGACCTGTCGCCGAAACCTATGAACCTTTATCCAAACA	824
Db	201	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro	220
QY	825	GGTGCATTTAAAGAAATTAAGGCTTCATTAAGCTGACTTTAAGAAATTAATTTGATAGTTTA	884
Db	221	GlyAlaPheLysGluIleArgLeuHisIbLysLeuThrLeuArgAsnAsnPheAspSerLeu	240
QY	885	AATGTAATGAAGAAACTTGTAATTCAGAGTCTGGCTGGTTTGAAGTCCATCGTTTGCTG	944
Db	241	AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu	260
QY	945	GGAGAAATTTAGAAATGAAGAGAACTTGAGAAAGTTTGCAAAATGGCTCTAGAGGGCTG	1004
Db	261	GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu	280
QY	1005	TGCATATTTGACCATTTGAAGAAATTCGATTAAGCATCTAGACTACTACCTTCGATGAATTT	1064
Db	281	CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle	300
QY	1065	ATTGACTTATTTAATTTGTTTGACAAATGTTTCTTCATTTCCCTGGTGAGTGTACATTT	1124
Db	301	IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	320
QY	1125	GAAAGGGTAAGAAAGCTTTCTTATTAATTTGGATGGCAACATTTAGAAATTAAGTTAACTGT	1184
Db	321	GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisIleGluLeuValAsnCys	340
QY	1185	AAATTTGACAGTTTCCGACATTTGAACCTCAAACTCTCAAAAGGCTTACTTCACTTCC	1244
Db	341	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer	360
QY	1245	AACAAAGGTGGAGTCTTTTTCAGAGTTGATCTACCAAGCTTGAGTTCTAGATCTC	1304
Db	361	AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu	380
QY	1305	AGTACAANAATGGCTGAGTTTCAAGAGTGGCTGTTCTCAAGTGAATTTGGGACAAACAGC	1364
Db	381	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	400
QY	1365	CTAAAGTATTTAGATCTGAGCTTCATGCTGTTTATTAACAAGATTCAAACTTCTTGGGC	1424
Db	401	LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly	420
QY	1425	TTAGAACCAACTAGAACATCTGAGATTTCCAGCAATTCGAATTTGAACAAATAGTAGATTT	1484
Db	421	LeuGluGlnLeuGluHisIleuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe	440
QY	1485	TCAGTAATTCCTATCACTCAAGAAACCTCATTTAACCCTGACATTTCTCATACTCAACACGA	1544
Db	441	SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisIleHisIleArg	460
QY	1545	GTTGCTTTCAATGGGACCTTCATAGGCTGTGCACCTCCGAAGCTTGAAATGGCTGGC	1604
Db	461	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly	480
QY	1605	AATTTCTTCCAGAGAAACTTCCTTCAGATATCTTCACAGAGCTGAGAACTTGACCTTC	1664
Db	481	AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe	500
QY	1665	CTGGAACCTCTCTCACTGTCACTGAGACAGTTGTCTCAACAGCAATTTAACTCACTCTCC	1724
Db	501	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer	520
QY	1725	AGCTTCAAGGTACTAAATATATGACCAACAAACTCTTTGATTTGGATAGCGTTTCTAT	1784
Db	521	SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr	540
QY	1785	AAGTCTCTGAACCTCCCTCAGGTTCTTGATTTACAGTCTCAATTCACATATATGACTTCCAA	1844

[illegible]

XX WO2003034984-A2.
 XX PD 01-MAY-2003.
 XX PF 15-OCT-2002; 2002WO-US033070.
 XX PR 19-OCT-2001; 2001US-0340083P.
 XX (GETH) GENENTECH INC.
 XX PI Goddard A, Gurney AL;
 XX DR WPI; 2003-481990/45.
 XX DR N-PSDB; ADC78784.
 XX PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 XX PT medicament for diagnosing or treating cancer or inflammatory bowel
 XX PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX PS Claim 12; SEQ ID NO 14; 327pp; English.
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for
 CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.
 XX SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 95.45% Mismatches: 0
 Query Match: 64.32% Indels: 40
 DB: 7 Gaps: 1
 US-09-396-985B-3 (1-3811) x ADC78785 (1-839)

DB 121 AlpheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCAATCTGACATCTCAAAACTTTGAAAGAACTTAATGTGCTCAAT 644
 DB 141 LeuGlnAsnPhenProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
 QY 645 CTTATCCAACTTTTAAATTAACCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTG 704
 DB 161 LeuIleGlnSerPheLeuSerLeuProGluLysPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 705 GACCTTCCAGCAACAAGATTCAAAGTATTTATTCACAGACTTGGGGCTTACATCAA 764
 DB 181 AspLeuSerSerAsnLysIleGlnSerIleTyrcSerThrAspLeuArgValLeuHisGln 200
 QY 765 ATGCCCTTCTCAATCTCTTTAAGCTGTGCTCCGACCCCTTAAGAACTTTATCCACCA 824
 DB 201 MetProLeuLeuAsnLeuSerLeuAsnPhenLeuAsnProMetAsnPhenIleGlnPro 220
 QY 825 GGTCGATTTAAAGAAATTAGCTTCATPAAAGCTTGAAGTAAAGAAATTTGATAGTTA 884
 DB 221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPhenAspSerLeu 240
 QY 885 AATGTATGAAATACTTGTATTCAGAGCTGTGCTGCTTTAGAAATCCATGCTTGGTCTG 944
 DB 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 945 GGAGAAATTTAAGAAATGAGAGAAACTTGGAAAAGTTTGACAAATTCGCTTAAAGGCTTG 1004
 DB 261 GlyGluPheArgAsnGlnGluLysAsnLeuGluLysPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 1005 TGCATTTGACCATTTGAAGAATTCGATAGACTTACATCTGATGATGATTT 1064
 DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrlLeuAspLysTyrlLeuAspLys 300
 QY 1065 ATTGACTTATTTAATGTTTGAACAATGTTTCTTATTTTCCCTGAGTGTACTATT 1124
 DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerAlaThrIle 320
 QY 1125 GAAAGGTTAAAGACTTTCTTATTAATTCGATGGCAACATTGATTAATGATCTG 1184
 DB 321 GluArgValLysAspPheSerTyrlAsnPhenGlyTyrlGlnHisLeuGluLeuValAsnCys 340
 QY 1185 AATTTGACAGTTTCCCAATTTGAACCTCAAACTCTCAAAAGCTTACTTCACTTCC 1244
 DB 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
 QY 1245 AACAAAGGTGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTCTAGATCTC 1304
 DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAlaAspLeuProSerLeuGlnPheLeuAspLeu 380
 QY 1305 AGTAAATGCTTGAATTTCAAGGTGCTGTTCTCAAGTATTTGGGCAACACGAC 1364
 DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1365 CTAAAGTATTTGATCTGAGCTTCAATGCTTATTAACATAGATTTCAAACTTTGGGCG 1424
 DB 401 LeuLysTyrlLeuAsnLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTAGAAACAATGACATCTGATTTTCCAGATTCGATTTGAAACAAATGAGTAGTGT 1484
 DB 421 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
 QY 1485 TCAATATCTCTATCTCAGAAACCTCATTTACCTTGACATTTCTCATACACACAGA 1544
 DB 441 SerValPheLeuSerLeuAsnLeuIleTyrlLeuAspIleSerHisThrHisThrArg 460
 QY 1545 GTTGCTTTCAATGGGATCTTCAATGGCTTGTCAATCTGCAAGTCTTGAAAATGGCTGGC 1604
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 480
 QY 1605 AATTTCTTCCAGGAAACCTTCCCTTCAGATATCTTCACAGAGCTGAGAAACTTGACCTTC 1664

Db 481 AaSerPheGlnGluAaPheLeuProAapIlePheThrGluLeuArgAaLeuThrPhe 500
QY 1665 CTGACCTCTCTCAAGTCACTGAGCAGATTGTCTCAACAGCATTTAACTCACTCTCC 1724
Db 501 LeuAaPheLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAaSerLeuSer 520
QY 1725 AGTCTTCAAGTACTAAATATAGCCCAACAACCTCTTTTTCATTGATACGTTCTTAT 1784
Db 521 SerLeuGlnValLeuAaSerSerHisAaAaPhePheSerLeuAaPheThrProTyr 540
QY 1785 AAGTCTCAAGTCCCTCCAGGTTCTTGATTAACGCTCAATCAACAATTAAGCTTCCAA 1844
Db 541 LysCysLeuAaSerLeuGlnValLeuAaPyrSerLeuAaSerHisLeuMetThrSerLys 560
QY 1845 AAACAGGAACCTACAGCATTTTCCAAAGTACTAGCTTTCTTAAATTTTCTCAGAAATGAC 1904
Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuHisPheLeuAaSerLeuThrGlnAaAaP 580
QY 1905 TTTGCTTGACTTGATGACACACAGATTCTCTGCAATGATCAAGACCAAGACGAGCTTC 1964
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAaPglAaArgGlnLeu 600
QY 1965 TTGCTGGAAGTGAAGAAATGGAATGGAACCTTCAAGATGAGAGGACGAGCTCTG 2024
Db 601 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAaPylGlnGlyMetProVal 620
QY 2025 CTGAGTTGAATATACCTCTGACATGATGAATGAACCATCATGATGCTGCTCAGT 2084
Db 621 LeuSerLeuAaSerHisPheCysGlnMetAaHisPheThrIleIleGlyValSerValLeuSer 640
QY 2085 GTGCTTGATGATCTGTGTGAGACGTTGCTGTATAGTTCTTATTTTCACTGATGCTT 2144
Db 641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 660
QY 2145 CTTCGCTGCTGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2204
Db 661 LeuAlaGlyCysIleLysThrGlyArgGlyGlnAaSerHisPheValIleTyr 680
QY 2205 TCAGCAGCAGATGAGGAGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2264
Db 681 SerSerGlnAaPglAaSerPyrValAlaArgAaGlnLeuValLysAaSerLeuGlnGlyVal 700
QY 2265 CCTCATTTCAAGTCTGCTCTTCACTACAGACATTTATTTCCCGGTGGCCATTGCTGCC 2324
Db 701 ProProPheGlnLeuCysLeuHisTyrArgAaPheIleProGlyAlaIleAlaIle 720
QY 2325 AACATATCATGAAGTTCATTCATTAAGCCGAAGGATGTTGTTGTTGCCAGCAC 2384
Db 721 AaHisLeuHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHis 740
QY 2385 TTCAATCAGAGCCGCTGATCTTTGAATATGATGATGATGATGATGATGATGATGATGAT 2444
Db 741 PheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnHisThrPglAaPheLeu 760
QY 2445 AGCAGTCTGCTGATTCATTTCTTCTGACAGAGTGAAGAACCTGCTCAGG 2504
Db 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuAaArg 780
QY 2505 CAGCAGTGAAGTGAAGCCCTTCCAGCAGGAACAATCACTGAGTGAAGGAGCAGT 2564
Db 781 GlnGlnValGlnLeuTyrArgLeuSerSerArgAaThrTyrLeuGlnLysPglAaPheSer 800
QY 2565 GTCTCTGGGCGGACATCTTCTGAGAGACATCAGAAAGCCCTGATGATGATGATGATGAT 2624
Db 801 ValLeuGlyArgHisIlePheThrPglAaGlnLeuArgLysAlaLeuLeuAaPglLysSer 820
QY 2625 TGGATTCAGAAAGAACAGTGGGATCAGAGATGCAATTTGACAGGAACCAATCTATC 2681
Db 821 TrpAaSerProGlnGlyThrValGlyThrGlyCysAaThrPglGlnLysAlaThrSerIle 839

XX AC ADD48826;
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX DT
XX DE Human Protein AAF05316, SEQ ID NO 14536.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNR; Chung.
XX OS Homo sapiens.
XX OS Unidentified.
PN MO2003016475-A2.
XX 27-FEB-2003.
PD 14-AUG-2002; 2002WO-US025765.
XX PF 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0335347P.
XX PA (GENO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAF05316.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNR)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (described in Table 3
of the specification) which is differentially expressed during pain.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4325.00 Matches: 839
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 0

Query Match: 64.32% Indels: 40
DB: 7 Gaps: 1
US-09-396-985b-3 (1-3811) x ADD48826 (1-839)

QY 45 ATGATGTGCTGCGGCGCTGGCTGGAGCTTGATCCAGCACTGGCTTCTCTCTGC 104
DB 1 MetMetSerLaserLagLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 105 GTGAGCCGGAAGCTGGGAGCGCCTGGCTGGAGACTTGGCCCTAAACCAACAGAGAGC 164
DB 21 ValArgProGluSerThrGluProCysVal----- 30
QY 165 TGGCATGAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCCTTCAACCCGATTCCATTG 224
DB 30 ----- 30
QY 225 CTTCTGTAAATGCTGCGCTTTTATCAGAGAGTGCTTCTAATATTACTTATCAATGC 284
DB 31 -----GluValValProAsnIleThrTyrgInCys 40
QY 285 ATGAGCTGAATTTTCTCAAAATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 344
DB 41 MetGluLeuAsnPhetYrYsIleProAspAsnLeuProPheSerThrLyAsnLeuAsp 60
QY 345 CTGAGCTTATATCCCTGAGGCACTTGAAGCACTATAGCTTCTCAGTTTCCAGAACTG 404
DB 61 LeuSerPheAsnProLeuAsnIleGlySerTySerPhePheSerPheProGluLeu 80
QY 405 CAGTCTCGATTTATTCAGAGTGTGAATTCAGACAAATTGAAGATGGGCAATACAGAGC 464
DB 81 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrgInSer 100
QY 465 CTAAAGCACTCTCTTCTTAAATATTGACAGGAAACCCCATCCAGAGTTTGAAGCTGGGA 524
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 525 GCCTTTTCTGACTATCAAGTTTACAGAAAGCTGTGGCTGTGGAGCAAACTTACAGACT 584
DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGluThrAsnLeuAlaSer 140
QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAACTTATGTGCTCACAAT 644
DB 141 LeuGluAsnPheProIleGlyHisLeuIlyThrLeuIleGluLeuAsnValAlaHisAsn 160
QY 645 CTTATCCAACTTTTCAAAATTAAGCTGAGTATTTTCTAATTTGACCAATCTAGAGCACTG 704
DB 161 LeuIleGlnSerPheLeuSerProGluTyPheSerAsnLeuThrAsnLeuGluHisLeu 180
QY 705 GACCTTTCAGAAACAAGATTCAAGATTTATTTGACAGACTTGGGGGTTCTACATCA 764
DB 181 AspLeuSerSerAsnIlyIleGlnSerIleTyCysThrAspLeuArgValLeuHisGln 200
QY 765 ATGCCCTTCACTCAATCTCTTTTGAAGCTGTCCCTGAGCAACCTTGAACCTTATCCAGCA 824
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 825 GGTGCTTTTAAAGAAATTAAGCTTCAAGCTGACCTTAAAGAAATTAATTTGATAGTTTA 884
DB 221 GlyAlaPheLeuSerGluIleArgLeuHisIlyLeuThrLeuAsnAsnPheAspSerLeu 240
QY 885 AATGTATGAAAACTGTATTTCAAGGCTGGCTGGTGTGTTAGAGTCCATGTTGGTTGCTG 944
DB 241 AsnValMetLeuIlyThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAsnGluValLeu 260
QY 945 GGAGAAATTTAGAAATGAAGAAACTTGAAGAACTTTGACAAATCTGCTTAGAGGGCTG 1004
DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluIlyPheAspLySerAlaLeuGluGlyLeu 280
QY 1005 TGGAAATTTGACCTTGAAGAAATTCGATTGACCTTACTTGAAGCTTACTGCTGATGATATT 1064
DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyLeuAspTyTyLeuAspAspIle 300

QY 1065 ATTGACTTATTTAATTGTTGACAAATGTTTCTTCAATTTCCCTGGTAGTGACTATT 1124
DB 301 IleAspLeuPheAsnCysIleuThrAsnValSerSerPheSerLeuValSerValThrIle 320
QY 1125 GAAAGGTTAAAGACTTTTCTTAAATTTTCGGATGGCAACTTTAGAAATTAAGTAACTGT 1184
DB 321 GluArgValIlyAspPheSerTyAsnPheGlyTyTPGlnHisLeuGluLeuValAsnCys 340
QY 1185 AAATTGGAACAGTTTCCCATTTGAACCTCAATCTCTCAAAAGCTTCTTCACTTCC 1244
DB 341 LysPheGlyGlnPheProThrLeuIlySerLeuIlySerLeuIlyArgLeuThrPheThrSer 360
QY 1245 AACCAAGTGGGAATGCTTTTTCAGAAAGTTGATCTTCAAGCCTTGAGTTTCTAGATCTC 1304
DB 361 AsnIlyGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1305 AGTAGAAATGGCTTGAGTTTCAAGGCTGTCTGTTCTCAAGTGAATTTTGGAGAACACAGC 1364
DB 381 SerArgAsnGlyLeuSerPheIlyGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAAGTATTTAGATGAGCTTCAATGAGTGTATTAACATGATGATCAAACTTCTGGGCG 1424
DB 401 LeuIlyTyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1425 TTAGAACAACACTGAACATCTGATTTCCAGACTTCCAAATTTGAACAAATGAGTGATTT 1484
DB 421 LeuGluGlnLeuGlnHisIleuAspPheGlnHisSerAsnLeuIlySerGlnMetSerGluPhe 440
QY 1485 TCAGTATTTCTTATCACTCAAGAACTCAATTTTACCTTGAATTTCTCATCTCACACCAGA 1544
DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHisThrHisThrArg 460
QY 1545 GTTGTCTTAAAGGACTCTTCAATGCTGTGCTGCAAGTCTGGAAGTCTTGAAGTGGCTGCG 1604
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIlyMetAlaGly 480
QY 1605 AATTCTTTCAGAGAAACTTCTCCATGATATCTTCCAGAGCTGAGAACTTGACCTTC 1664
DB 481 AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1665 CTGAACTTCTCAAGTGTCACTGAGAGCAAGTTGTCTCAACAGACATTTAACTCACTCTCC 1724
DB 501 LeuAspLeuSerGlnCysGlnLeuGlnIlyLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1725 AGTCTTCAAGTACTAAATATGAGCCACAACTTCTTCAATGATACGTTTCTCTTAT 1784
DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 540
QY 1785 AAGTGTGAATCTCCCTCCAGAGTTCTTGATTAACGTCAATCACTAATGAAGCTTCCAA 1844
DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTyIlySerLeuAsnHisIleMetThrSerIly 560
QY 1845 AAACAGAACTACAGCAATTTTCAAGTATGCTAGCTTTCTTAAATCTTACAGAAATGAC 1904
DB 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1905 TTTGCTTGAATCTTGGAAACACAGAGTTTCTCGCAATGATTAAGAACACAGAGCAAGCTC 1964
DB 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyIlyLysAspGlnArgGlnLeu 600
QY 1965 TTGTGTGAAGTTGAAGAAATGGAATGTGCAACACTTGAATGATAGAGAGGAGCTGTG 2024
DB 601 LeuValGluValGluArgMetGlyCysAlaThrProSerAspIlyGlnIlyMetProVal 620
QY 2025 CTGAGTTGAATATCACTGTGAGATGAATGAAGCAATCATTTGTTGTGCTCTCACT 2084
DB 621 LeuSerLeuAsnIleThrCysGlnMetAsnIlyThrIleIleGlyAlaSerValLeuSer 640
QY 2085 GTGCTTGAATATCTGTTGTAGCACTTCTGCTATTAAGTTCTATTTTCACTGATGCTT 2144
DB 641 ValLeuValValSerValValAlaValLeuValTyLysPheTyPheHisLeuMetLeu 660
QY 2145 CTTGCTGCTGATGAAGATGATGAGGTGAAGAAATCTATGATGCTTTGTATCTTAC 2204

Db 180 LeuSerSerAsnLysIleGlnSerIleYrCysThrAspLeuArgValLeuHisGlnMet 199
 QY 768 CCCCTACTCAATCTCTCTTAGACCTGTCCCGAACCCTATGAACTTATCCAAACGAGT 827
 Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnProIleGlnProGly 219
 QY 828 GCATTTAAAGAAATTAAGCTTCAAGCTTCAAGCTTAAAGAAATTAATTTGATAGTTAAAT 887
 Db 220 AlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 QY 888 GTAAATGAAAATCTTGATTCAGAGCTGTGGCTGTTTGAAGTCCATCGTTTGGTTGGGA 947
 Db 240 ValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlyValHisArgLeuValLeuGly 259
 QY 948 GAATTTAGAAATGAAGAAATCTGGAAAGTTTGACAAATCTGCTCTAGAGGGCCGTGTC 1007
 Db 260 GluPheArgAsnGlnIleArgLeuHisLysPheAspLysSerAlaLeuGlnGlyLeuCys 279
 QY 1008 AATTGACCAATTGAAGAAATCCGATTAGCATTAAGTACTAGTACTGATGATATTAT 1067
 Db 280 AsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAlaIle 299
 QY 1068 GACTATTTAATGTTTGAACAAATGTTTCTCAATTTCCCTGGTGAAGTGTGACTATTGAA 1127
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
 QY 1128 AGGGTAAAGACTTTCTTATATTTCCGATGGCACTTTAAATTAAGTAACTGTAAT 1187
 Db 320 ArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnCysLys 339
 QY 1188 TTGTGACAGTTCCCATGAAACTCAATCTCTGAAAAGCTTACTTCACTTCCAC 1247
 Db 340 PheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheMetAsn 359
 QY 1248 AAAGGTGGAAATGCTTTTTCAGAAATGATCTACCAAGCTTGAAGTTTCTGATCTCAGT 1307
 Db 360 LysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
 QY 1308 AGAAATGGCTTGAGTTTCAAAAGTGTCTGTCTCAAAAGTATTTGGAGACCAACGACT 1367
 Db 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
 QY 1368 AAGTATTTGATGTGAGCTTCAATGGTGTATTACCATGAGTCAAACTCTTGAGGCTTA 1427
 Db 400 LysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
 QY 1428 GAACTAGTAAATCTGATTTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATTTCA 1487
 Db 420 GlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPheSer 439
 QY 1488 GTATTCCTATCACTCGAAACCTCATTTACCTTGAACATTTCTATACTCACACCAAGATT 1547
 Db 440 ValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrArgVal 459
 QY 1548 GCTTTGAATGGGACTTTCATAGGCTGTCCAGTCTGAGTCTTGAATTTGCTGCGCAAT 1607
 Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsn 479
 QY 1608 TCTTTTCAGAAAATCTCTTCAGATATCTTCAGAGCTGAGAACTTGACCTTCCCTG 1667
 Db 480 SerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeu 499
 QY 1668 GACCTCTCTCAGTGTCACTGAGCAAGTGTCTTCAACAGCATTTAACTCATCTCCAGT 1727
 Db 500 AspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
 QY 1728 CTTGAGTGTCTAAATTAAGCAACAATCTTTTCAATGATGATGCTTCTTATG 1787
 Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
 QY 1788 TGTCTGAACCTCCCTCCAGGTTCTTGATTACAGTCTCAATCACTTAATGACTTCAAAA 1847

Db 540 CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysLys 559
 QY 1848 CAGGAATCAAGACATTTTCCAGTAGTCTAGCTTTCTTAATCTTACTCAGAAATGACTT 1907
 Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
 QY 1908 GCTTGTACTTGTGAACACCAAGATTCTTCAATGGATCAAGGACCAAGGAGCTCTTG 1967
 Db 580 AlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeuLeu 599
 QY 1968 GTGGAAGTTGAAAGAAATGGAATGTGCAACACTTCAATTAAGCAAGGCACTGCTGTGCTG 2027
 Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu 619
 QY 2028 AGTTGAATATCACTGTCAGATGAATGAATGAAATCAATCATTTGGTGTGCGGCTCACTGTG 2087
 Db 620 SerLeuAsnHisLeuThrCysGlnMetCysLysHisIleIleGlyValSerValLeuSerVal 639
 QY 2088 CTGTGATATCTGTGTAGCAAGTTCGTGATCTTAAGTCTTATTTTCACTGATGCTTCTT 2147
 Db 640 LeuValValSerValAlaAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeu 659
 QY 2148 GCTGCTGCATTAAGTATGATGTGAGGTGAAAACATTATGATGCTTTGTATCTACTCA 2207
 Db 660 AlaGlyCysIleIleTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyrSer 679
 QY 2208 AGCCAGGATGAGGACTGGGTAAAGGATGAGCTAGTAAAGAAATTTAGAAAGGGGCGCT 2267
 Db 680 SerGlnAspGlnAspTyrAlaArgAsnGlnLeuValLysAsnLeuGlnGlyValPro 699
 QY 2268 CCATTTCACTGTGCTTCACTACAGAGACTTATTCCTGGTGTGCGCACTTGTGCGCAAC 2327
 Db 700 ProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAlaAsn 719
 QY 2328 ATCATCATGAAGTTTCCATAAAGCCGAAAGGTGATTTGTGTGTGCCAGACTTC 2387
 Db 720 IleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHisPhe 739
 QY 2388 ATCCAGAGCGGTGCTGTATCTTTGAATTAAGATTGATGCTCAGACCTGGAGTTCTGAGC 2447
 Db 740 IleGlnSerArgTyrPheIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeuSer 759
 QY 2448 AGTCGTGCTGATCATCTTCAATTTGCTGCGAAGGTGAGCAAGCACTGCTCAGAGCAG 2507
 Db 760 SerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuAsnGln 779
 QY 2508 CAGGTGAGCTGTACCGCTTCTCAGACAGAACTTACCTGAGTGGAGAGCAGTGTCTC 2567
 Db 780 GlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSerVal 799
 QY 2568 CTGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCCTGTGATGGTAAATGATG 2627
 Db 800 LeuGlnArgHisIlePheThrArgArgLeuAspGlyValAlaLeuLeuAspGlyLysSerTyr 819
 QY 2628 AATCCAGAGAAACAGTGGGTACAGATGCAATTTGGCAGAAACATCTATC 2681
 Db 820 AsnProGlnGlyThrValGlyThrGlyCysAsnThrProGlnGlnAlaThrSerIle 837
 Db
 RESULT 7
 AAE16102
 ID AAE16102 standard; protein; 837 AA.
 AC AAE16102;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 XX
 DB Human DNAX Toll like receptor (DTLR) 4 #2.
 DB
 KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KW Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX
 XX Homo sapiens.
 XX

PN WO200190151-A2.
 XX 29-NOV-2001.
 XX 23-MAY-2001; 2001MO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 XX Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;
 XX WPI; 2002-083085/11.
 XX N-PSDB; AAD26292.
 PT New DNAJ Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS Claim 3; Page 41; 297pp; English.
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAJ Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detection or diagnosing various immunological conditions related to
 CC expression of DTLR or cells that express it. The present sequence is
 CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAE16116). However these sequences differ
 CC at several locations
 CC
 XX
 XX
 SQ Sequence 837 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4315.50 Matches: 837
 Percent Similarity: 95.33% Conservative: 0
 Best Local Similarity: 95.33% Mismatches: 0
 Query Match: 64.18% Indels: 41
 DB: 5 Gaps: 1
 US-09-396-985B-3 (1-3811) x AAE16102 (1-837)
 QY 48 ATGTCTGCTGGCGCTGGAGCTGTGATCCAGCCATGAGCTTCTCTCTCGCG 107
 Db 1 MetSerLaseRArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
 QY 108 AAGACCGAAGAGCTGGAGCGCTCGGTGAGACTTGGCCCTTAACCAACAGAAAGAGCTGG 167
 Db 21 ArgProGlnSerIlePrlGluProCysValGlu----- 30
 QY 168 CATGAACCCAGAGCTTTCAGACTCCGAGAGCTCAGCCCTTCAACCCGATTCATTGCTT 227
 Db 30 ----- 30
 QY 228 CTGTGCTAAATGCTGCGGTTTTCACAGAGGTGGTCTTAATATTACTTATCAATGATG 287
 Db 31 -----ValProAsnIleThrIleGlnCysMet 39
 QY 288 GAGCTGAATTTTCTACAAATCCCGCAACACTCCCTTCTCAACCAAGAACTGGAGCTTG 347
 Db 40 GluLeuAsnPheTyrIlePrlProAsnLeuLeuProPheSerThrIleAsnLeuAsnLeu 59

QY 348 AGCTTTAATCCCTGAGGCAATTTAGGCACTATAGCTTCTGAGTTTCCAGAACTGCAG 407
 Db 60 SerPheAsnProLeuAsnIleGlnIleSerIleTyrSerPhePheSerPheProIleuGln 79
 QY 408 GTGCTGATTTTATCCAGGTGTGAAAATCCAGCAATTAAGATGGGCAATATGAGACCTTA 467
 Db 80 ValLeuAspLeuSerArgCysGluIleGlnIleThrIleGlnAspGlyAlaTyrGlnSerIleu 99
 QY 468 AGCCACCTCTCTACCTTAATATTGACAGAAAACCCCATCCAGAGTTTAGCCCTGGAGCC 527
 Db 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 QY 528 TTTTTCGAGCTATCAAGTTTACAGAGCGGTGGCTGGAGACAATCTAGCATCTCTTA 587
 Db 120 PheSerGlyLeuSerSerIleuGlnIleuValAlaValGluThrAsnLeuAlaSerLeu 139
 QY 588 GAGAACTTCCCATTTGACATCTCAAAAATTGAAAAGAACTTAATGTGGCTCACAATCTT 647
 Db 140 GluAsnPheProIleGlyHisIleuLysThrIleuLysGluLeuAsnValAlaHisAsnLeu 159
 QY 648 ATCCAAATCTTTCAATTTACCTGAGTATTTTCTAATCTGACCAATCTGAGACCTTGAC 707
 Db 160 IleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisIleuAsp 179
 QY 708 CTTTCCAGCAACAAGTTCAAAGTATTTATTCACAGACTTGGGGTTCTCATCAATG 767
 Db 180 LeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
 QY 768 CCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTTGAACCTTATTCACACAGGT 827
 Db 200 ProLeuAsnLeuSerSerLeuAspSerLeuAsnProMetAsnPheIleGlnProGly 219
 QY 828 GATTTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATTAATTTGATAGTTAAT 887
 Db 220 AlaPheLysGluIleArgLeuHisLysLeuThrIleuAspAsnPheAspSerLeuAsn 239
 QY 888 GTAATGAAAACCTGTATTCACAGCTCGGCTGTTTGAAGCTCATCGTTTGTCTGGGA 947
 Db 240 ValMetLysThrCysIleGlnIleuValAspGlyLeuValHisArgLeuValLeuGly 259
 QY 948 GAATTTAGAAATGAAGAACTTGGAAAATTTGAACAATCTGCTCTAGAGGCGCTGTGC 1007
 Db 260 GluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluIleuCys 279
 QY 1008 AATTGACCATTTGAAGAAATCCGATTAGCATCTTAGACTACTGATGATATATATT 1067
 Db 280 AsnLeuThrIleGlnIleuPheArgLeuAlaTyrIleuAspTyrTyrIleuAspAspIleIle 299
 QY 1068 GACTTATTAAATTTGTTGCAAAATGTTCTTCAATTTCCCTGGTGAAGTGTGACTATTGAA 1127
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerIleuValSerValThrIleGlu 319
 QY 1128 AGGTTAAAGACTTTTCTTAATATTGCGATGGCAACAATTTGAATTAAGTTAAGTTAA 1187
 Db 320 ArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisIleuGluLeuValAsnCysLys 339
 QY 1188 TTTGAGACAGTTTCCCAATTTGAAGTCAAAATCTTCAAAAAGGCTTACTTCTCCAC 1247
 Db 340 PheGlyGlnPheProThrIleuLysLeuLysSerIleuLysArgLeuThrPheThrSerAsn 359
 QY 1248 AAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCTAGACTCTAGT 1307
 Db 360 LysGlyGlyAsnAlaPheSerGluValAspLeuProSerIleuGluPheLeuAspLeuSer 379
 QY 1308 AGAAATGGCTTGAGTTTCAAAAGTTGCTGTTCTCAAAATGATTTTGGACAACAAGCCTTA 1367
 Db 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerIleu 399
 QY 1368 AAGTATTTAGATCTGAGCTTCAATGCTGTATTTACATGAGATTTCAAACTTCTGGGCTTA 1427
 Db 400 LysTyrIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419

QY 1428 GAAACAAGTGAACATCTGATATTCAGACATTCAGATTTGAACAATGAGTGAAGTTTCA 1487
 DB 420 G|U|G|I|L|e|u|g|I|u|H|I|s|L|e|u|A|p|h|e|G|I|n|H|I|s|e|r|A|s|n|L|e|u|y|s|e|G|I|n|e|t|S|e|r|G|I|u|p|S|e|r| 439
 QY 1488 GTATTCCTATCATTCAGAAACCTCATTTACTTGACATTTCTCATACTCATCACCAGAGTT 1547
 DB 440 ValPheLeuSerLeuValrGaenLeuLeIeTyLeuAspLlIeSerHlstrHrLstrArGVal 459
 QY 1548 GCTTTCAGATGAGCATCTTCAGATGGCTTGTCAGTCTCGAATCTTGAATTAAGGCTGGCAAT 1607
 DB 460 AlApheAsnG|L|I|e|P|he|A|s|n|G|L|Y|L|e|u|S|e|r|S|e|r|L|e|u|G|I|U|L|e|u|y|S|e|C|A|G|L|Y|A|s|n 479
 QY 1608 TCTTTCAGAGAAAATCTCTTCAGATATCTTCAGACAGCTGAGAAAATTCAGCTTCCTG 1667
 DB 480 SerPheG|I|n|G|I|u|S|n|P|he|L|e|u|P|ro|A|s|P|I|e|P|he|T|H|G|I|u|e|u|r|g|a|n|L|e|u|H|r|P|he|L|e|u 499
 QY 1668 GACCTCTCTAGGTGTCACATGAGACAGTTGTCTTCAGACAGCATTTAACTCATCTCCAGT 1727
 DB 500 AspLeuSerG|I|n|G|I|u|S|n|P|he|L|e|u|G|I|U|L|e|u|S|e|r|P|ro|H|r|A|P|he|A|s|n|S|e|r|L|e|u|S|e|r| 519
 QY 1728 CTTCAGGTAATAATATGAGCCCAACAACATCTTTCATTTGATACGTTTCTTAAAG 1787
 DB 520 LeuG|I|n|V|a|L|e|u|S|n|e|t|S|e|r|H|s|A|s|n|P|he|S|e|r|L|e|u|S|p|H|r|P|he|P|ro|T|Y|r|Y|s| 539
 QY 1788 TGTCTGAACCTCCCTCCAGGTTCTTGATTAAGTCTCAATCACTAATGACTTCCAAAATA 1847
 DB 540 CyLeuAsnSerLeuG|I|n|V|a|L|e|u|A|s|P|T|Y|S|e|r|L|e|u|S|n|H|I|s|I|e|H|e|T|H|S|e|r|L|y|S|e| 559
 QY 1848 CAGGAACCTACAGCATTTTCCAGATGCTTACGTTTCTTAAATCTTACTCAGAAATGACTTT 1907
 DB 560 G|I|n|G|I|u|e|u|G|I|n|H|I|s|P|he|P|ro|S|e|r|L|e|u|A|P|he|L|e|u|S|n|L|e|u|H|r|G|I|n|A|s|n|A|s|P|he 579
 QY 1908 GCTTGTACTTGTAACAACCCAGATTCCTTCAGATTCAGATTCAGAGACAGGAGCTCTTG 1967
 DB 580 AlaCythrCyS|G|I|u|H|I|s|G|I|n|S|e|r|P|he|L|e|u|G|I|n|T|P|I|e|L|y|s|A|s|P|G|I|n|A|G|I|n|L|e|u| 599
 QY 1968 GTGGAAGTTGACGAATGGAATGGAATGCAACCTTCAGATTAAGAGGAGGATGCTGTGCTG 2027
 DB 600 ValG|I|V|a|G|I|u|r|g|e|t|G|I|u|C|Y|A|L|a|T|H|r|P|ro|S|e|r|A|s|P|S|e|G|I|n|G|I|U|Y|e|t|P|ro|V|a|L|e|u 619
 QY 2028 AGTTTGATATTCACCTGTCAGATGATTAAGACCATCATTCGTTGCTGCTCAGTGTG 2087
 DB 620 SerLeuAsnL|e|H|r|C|Y|S|G|I|n|e|t|A|s|n|L|y|T|H|r|I|e|L|I|e|G|I|Y|a|S|e|r|V|a|L|e|u|S|e|r|V|a|L 639
 QY 2088 CTGTGATGATCTGTGTAGAGATTCGCTATTAAGTCTATTTCACTTCAACCGAGCTTCTT 2147
 DB 640 LeuValValSerValValAlaValLeuValTyL|Y|S|P|he|Ty|r|P|he|H|I|s|L|e|u|K|e|t|L|e|u| 659
 QY 2148 GCTGCGTCGATAAGTATGATGATGAGGTAAGAAACATCATGATGCTTGTATCTACTCA 2207
 DB 660 AlAeG|I|C|Y|S|I|e|L|e|Y|r|G|I|Y|A|G|G|I|Y|G|I|U|S|n|L|I|e|T|r|A|s|P|A|L|A|P|he|V|a|L|I|e|T|r|Y|S|e|r 679
 QY 2208 AGCCAGATGAGAGACTGGGTAGGAATGAGCTAGTAAAGATTTAGAAAGAGGGGTGCTT 2267
 DB 680 SerG|I|n|A|s|P|I|u|A|s|P|T|P|V|a|L|A|G|A|s|n|G|I|U|L|e|u|V|a|L|y|S|a|n|L|e|u|G|I|U|G|I|Y|V|a|L|P|ro 699
 QY 2268 CCATTTACGCTCGCTTCCTACACAGACATTTATCCCGGTGTGGGCAATTCCTGCCCAAC 2327
 DB 700 P|ro|P|he|G|I|n|e|u|S|L|e|u|H|I|S|T|Y|r|A|G|A|s|P|P|he|I|e|r|P|o|I|Y|a|L|a|I|e|a|I|e|a|A|a|s|n 719
 QY 2328 ATCATCATGAGATTTCCATTAAGCCGAAAGGATGTTGTTGCTGCTCCAGCACTTC 2387
 DB 720 I|L|I|e|I|H|I|S|G|I|U|L|Y|P|he|H|I|S|Y|S|e|r|H|r|G|I|Y|V|a|L|I|e|V|a|L|V|a|L|S|e|r|G|I|n|H|I|S|P|he 739
 QY 2388 ATCCAGAGCGGCTGTGTATCTTGAATATGAGATTCCTCAGACCTGCGAGTTTCTGAGC 2447
 DB 740 I|L|E|G|I|S|e|r|A|T|P|C|Y|S|I|e|P|he|G|I|U|r|G|I|U|L|e|A|I|n|H|r|T|P|G|I|n|P|he|L|e|u|S|e|r 759
 QY 2448 AGTCGCTGCTGATCATCTTCATTCCTTCAGAGAGTGAAGAGACCCCTGCTCAGGAGC 2507
 DB 760 SerArG|A|L|G|I|Y|L|I|e|I|P|he|I|e|V|a|L|e|u|G|I|n|Y|V|a|G|I|U|Y|S|T|H|r|L|e|u|A|V|A|G|G|I|n 779
 QY 2508 CAGGTGAGCTGTACCGCTTTCAGAGGAACAATTACTGAGGTGAGAGACAGTGTG 2567

DB 780 G|I|n|V|a|G|I|u|L|e|u|T|Y|r|A|r|g|L|e|u|S|e|r|A|r|g|a|n|T|H|r|T|Y|L|e|u|G|I|u|r|T|P|G|I|u|S|e|r|V|a|L 799
 QY 2568 CTTGGGGGGGACACATCTCTCGAGAGACATCAGAAAAGCCCTGCTGATGGTAATCATG 2627
 DB 800 LeuG|I|Y|A|r|H|I|e|H|r|P|A|r|g|L|e|u|A|r|g|L|V|A|L|e|u|S|n|S|p|G|I|Y|S|e|r|T|P 819
 QY 2628 AATCCAGAGAGAACTAGTGGTACAGATCAATTCGTCAGAGAACATCTATC 2681
 DB 820 AsnProG|I|U|G|I|Y|T|H|r|V|a|L|G|I|Y|T|H|r|G|I|Y|C|Y|A|s|n|T|P|G|I|n|G|I|u|A|L|e|H|r|S|e|r|I|e 837
 RESULT 8
 ABU04776
 ID ABU04776 standard; protein; 837 AA.
 XX
 AC ABU04776;
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1442.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 OS Homo sapiens.
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PP 28-MAR-2001; 2001US-0279495P.
 XX
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 837 AA:

Alignment Scores:

Pred. No.:	0	Length:	837
Score:	4315.50	Matches:	837
Percent Similarity:	95.33%	Conservative:	0
Best Local Similarity:	95.33%	Mismatches:	0
Query Match:	64.18%	Indels:	41
DB:	6	Gaps:	1

US-09-396-985b-3 (1-3811) x ABU04776 (1-837)

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QY 48 AATGTCCTCGGCGCTGGCTGAGCTGATCCAGCCATGCGCTTCTCTCGCTG 107
DB 1 MeSeSeAlaSeSrIeGluIaGlyThrIleuIleProAlaMeValaIheSeuSerCyVal 20
QY 108 AGACCGAAAGCTGGAGCCCTGCTGGAGACTTGGCCCTAAACACACAGAAAGACTGG 167
DB 21 ArgProGluSerTrpGluProCyValGlu----- 30
QY 168 CATGAACCAAGAGCTTTCAGACTCGGAGAGCTCAGCCCTTACCCCGATTCCATTGCTT 227
DB 30 ----- 30
QY 228 CTGCTAAATGCTGCCGTTTATCACGAGGTGGTCTTAATATTACTTATCAATGCTAG 287
DB 31 -----ValProAsnIleThrTyrgInCybMet 39
QY 288 GAGCTGAATTTCTACAAATCCCGCAACCTCCCTTCTCAACCAAGAACTGGACTGG 347
DB 40 GluLeuAsnPhenTyriLysIleProAspAsnLeuProPheSerThriLysAsnLeuAspLeu 59
QY 348 AGCTTAATCCCTGAGGCACTTAGGAGCTATAGCTTCTTCACTTCCAGAACTGACG 407
DB 60 SerPheAsnProleuAsnTrgIleuGlySerTyriSerPhePheSerPheProGluLeuGln 79
QY 408 GTGCTGATTTATCAAGTGTGAATCAACACATTTGAAGATGGGCAATATCAGAGCTTA 467
DB 80 ValLeuAspLeuSerTrgCysGluIleGlnThrIleGluAspGlyAlaTyrgInSerLeu 99
QY 468 AGGCACTCTTACCTTAATATTGACAGAAACCCATCCAGAGTTTACGCCCTGGAGGC 527
DB 100 SerHisLeuSerThriLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 528 TTTTTCGACTATCAAGTTTACAGAGCTGGTGGCTGTGGAGACAATCTAGACTCTTA 587
DB 120 PheSerGlyLeuSerSerLeuGlnIlySleuValAlaValGluThrAsnLeuAlaSerLeu 139
QY 588 GAGAACTTCCCAATGGACATCTCAAAACTTTGAAAGAACTTAATGTGCTCAAACTTT 647
DB 140 GluAsnPhenProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsnLeu 159
QY 648 ATCCAAATCTTGAATTAATCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTTGGAC 707
DB 160 IleGlnSerPheLysLeuProGluTyriPheSerAsnLeuThrAsnLeuGluHisLeuAsp 179
QY 708 CTTTCAGAAACAAGTTCAAGATTAATTATTCAGACAGACTGGGGGTTCTCAACTCAAAAG 767
DB 180 LeuSerSerAsnLysIleGlnSerIleTyriCysThrAspLeuArgValLeuHisGlnMet 199
QY 768 CCCCTACTCAATCTCTTTAGACTGTCCCTGAACTTGAACCTTATGAACCTTATCAACAGGT 827
DB 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnHeIleGlnProGly 219
QY 828 GCATTTAAAGAAATTAGGCTTCAATAAGCTGACTTTAAGAAATAATTTGATAGTTTAAT 887
DB 220 AlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
QY 888 GTATATGAAGCTGTATTCAGAGCTGGCTGGTTTGAAGTTCATGCTGTTGGTTGGGA 947
DB 240 ValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
QY 948 GAATTTAGAATGAGGAAACTTGAAGAAAGTTTGACAAATCTGCTAGAGGCGCTGTGC 1007

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DB 260 GluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeuCyS 279
QY 1008 AATTGACCACTTGAAGAAATTCGATTAACATTAATCTAGACTAGTGAATTTATTT 1067
DB 280 AsnLeuThrIleGlnGluProPheArgLeuAlaTyriLeuAspTyriTyriLeuAspAspIleIle 299
QY 1068 GACTTATTTAATTTGTTTGCACAAATGTTTCTTCAATTTCCCTGGAGTGTGACTATTTGA 1127
DB 300 AspLeuPheAsnCyLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
QY 1128 AGGTTAAAGACTTTTCTTAATATTGCGATGGCAACTTTAGAAATTAGTTACTGTAA 1187
DB 320 ArgValLysAspPheSerTyriAsnPheGlyTrpGlnHisLeuGlnLeuValAsnCyLys 339
QY 1188 TTTTGACAGTTTCCCAATTTGAAGTCAAAATCTCCAAAAGGCTTACTTCCCTCCAC 1247
DB 340 PheGlyGlnPheProThrLeuLysLeuLysSerLysValArgLeuThrPheThrSerAsn 359
QY 1248 AAGGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTCAGT 1307
DB 360 LysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeuSer 379
QY 1308 AGAAATGCTTGAATTTCAAAAGCTTGTCTCAAGTATTTTGGACAAACAGCTTA 1367
DB 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1368 AAGTATTTAGATCTAGAGCTTCAATGTTGTTATTAACATGAGTTCAAACTTCTGGGCTTA 1427
DB 400 LysTyriLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1428 GAACAACCTAGAACATCTGATTTCCAGACTTCCAAATTTGAAACAATGAGTGAATTTTCA 1487
DB 420 GluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPheSer 439
QY 1488 GTATTTCTATCACTAGAAACCTCAATTAATCTTGAATCTCACTCAACAGAGTT 1547
DB 440 ValPheLeuSerLeuArgAsnLeuIleTyriLeuAspIleSerHisIleThrHisArgVal 459
QY 1548 GCTTCAATGGCATCTTCAATGCTTGTCCAGTCCGAAAGTTTGAAGATGGCTGGCAAT 1607
DB 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLysGluValLeuLysPheCysIleGlyAsn 479
QY 1608 TCTTTTCAGAAACCTTCCCTTCCAGATATCTTCAAGAGCTGAGAACTTGAACCTTCTG 1667
DB 480 SerPheGlnGluAsnPhenProAspIlePheThrGluLeuArgAsnLeuThrPheLeu 499
QY 1668 GACCTCTCAGTGTCAACTGGAGAGCTTGTCTCAACAGACTTTTAATCACTTCCAGT 1727
DB 500 AspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1728 CTTTCAGATCTTAATATGAGCCACAAACAATCTTTCATTCAGATACGTTTCTTAATAG 1787
DB 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyriLys 539
QY 1788 TGTCTGAATCTCCCTCAAGGTTCTTGAATPACGTCTCAATCACAATATGACTTCCAAAAA 1847
DB 540 CysLeuAsnSerLeuGlnValLeuAspTyriSerLeuAsnHisIleMetThrSerLysLys 559
QY 1848 CAGAACTACAGCAATTTTTCAGATGCTAGCTTTCTTAATCTTACTCAGAAATGACTTT 1907
DB 560 GlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY 1908 GCTTGACTTGGAGACACAGAGTTTCCCTGCAATGAGTAAAGACACAGAGGAGCTCTTG 1967
DB 580 AlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeuLeu 599
QY 1968 GTGGAAGTGAAGCAATGGAATGTGCAACACTTCAATATPACAGAGGCACTGCTGTGCTG 2027
DB 600 ValGluValGluArgMetGluCysAlaThrProSerAspLysGlnIlyMetProValLeu 619
QY 2028 AGTTGAATATCACTGTCAATGATGAATAAGACATCATTTGTGTGTGGTCTCAGTGTG 2087

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Db      620 SerIeuAsnIleThrCysGlnMetAsnIysThrIleIleGlyValSerValIleuSerVal 639
QY      2088 CTGTGAGTATCTGTGTAGACAGTCTGTGCTATAGTCTATTTGACCGTACGTTCTT 2147
Db      640 LeuValValSerValValAlaValIleValIleValIleValIleValIleValIleValIleVal 659
QY      2148 GCTGCGTGCATTAAGTATGTTAGAGGTGAAACATCATGATGCTTTGTTATCTACTCA 2207
Db      660 AlaGlyCysIleIleThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIleThr 679
QY      2208 AGCCAGATGAGAGCATGGGTGAGAGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 2267
Db      680 SerGlnAsnIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 699
QY      2268 CCATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2327
Db      700 ProIleGlnIleuValSerValIleValIleValIleValIleValIleValIleValIleValIle 719
QY      2328 ATCATTCATGAAAGTTTCCATTAAGACCCGAAAGGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTT 2387
Db      720 IleIleIleGlnIleuValSerValIleValIleValIleValIleValIleValIleValIleVal 739
QY      2388 ATCCAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2447
Db      740 IleGlnSerValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 759
QY      2448 AGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2507
Db      760 SerValIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 779
QY      2508 CAGGTGAGACTGATCCGCTCTTCCAGAGAGAACCTTACCTGAGTGGAGAGACAGTGTCT 2567
Db      780 GlnValGlnIleuValIleValIleValIleValIleValIleValIleValIleValIleVal 799
QY      2568 CTGGGCGCGCACATCTTCTGAGAGACATCAGAAAGCCCTGCTGATGCTAAATCATGCG 2627
Db      800 LeuGlyArgHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 819
QY      2628 AATCCAGAGAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2681
Db      820 AsnProGlnIleuValIleValIleValIleValIleValIleValIleValIleValIleVal 837

RESULT 9
AAE16116
ID      AAE16116 standard; protein; 837 AA.
AC      AAE16116;
DT      26-MAR-2002 (first entry)
DB      Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX      Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW      Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX      Homo sapiens.
OS      Homo sapiens.
XX      Key Location/Qualifiers
FH      Misc-difference 211
FT      /label= Unknown
FT      /note= "Encoded by AAY"
XX      MO200190151-A2.
XX      29-NOV-2001.
XX      23-MAY-2001; 2001WO-US016766.
XX      25-MAY-2000; 2000US-0207558P.
XX      (SCHE ) SCHERING CORP.
XX      Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;
PI

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XX      WI: 2002-083085/11.
DR      N-PSDB; AAD26306.
XX      New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT      conditions exhibiting abnormal expression of the receptors of their
PT      ligands, particularly abnormalities manifested by immunological
PT      disorders.
XX      Claim 3; Page 240-243; 297pp; English.
XX      The invention relates to mammalian receptor proteins, e.g., primate,
XX      human DNAX Toll like receptor (DTLR) protein and their corresponding
XX      nucleic acids. The DTLR is useful for treating conditions exhibiting
XX      abnormal expression of the receptors of their ligands. Such abnormality
XX      is manifested by immunological disorders. In particular, the DTLR is
XX      useful for treating various disease or disorders associated with abnormal
XX      expression or abnormal triggering of response to a ligand. The DTLR is
XX      also useful as an immunogen for the production of antisera or antibodies
XX      specific, e.g., capable of distinguishing between other interleukin (IL)-1
XX      receptor family members, for the DTLR or its various fragments. The
XX      purified DTLR can be used to screen monoclonal antibodies or antigen-
XX      binding fragments. The antibodies are useful for screening expression
XX      libraries for particular expression products. These are useful for
XX      detecting or diagnosing various immunological conditions related to
XX      expression of DTLR or cells that express it. The present sequence is
XX      human DTLR4 protein, alternative version. The DTLR4 gene is located on
XX      chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
XX      be similar to the sequence shown in page 41 (AAE16102). However these
XX      sequences differ at several locations
SQ      Sequence 837 AA;
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 4308.50 Matches: 836
Percent Similarity: 95.22% Conservative: 0
Best Local Similarity: 95.22% Mismatches: 1
Query Match: 64.08% Indels: 41
DB: 5 Gaps: 1

US-09-396-985B-3 (1-3811) x AAE16116 (1-837)
QY      48 ATGTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107
Db      1 MetSerAlaSerArgIleuAlaGlyThrIleuIleProAlaMetAlaIleuSerCysVal 20
QY      108 AGACCAAGAAAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 167
Db      21 ArgProGlnIleuSerTrpGlnProCysValGlu 30
QY      168 CATGAACCCAGAGCTTTCAGACTCCGAGGCTCAGCCCTTACCCGATTCATTGCTT 227
Db      30 30
QY      228 CTGTGCTAATGCTGCGCTTTTATCAAGAGTGGTCTCTAATATTACTTATCAATGATG 287
Db      31 ValProAsnIleThrIleGlnCysSer 39
QY      288 GAGCTGAATTTCTACAAATCCCGCAACCTCCCTTCTCAACCAAGAACCTGACCTG 347
Db      40 GluIleuAsnPheThrIleIleProAsnIleuProPheSerThrIleAsnIleuSerIleu 59
QY      348 AGCTTTAATCCCTGAGGCTTATGAGCAGCTATAGCTTTCTTCAAGTTCCCAAGATGCGAG 407
Db      60 SerPheAsnProIleuArgHisIleuGlySerIleuPhePheSerPheProGlnIleuGln 79
QY      408 GTGCTGATTTATCCAGGTGTAATCCAGAAATGGAATGAGTGGGCAATGAGGCCCTA 467
Db      80 ValIleuAsnIleuSerArgCysGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 99
QY      468 AGCCAGCTCTTACCTTAATTTGACAGAAACCCCATTCAGATTTAGCCCTGGAGCC 527

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Db SerHisLeuSerThrIleuLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 528 TTTTCGAGCTATCAAGTTTACGAGCTGGTGGCTGGAGCAAAATGACATCTCA 587
Db 120 PheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
QY 588 GAGAACTTCCCACTTGACATCTCAAAAATTGAAAAGAACTTAAATGGCTCAAACTTT 647
Db 140 GluAsnPheProIleGlyHisLeuIySthrIleuLyGluLeuAsnValAlaHisAsnLeu 159
QY 648 ATCCAACTTTCAATTAACCTGAGATATTTTCTAATCTGACCAATCTTAAGACCTTGAC 707
Db 160 IleGlnSerPheIySLeuProGlnIyPheSerAsnLeuThrAsnLeuGlnIlySLeuAsp 179
QY 708 CTTTCAGAGCAAGATGAAAGTATTTATTTATGACAGACTTGGGGTCTTACATCAAG 767
Db 180 LeuSerSerAsnIySleGlnSerIleIyYrCySthrAspLeuArgAlaLeuHisGlnMet 199
QY 768 CCCCTACATCTCTCTTGAACCTGTCCCTGAACTTGAACCTTAACTTCAACAGAGT 827
Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeu***ProMetAsnPheIleGlnProGly 219
QY 828 GCATTTAAAGAAATTAAGCTTCAATAGCTGACTTTAAAGAAATATTTGATAGTTAAAT 887
Db 220 AlaPheLyGlnIlyLeuArgLeuHisIySLeuThrIleuAlaArgAsnAsnPheAspSerLeuAsn 239
QY 888 GTAATTAAGAACTTGATTCAGAGCTGGCTGGCTTGAAGTCCATGGTTGGTCTGGGA 947
Db 240 ValMetLySthrCySleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
QY 948 GAATTTAGAAATGAGAAACTTGAAGAAAGTTGACAAATCTGCTAGAGGCTGTGC 1007
Db 260 GluPheArgAsnIyGlnIyAsnLeuGlnIyYrPheAspIySLeuAlaLeuGlnIyLeuCyS 219
QY 1008 AATTTGACCATGAGAAATTCGATTAAGCATTAAGTACTTAAGTCTGATGATTAAT 1067
Db 280 AsnLeuThrIleGlnIyPheArgLeuAlaIyYrLeuAspIyYrIyLeuAspAspIleIle 299
QY 1068 GACTTTTAAATGTTGACAAATGTTTCTCATTTTCCCTGGTGGTGGTACTATTA 1127
Db 300 AspLeuPheAsnCySLeuThrAsnValSerSerPheSerLeuValSerValIlnrIleGln 319
QY 1128 AGGGTAAAGACTTTCTTAATAATTCGATGAGCAATTTAGAAATTAAGTTAACTGAAA 1187
Db 320 ArgValIyAspAspPheSerIyYrAsnPheGlyYrGlnHisIleuGlnLeuValAsnCySlyS 339
QY 1188 TTTGACAGCTTCCACATTAAGATCTCAAACTCTCAAAAGCTTACCTTCACTCCAC 1247
Db 340 PheGlyGlnPheProThrIleuIySLeuIySLeuIySLeuIySLeuIySLeuIySLeuIySLeu 359
QY 1248 AAGGTGGGGAATGCTTTTCAAGATTAAGTCAAGCTTGAAGCTTGAAGTCTGAGT 1307
Db 360 LySgLyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
QY 1308 AGAAATGCTTGAAGTTCAAGGTTGCTGTCTCAAGTGAATTTGGGCAACAGAGCTTA 1367
Db 380 ArgAsnGlyLeuSerPheIySgIyCySlySerGlnSerAspPheGlnIlnrIlnrSerLeu 399
QY 1368 AAGTATTTAGATGAGCTTCAATGGTGTATTAACCATGAGTTCAAACTTTGGGCTTA 1427
Db 400 LyYrIyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1428 GAACAATGAGAACTGGAATTTCCAGACTTCCAAATTTGAACAAATGAGTGAAGTTTCA 1487
Db 420 GlnGlnLeuGlnIlyHisLeuAspPheGlnHisSerAsnLeuIySglnMetSerGlnPheSer 439
QY 1488 GATTCCTATCACTGAGAAACTCAATTACCTTGAACATTTCTCATACTCACAGAGTT 1547
Db 440 ValPheLeuSerLeuArgAsnLeuIleIyYrLeuAspIleSerHisIlnrHisIlnrArgVal 459
QY 1548 GCTTTCAATGGCATTTCAATGGCTTGTCCAGTCTCCAGAGTCTTGAATGGCTGGCAAT 1607
Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValIleuIySMeAlaGlyAsn 479

QY 1608 TCTTCCAGAAAACCTTCCAGATATCTTCAAGAGCTGAGAACTTGAACCTTCCGTG 1667
Db 480 SerPheGlnIyAsnPheLeuProAspIlePheThrGlnLeuAlaArgAsnLeuThrPheLeu 499
QY 1668 GACCTCTCTCAGTGTCAACTGGAGAGCTTGTCTCAACAGCAATTTAACTCACTCCAGT 1727
Db 500 AspLeuSerGlnCyGlnLeuGlnIyGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1728 CTTTCAGATCTAAATATGAGCCCAACAACTTCTTTCATTTGGAATGAGTTTCCCTTAAG 1787
Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspPheProIyYrIyS 539
QY 1788 TGTGTGAACCTCCCTCCAGAGTCTTGAATTAAGTCAAGTCAATCAATATGACTTCAAAAAA 1847
Db 540 CySLeuAsnSerLeuGlnValLeuAspIySLeuAsnHisIleMetHisSerIySlyS 559
QY 1848 CAGGAATCAAGCAATTTTCAAGTACTAGCTTCTTAATCTTAACTCAAGATGACTTT 1907
Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY 1908 GCTTGTACTTGGAAACACAGAGTTTCTGCAATGGAATCAAGACACAGAGGAGCTTGG 1967
Db 580 AlaCySthrCySglnHisGlnSerPheLeuGlnIlnrIlySAspGlnArgGlnLeuLeu 599
QY 1968 GTGGAAGTTGAACGAATGGATGTGCAACACTTCAAGATTAAGCAGAGGAGCTGTGCTG 2027
Db 600 ValGlnValGlnIyArgMetGlnCySAlaThrProSerAspIyGlnIyMetProValLeu 619
QY 2028 ACTTTGAATATCACTGTCAAGATGAATGAATGAACCAATCATTTGCTGTGCTCTCAGTGTG 2087
Db 620 SerLeuAsnIleThrCyGlnIlnrAsnIySthrIleIleGlyValSerValLeuSerVal 639
QY 2088 CTTTGTAGTATCTGTTGTAGCACTTGTGCTATTAAGTTCTATTTCACTGATGCTTCTT 2147
Db 640 LeuValValSerValValAlaValLeuValIyYrIySlyPheIyYrPheHisIleuMetLeuLeu 659
QY 2148 GCTGCTGCATTAAGATGATGTAGAGGTGAAAACATCTATGAGCCTTGTGTATTACTCA 2207
Db 660 AlaGlyCySAlaIlySlyYrGlnArgGlnIyGlnIyAsnIleIyYrAspAlaPheAlaIleIyS 679
QY 2208 ACCCAGATGAGAGACTGGGTAAAGATGAGTAAAGATTAAGAAATTTAGAGAGGGTGGCT 2267
Db 680 SerGlnAspGlnAspIyYrValIyArgAsnGlnLeuValIySAsnLeuGlnIyGlnIyAlaPro 699
QY 2268 CCATTTACAGCTTGTGCTTCACTAAGAGACTTTATTTCCGGGTGGCCATTTCTCCCAAC 2327
Db 700 ProPheGlnLeuCySLeuHisIyYrIyArgAspPheIleProGlyValAlaIleAlaAsn 719
QY 2328 ATCATCATGAGAGTTTCCATTAAGCCGAAAGGTGATTTGTTGGGTGCCAGCACTTC 2387
Db 720 IleIleHisGlnIyGlnPheHisIySLeuArgIySValIleValValSerGlnHisPhe 739
QY 2388 ATCCAGAGCCGCTGTGTATCTTTGAATATGAAGATTTGCTCAGACCTGGCAGTTTCTGAC 2447
Db 740 IleGlnSerArgIyYrCySlePheGlnIyYrGlnIleAlaGlnIlnrIlnrPheLeuSer 759
QY 2448 AGTCGTGCTGTATCATCTTCAATGTCCTGCGAAGAGTGGAGAAACCTTGGCTCAGGCGAG 2507
Db 760 SerArgAlaGlyIleIlePheIleValLeuGlnIySValGlnIySLeuThrLeuLeuArgGln 779
QY 2508 CAGGTGAGCTGTAACCGCTTCTCAGCAGAGAAACATTTACCTGAGTGGAGGAGCACTGTGC 2567
Db 780 GlnValGlnLeuIyYrArgLeuLeuSerArgAsnIlnrIyYrLeuGlnIyYrIlnrAspSerVal 799
QY 2568 CTGGGGCGGACATCTTCTGAGACGACTCAGAAAAGCCCTGTGATGATGAATATGAG 2627
Db 800 LeuGlnIyArgHisIlePheThrArgIyLeuAlaGlyValAlaLeuLeuAspIlyIySleSerTrp 819
QY 2628 AATCCAGAAAGAACAGTGGGTACAGAGTGCATTTGGCAGAGAAAGCAATCTATC 2681
Db 820 AsnProGlnIyYrThrValGlnIyYrThrGlyCySAsnIlnrGlnIyAlaIlnrThrSerIle 837

XX	AD057782	standard; protein; 808 AA.
XX	AD057782	
AC	AD057782;	
XX	12-AUG-2004	(first entry)
XX	Chimpanzee toll-like receptor 4	SEQ ID NO:3.
DE	toll-like receptor 4; TLR4; old world monkey; antibacterial;	
XX	immunosuppressive; antiasthmatic; Gran-negative bacterial infection;	
KM	sepsis; severe sepsis; septic shock; asthma; chimpanzee.	
XX	Pan troglodytes.	
OS	MO2004042365-A2.	
XX	21-MAY-2004.	
PN	03-NOV-2003; 2003MO-US036247.	
XX	01-NOV-2002; 2002US-0423113P.	
XX	(EVOL-) EVOLUTIONARY GENOMICS LLC.	
PA	Messier W;	
PI	WPI; 2004-400726/37.	
XX	N-PSDB; AD057780, AD057781.	
DR	Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful	
PT	in treating sepsis and asthma, by comparing the TLR4 polynucleotide	
PT	sequence of the Old World monkey with that of a human.	
XX	Example 1; SEQ ID NO 3; 11pp; English.	
PS	The invention relates to a novel method for identifying a nucleotide	
XX	change in a TLR4 polynucleotide sequence of an old world monkey	
CC	comprising comparing the TLR4 polynucleotide sequence of a human. The	
CC	monkey with corresponding TLR4 polynucleotide sequence of a human. The	
CC	method of the invention has antibacterial, immunosuppressive, and	
CC	asthmatic activity. The method is useful in identifying a nucleotide	
CC	change in a TLR4 polynucleotide sequence of an Old World monkey where the	
CC	change may be associated with reduced sensitivity to Gran-negative	
CC	bacterial infection. The methods, agents and composition are useful in	
CC	treating sepsis, severe sepsis or septic shock and asthma. The present	
CC	sequence represents chimpanzee TLR4.	
XX	Sequence 808 AA;	
SQ		
Alignment Scores:		
Pred. No.:	0	Length: 808
Score:	4178.00	Matches: 805
Percent Similarity:	99.88%	Conservative: 2
Best Local Similarity:	99.63%	Mismatches: 1
Query Match:	62.14%	Indels: 0
DB:	8	Gaps: 0
US-09-396-985B-3	(1-3811) x AD057782	(1-808)
OY	GTGGTTCCTCAATATTTACTTATCAAGACGAGAGCTGAATTTCTACAAAATCCCGACAC	3177
Db	1 ValValProAsnIleThiTyrlncYsMetGcIuLsAaAmpHeTyYlVslleProAspAsn	20
OY	CTCCCTTCGACCAAGAACCTGACCTGACCTTAAATCCCTGAGGACATTAGGAGC	3777
Db	21 LeuProGheserThiTyrsAsnLeuAmpLeuSerPheAaAmpProLeuAghIleuGlySer	40
OY	TATAGCTTCCTCAAGTTCCTCCAGACGCGAGCTGCGATTTATTCAGTGGTGAATCAG	4377
Db	41 TySerPheGheserPheProGluLeuGlnValIleuAmpLeuSerAArgCYsGlnIleGln	60

Qy	438	ACAAATTGAAAGTGGGGCATATTCAGAGCCTTAAGCCACCTCTGACCTTAATATATGACAGA	497
Db	61	ThrlleGIuapBpGylalatyGlnSerleuSerHisleuSerThrleuIleuThrGly	80
Qy	498	AACCCCATCCAGAGTTTAAAGCCCTGGAGACCTTTTCTGACACTATCAAGTTTACAGAACTG	557
Db	81	AsnProIleGlnSerleuAlaIleuGIyAlaIleuSerGIyIleuSerSerleuGlnIlySer	100
Qy	558	GTGGCTGTGGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACT	617
Db	101	ValAlaValGIuThrAsnleuAlaSerleuGluAsnProIleGIyHisleuIlySer	120
Qy	618	TTGAAAGACCTTAATGTCGGCTCAACAATTTATGCCATCTTTCAATTTACCGTAGATATT	677
Db	121	LeuIySGIuIleuAsnValAlaHisAsnleuIleGlnSerPheIyIleuProGIuIyTrp	140
Qy	678	TCTAATCTGACCAATCTAGAGCATGTGGACCTTTCCACCAACAATTTCAAGTATTAT	737
Db	141	SerAsnleuThrAsnleuGluHisIleuAspIleuSerSerAsnIlyIleGlnSerIleIyTr	160
Qy	738	TGCACAGACTTGGGGTTCTACATCAATGCCCTACTCAATCTCTCTTTAGACCTGTCC	797
Db	161	CysThrAspIleuArgValIleuHisIleGlnIleProIleuIleuAsnleuSerleuAspIleuSer	180
Qy	798	CTGAACCCCTATGAACCTTATTCACACCGAGTGCATTTAAAGAAATTAGGCTTCATAAGCTG	857
Db	181	LeuAsnProIleuAsnProIleGIleGlnProGIyAlaPheIySGIuIleArgIleuHisIlySer	200
Qy	858	ACCTTAAGAAATTAATTTTGATAGTTTAAATGTATAGAAACTGTGATTTCAAGGCTGGCT	917
Db	201	ThrleuIyArgAsnAsnPheAspSerleuAsnValIleCysIlySerGIyIleGlnIyIleuAla	220
Qy	918	GGTTTAGAAGTCATCGTTTGGTTCTGGAGAAATTTAGAAAATGAGAAACTTGGAAAAG	977
Db	221	GIyIleuGIuIyAlaHisArgIleuValIleuGIyGIuIleuArgAsnGIuGIyAsnleuGIuIyS	240
Qy	978	TTTGACAAATCTGCTCTAGAGGGCTGTGCAATTTGACATTTGAAGAATTCGGATTAGCA	1033
Db	241	PheAspIySerAlaIleuGIuGIyIleuCysAsnleuThrIleGIuGIuIleuArgIleuAla	260
Qy	1038	TACTTAGACATCACCTCGATGATATTAATTAAGCTTAATTAATGTTTGACAAATGTTTCT	1097
Db	261	TyIleuAspIlyTrIyIleuAspAspIleIleAspIleuPheAsnCysIleuThrAsnValSer	280
Qy	1098	TCATTTTCCCTGTGAGTGTGACTATTGAAAAGGTAAGAACTTTCTTAATATTTCCGA	1157
Db	281	SerPheSerleuValSerValThrIleIySerIleValIyAspPheSerTrIyAsnIyPheGIy	300
Qy	1158	TGGCAACATTTAGAAATTAAGTTAACTGTAAATTTTGACAGTTTCCCACTTGAACCTCAA	1217
Db	301	TrpGIuHisIleuGIuIleuValIleAsnCysIySerPheGIyGlnPheProThrIleuIySerIyS	320
Qy	1218	TTCTCTCAAAAGGCTTACTTTCACTTCCACAAAGAGTGGGAATGCTTTTCCGAAGTTGAT	1277
Db	321	SerIleuIySArgIleuThrPheThrSerAsnIySGIyIleAsnAlaPheSerGIyValIyAsp	340
Qy	1278	CTACCAAGCCTTGAGTTTCTAGATCTCAGTGAAGAATGGCTTGAGTTTCAAGAGTTGCTGT	1333
Db	341	IleuProSerIleuGIuIleuPheIleuAspIleuSerArgAsnGIyIleuSerPheIySGIyCys	360
Qy	1338	TCTCAAAAGTAAATTTGGGACACACCGACTTAAAGTATTTAGATCTTGAGCTTCAATGGTGT	1397
Db	361	SerGIuIleuAspPheGIyThrThrSerIleuIySerIyIleuAspIleuSerPheAsnGIyAla	380
Qy	1398	ATTACCATTGAGTTTCAACTTCTGGGCTTGAACAACATGAACATCTCGAATTTCCAGCAT	1457
Db	381	IleThrMetSerSerAsnPheIleuGIyIleuGIuIleuGIuHisIleuAspPheGIuHis	400
Qy	1458	TCCAAATTTGAAACAATAGAGAGTTTTCAGTATTTCTCATCTACACAGAACTCTCATTTAC	1517
Db	401	SerAsnleuIySGIuIleuSerGIuIleuPheSerAlaPheIleuSerIleuArgAsnleuIleIyTr	420
Qy	1518	CTTGACATTTTCTCACTACACACCAAGATGCTTTCAATGGCATCTTCAATGGCTTGCC	1577


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Db      421  LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY      1578  AGTCTGGAAGTCTTGAAGAAATGCTGGCAATTTCTTCCAGAGAAATCTCTCCAGATATC 1637
Db      441  SerLeuGlnValLeuIleuSerMetAlaGlyAsnSerPheGlnIleuAsnPheLeuProAspIle 460
QY      1638  TTCACAGAGCTGAGAAATCTGACCTTCTGAGACCTCTCTGAGTGCATAGTACAGAGATTG 1697
Db      461  PheThrGlnIleuArgAsnLeuThrPheLeuAspLeuSerGlnGlnIleuGlnIleu 480
QY      1698  TTCCTCAACAGCATTTAACTCACTCTCCAGTCTTCAAGTACTAAATATGACCAACAAC 1757
Db      481  SerProThrAlaPheAsnSerLeuSerSerLeuGlnValIleuAsnMetSerHisAsnAsn 500
QY      1758  TTCTTTTCATGGATACGTTTCTCTTAATGATGTCTGACCTCCCTCCAGAGTTCTTGATTC 1817
Db      501  PhePheSerLeuAspThrPheProGlyLysCysLeuAsnSerLeuGlnValIleuAspGly 520
QY      1818  AGTCTCAATCACTAATATGACTTCCAAAAACAGAACTACAGAGATTTTCCAGATGACTTA 1877
Db      521  SerLeuAsnHisIleMetThrSerLysLysGlnIleuGlnIleuPheProSerSerLeu 540
QY      1878  GCTTTCTTAATCTTACTCAGAAATGACTTTGCTTGTGTAATTTGTGAACAACAAGATTCTG 1937
Db      541  AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleuGlnIleuSerPhe 560
QY      1938  CAATGATCAAGACCAAGAGAGGAGCTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1997
Db      561  GlnTrpLysAspGlnArgGlnLeuValGlnValGlnValGlnValGlnValGlnValGln 580
QY      1998  CCTTCAGATAGAGAGGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2057
Db      581  ProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsnLys 600
QY      2058  ACCATCATTTGGTGTGCTGCTCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2117
Db      601  ThrIleIleGlyAlaSerValLeuSerValLeuValSerValAlaIleValLeuVal 620
QY      2118  TATTAAGTTCTATTTTTCACCTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2177
Db      621  TyrLysPheThrPheHisLeuMetLeuValGlyCysIleLysTyrGlyArgGlyGln 640
QY      2178  AACATCATGATGCTTGTATCTACTACTAAGCCAGAGATGAGAGCTGCTGCTGCTGCTGCTG 2237
Db      641  AsnIleTyrAspAlaPheValIleTyrSerSerGlnAspLysTrpValArgAsnGln 660
QY      2238  CTAGTAAAGAAATTTAGAAAGAGGAGTGCCTTCATTTGAGCTTGCCTTCACTACAGAGAC 2297
Db      661  LeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAsp 680
QY      2298  TTTATTTCCCGGTGTGGCATTTGCTGCTGCCAATCATCATGAAAGTTTCCATAAAGCCCA 2357
Db      681  PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSerArg 700
QY      2358  AAGGTGTTGTTGGTGTGCTCCAGCACTTCACTCAGAGCCGCTGCTGCTGCTGCTGCTGCTG 2417
Db      701  LysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnTyr 720
QY      2418  GAGATTGCTCAGACTTGGCAGATTCTGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2477
Db      721  GlnIleLeuGlnIleuThrTrpGlnPheLeuSerSerArgLysGlyIleIlePheIleValLeu 740
QY      2478  CAGAAAGTGAAGAAAGACCTGCTCAGCAGCAGGTGAGCTGTACCGCTTCTCAGAGAG 2537
Db      741  GlnLysValGlnLysThrLeuLeuArgGlnValGlnLeuTyrArgLeuLeuSerArg 760
QY      2538  AACACTTACCTGAGTGAAGAGACAGTGTCTGAGGAGGAGCAATCTTCTGAGAGCACTC 2597
Db      761  AsnThrTyrLeuGlnTrpGlnLysSerValLeuGlnLysGlnIlePheTrpArgAlaGln 780
QY      2598  AGAAAGCCCTGTGATGTGTAATCAATGAAATCCAGAAAGAAACAGTGGGTACAGATGC 2657

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Db      781  ArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGlyCys 800
QY      2658  AATTGGCAGAGCAACAACCTATC 2681
Db      801  AsnTrpGlnGlnAlaThrSerIle 808

RESULT 11
AD057785
ID AD057785 standard; protein; 808 AA.
XX
AC AD057785;
DT 12-AUG-2004 (first entry)
XX
DB Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN MO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003MO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messter W;
DR WPI; 2004-400726/37.
DR N-PSDB; AD057783, AD057784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111bp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;
XX

Alignment Scores:
Pred. No.: 0 Length: 808
Score: 4167.00 Matches: 803
Percent Similarity: 99.75% Conservative: 3
Best Local Similarity: 99.38% Mismatches: 2
Query Match: 61.97% Indels: 0
DB: 8 Gaps: 0

US-09-396-985B-3 (1-3811) x AD057785 (1-808)

QY      258  GTGGTCTTAATATTACTATCATGATGAGAGCTGAATTTCTTCAAAAATCCCGACAC 317
Db      1  ValValProAsnIleThrTyrGlnCysMetGlnLeuAsnPheTyrLysIleProAspAsn 20
QY      318  CTCCTCTTCAACCAAGAACTGACCTGACCTTAACTCCCTGAGGACATTTAGGACAC 377

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Db 21 LeuProPheSerThrIrysaenLeuAspLeuSerPheasnProleuArghIleuGlySer 40
 QY 378 TATAGCTCTTCAGTTCCAGAACTGAGCTGCTGATTTATCCAGGTGTAATCCG 437
 Db 41 TyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIleGln 60
 QY 438 ACAATGAAAGATGGGCGATATCAGAGCCTTAAGCCACCTCTCTCAATTAATATGACAGA 497
 Db 61 ThrIleGluAspIleValTyrGlnSerLeuSerHisleuSerThrIleuIleuThrGly 80
 QY 498 AACCCCATCCAGAGTTTAGCCCTGGAGACCTTTTCTGAGCTATCAAGTTTACAGAACTG 557
 Db 81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlySleu 100
 QY 558 GTGGCTGTGGAGCAATCTAGACATCTTAGAGAACTTCCCACTTGGACATCTCAAAACT 617
 Db 101 ValAlaValaGlnThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuIlySthr 120
 QY 618 TTGAAGAATTAATATGTGGCTCAACAATCTTATCCAAATCTTCAAAATTAATGAGTATTT 677
 Db 121 LeuIyGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIySleuProGluTyrPhe 140
 QY 678 TCTAATCTGACCAATCTTAGAGCACTTGGACCTTTCCAGCAACAAGTCAAGTATTTAT 737
 Db 141 SerAsnLeuThrAsnLeuGluTyrLeuAspLeuSerSerAsnIlyIleGlnSerIleTyr 160
 QY 738 TGGACAGACTTGGGGTTCACATCAAAATGCCCTTACTCAATCTCTTTAGACCTGTGC 797
 Db 161 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
 QY 798 CTGAACCTATGAACTTATCCAAACAGAGGTCATTTAAAGAAATTAAGGCTTCAATAGCTG 857
 Db 181 LeuAsnProMetThrPheIleGlnProGlyAlaPheIySgluIleArgLeuHisIlySleu 200
 QY 858 ACTTAAGAATAATTTTGAATGATTAATTAATGATAAGAACTTGATTCAGAGCTGTGCT 917
 Db 201 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetIyThrCysIleGlnIlyLeuAla 220
 QY 918 GGTTTGAAGTCCATGTTGGTTCCTGGGAGAAATTTAGAAATGAGAAACTTGGAAAG 977
 Db 221 GlyLeuGlnValaArgArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGluIlyS 240
 QY 978 TTGGAACAATCTGCTCTAGAGGGCTGTGCAATTTGACATTTGAGAAATTCGATTAGCA 1037
 Db 241 PheAspIySerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuAla 260
 QY 1038 TACTTAGACTACTGCTGATGATGATATTAATGATTAATTAATGATTTGACAAATGTTTCT 1097
 Db 261 TyrLeuAspIlyTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSer 280
 QY 1098 TCAATTTCCCTGGTGAAGTGTGATCTATTTGAAAGGTAAGAACTTTCTTAATTTGCGA 1157
 Db 281 SerPheSerLeuValSerValThrIleGluArgValIlyAspPheSerTyrAsnProGly 300
 QY 1158 TGGCAACATTTAGAAATTAATTAATTTGACAGTTTCCCACTTGAACCAATCAAACTCAA 1217
 Db 301 TrpGlnHisLeuGlnLeuValaIleAsnCysIlySphGlyGlnPheProThrLeuIlySleuIlyS 320
 QY 1218 TCTCTCAAAAGGCTTACTTCACTTCCAAACAAAGTGGAGATCTTTTTCAGAACTTGAT 1277
 Db 321 SerLeuIlyArgLeuThrPheThrSerAsnIlyGlyGlyAsnAlaPheSerGluValaAsp 340
 QY 1278 CTRCCAGAGCTTAGATTTCTAGATCTCAGTGAAGAAATGGCTTGAAGTTTCAAGGTGCTG 1337
 Db 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheIySgluCysCys 360
 QY 1338 TCTCAAGATGATTTGGGACCAACAGCCTAAAGTATTTAGATGAGCTTCAATGGATTT 1397
 Db 361 SerGlnSerAspPheGlyThrThrSerLeuIlySyrLeuAspLeuSerPheAsnGlyVala 380
 QY 1398 ATTACATGATTCAAACTTCTTGGGCTTAGAACAACTAGAACATCTGATTTCCAGCAT 1457
 Db 381 IleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisIleuAspPheGlnHis 400

QY 1458 TCCAAATTTGAACAAATGAGTGAAGTTTTCAGTATTCCTATCACTCAGAAACCTCATTTAC 1517
 Db 401 SerAsnLeuIlyGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTyr 420
 QY 1518 CTTGACATTTCTCATACTCACAACAGAGTTGCTTCAATGAGCAATCTTCAATGGCTTGTCC 1577
 Db 421 LeuAspIleSerHisThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
 QY 1578 AGCTTCGAAAGTCTTGAAAATGGCTGGCAATTCCTTCCAGAGAAACTTCTTCCAGATATC 1637
 Db 441 SerLeuGlnValLeuIlySmetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle 460
 QY 1638 TTCACAGAGCTGAGAAACTTGAACCTTCCGAGACCTTCCAGTGTCAACTGAGCAGTTG 1697
 Db 461 PheThrGlnLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIlyLeu 480
 QY 1698 TCTCCAAACAGCAATTAATCACTCTCCAGCTTTCAGGTACTAAATATGAGCCAAACAC 1757
 Db 481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
 QY 1758 TTTCTTTTCACTGGATACGTTTCTTATTAAGTGTGCAATCCCTCCAGGTTCTTGATTC 1817
 Db 501 PhePheSerLeuAspThrPheProTyrIlySyrCysLeuAsnSerLeuArgValIleuAspTyr 520
 QY 1818 AGCTTCATCACATPATGACTTCCAAAACAGAGCACTACAGACATTTTCCAGTAGTCTTA 1877
 Db 521 SerLeuAsnHisIleMetThrSerIlySyrGlnIlyLeuGlnHisPheProSerSerLeu 540
 QY 1878 GCTTTCTTAATCTTAATCTCAGATGACTTGTGCTGTGATCTTGTGAACACAGAGTTTCTG 1937
 Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
 QY 1938 CAATGATACAGACCAAGGAGGCTCTTGGTGAAGTTGAACGAATGAATGTGCAACA 1997
 Db 561 GlnTrpIleIlyAspGlnArgIleuLeuValaGluValaGluArgMetGluCysAlaThr 580
 QY 1998 CCTTCAGATTAACAGGAGCAATGCTGTGCTGCACTTGAATATGACCTGTGAGATTAAG 2057
 Db 581 ProSerAspIlyGlnGlyMetProValLeuSerLeuAsnHisIleThrCysGlnMetCysIlyS 600
 QY 2058 ACCATCATGTGTGTGCTGCTCCTCAGTGTGCTGTGATCTGTGTGACAGTCTGTGC 2117
 Db 601 ThrIleIleGlyValaSerValLeuSerValLeuValaSerValaAlaIleuVal 620
 QY 2118 TATTAAGTTATATTTTCACTGATGCTTCTTGTGCTGTGATGAATGATGATGAGTGA 2177
 Db 621 TyrIlySphTyrPheHisIleuMetLeuAlaGlyCysIleIyTyrGlyArgGlyIly 640
 QY 2178 AACATCTAGAGCCTTGTGTATCTTCAACCAACAGAGAGAGACCTGGTAAAGATGAG 2237
 Db 641 AsnValTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValaArgAsnGln 660
 QY 2238 CTAGTAAGAATTTGAAAGAGAGGAGCTCCATTTACACTGCTGCTTCACTACAGAGAC 2297
 Db 661 LeuValIlyAsnLeuGlnIlyValaIleProPheGlnLeuCysLeuHisIlyTrpArgAsp 680
 QY 2298 TTTATTTCCGCTGTGAGCAATCTGCAACATCATCATGAAAGTTTCCATTAAGCCGA 2357
 Db 681 PheIleProGlyValaIleAlaIleAlaIleAsnIleIleHisGlnGlyPheHisIlySerArg 700
 QY 2358 AAGGTGATTTGTGTGTGCTCCAGACATTCACCAAGCCGCTGGTATCTTGAATAT 2417
 Db 701 IlyValIleValaValaSerGlnHisPheIleGlnSerArgTrpCysIlePheGluIly 720
 QY 2418 GAGATTTGTCAGACCTGGAGATTTTCTGAGCAGCTGTGCTGATATCTTCAATGCTGCTG 2477
 Db 721 GluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValaIleu 740
 QY 2478 CAGAAAGTGGAGAGACCTGTCTCAGCAGCAGAGGTGAGCTGTACCGCTTCCAGACAG 2537
 Db 741 GlnIlySValaGlnIlyThrLeuLeuArgGlnGlnValaGluLeuTyrArgLeuLeuSerArg 760

QY 2538 AACACTTACCTGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTGTGAGACGACATC 2597
 |||||
 Db 761 AenThThyLeuGlutTrpGluApsSerValLeuGlYArgHisIleIleThrpAgaGleu 780
 |||||
 QY 2598 AGAAAAGCCCTGCTGATGGTAATCATGGATCCAGAGAAACAGTGGGTACAGGATGC 2657
 |||||
 Db 781 ArgYAlaIleuLeuApsGlyIysSerTrpApsProGluGlyThrValGlyThrGlyCys 800
 |||||
 QY 2658 AATTGGCAGGAGACACATCTATC 2681
 |||||
 Db 801 AenTrpGlnGlnAlaThrSerIle 808
 |||||
 RESULT 12
 ADO57803
 ID ADO57803 standard; protein; 808 AA.
 AC ADO57803;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
 XX
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 XX
 OS Pan troglodytes.
 XX
 PN WO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003MO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Messier W;
 XX
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADO57801, ADO57802.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 24; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 808
 Score: 4164.00 Matches: 803
 Percent Similarity: 99.63% Conservative: 2
 Best Local Similarity: 99.38% Mismatches: 3
 Query Match: 61.93% Indels: 0
 DB: 8 Gaps: 0
 US-09-396-985B-3 (1-3811) X ADO57803 (1-808)

QY 258 GTGTTCCTTAATATTACTTATCATGATGAGAGCTGAATTTTCAAAAATCCCGACAAC 317
 |||||
 Db 1 ValValProAsnIleThrTyroIncySmetGluLeuAenPheTyIleIleProAsn 20
 |||||
 QY 318 CTCCTCTTCTCAACAGAACCTGGACCTGACCTTTAATCCCTGAGCATTTAGGCAC 377
 |||||
 Db 21 LeuProPheSerThrIleAsnLeuApsLeuSerPheAsnProLeuArgHisIleuGlySer 40
 |||||
 QY 378 TTTAGCTTCTTAGTTTCCCGAAGCTGAGGTCGAGTTTATCCAGGTCGAAATCCAG 437
 |||||
 Db 41 TyrSerPhePheSerPheProGluLeuGlnValLeuApsLeuSerArgCysGluIleGln 60
 |||||
 QY 438 ACAATTGAAGATGGGACATATCAGAGCCCTAAGCCACTCTTACCTTATATTATGACAGA 497
 |||||
 Db 61 ThrIleGluApsGlyAlaTyroInserIleuSerHisIleuSerThrIleuIleuThrGly 80
 |||||
 QY 498 AACCCCATCAGAGTTTAAAGCCCTGGAGACCTTTTGTGACATACAGATTACAGAACTG 557
 |||||
 Db 81 AsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerIleuGlnIysLeu 100
 |||||
 QY 558 GTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGAGCATCTCAAAACT 617
 |||||
 Db 101 ValAlaValAlaGluThrAsnLeuAlaSerIleuGlnApsPheProIleGlyHisIleuYsThr 120
 |||||
 QY 618 TTGAAGAAGACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTAAGCTGATTTT 677
 |||||
 Db 121 LeuYsGluLeuAsnValAlaHisIleAsnLeuIleGlnSerPheYsLeuProIuYrPhe 140
 |||||
 QY 678 TCTAATCTGACCAATCTAGAGCATTTGACCTTTCCAGCACAGAAATTCAAAGTATTAT 737
 |||||
 Db 141 SerAsnLeuThrAsnLeuGluHisIleuApsLeuSerSerAsnIlyIleGlnSerIleTyx 160
 |||||
 QY 738 TGCACAGACTTGGCGGTCTTATACATAAATGCCCTACATCTCTTTAACCTGCTGCC 797
 |||||
 Db 161 CysThrAspLeuArgValLeuHisIleGlnMetProLeuLeuAsnLeuSerIleuApsLeuSer 180
 |||||
 QY 798 CTGAACCCATGAACTTATTCACACAGGTGATTTAAGAAATTAAGCTTCATAGCTG 857
 |||||
 Db 181 LeuAsnProMetAsnPheIleGlnProGlyAlaPheYsGluIleArgIleuHisIysLeu 200
 |||||
 QY 858 ACTTTAAGAAATTAATTTTGTATAGTTTAAATGTAATGAAGAACTTGTATTCAGGCTCGCT 917
 |||||
 Db 201 ThrIleArgAsnAspPheAspSerIleuAsnValMetIysThrCysIleGlnIlyLeuAla 220
 |||||
 QY 918 GGTTTAAGAGTCCATCGTTGTTCTCGGAGAAATTTAGAAATGAAGAAACTTGAAGAAAG 977
 |||||
 Db 221 GlyLeuGluValHisArgIleuValIleuGlyGluPheArgAsnGluGluAsnLeuGluYs 240
 |||||
 QY 978 TTTGACAAATCTGCTCTAGAGGCGCTGTGCAATTTGACCATTTGAAGAAATTCGATTAGCA 1037
 |||||
 Db 241 PheAspYsSerHisIleuGlnIleuGlyLeuYsAsnLeuThrIleGlnIleuPheArgLeuAla 260
 |||||
 QY 1038 TACTTAGACTACTACCTCGATGATATTAATTAAGCTTAATTTATTTGTTGACAAATGTTCT 1097
 |||||
 Db 261 TyrLeuAspTyroTyroLeuApsPheIleIleAspLeuPheAsnCysLeuThrAsnValSer 280
 |||||
 QY 1098 TCATTTTCCCTGCTAGAGCTGACTTATGAAGGCTAAAGACTTTTCTATATATTCGGA 1157
 |||||
 Db 281 SerPheSerLeuValSerValThrIleYsSerValYsAspPheSerYrsnPheGly 300
 |||||
 QY 1158 TGGCAACATTTAGAAATTAAGTAACTGTAATTTGACAGTTTCCCATTTGAAACTCAAA 1217
 |||||
 Db 301 TrpGlnHisIleuGlnIleuValIysCysYsPheGlyGlnPheProThrIleuYsLeuYs 320
 |||||
 QY 1218 TCTCTCAAAAGGCTTACTTCACTTCCAACAAAAGTGGGAATGCTTTTCAAGAGTTGAT 1277
 |||||
 Db 321 SerLeuYsArgLeuThrPheThrSerAsnYsGlyAlaAsnAlaPheSerGluValAps 340
 |||||
 QY 1278 CTACCAAGCTTGAAGTTTATAGATCTCAGTAGAAATGCTTGAAGTTTCAAGAGTCTCT 1337
 |||||
 Db 341 LeuProSerLeuGluPheLeuApsPheSerArgAsnGlyLeuSerPheYsGlyCysCys 360
 |||||
 QY 1338 TCTCAAGATGATTTTGGGACCAACGACCTAAAGTATTATGATCTGAGCTTCAATGCTGT 1397
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Db      ||| 361 SerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyVal 380
Qy      ||| 1398 AATACCGTAGGTCGAACCTCTGGGGCTTAGAACATAGAAATCGGATTTCCAGCAT 1457
Db      ||| 381 IleThrIleSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnIuhIleuAspPheGlnHis 400
Qy      ||| 1458 TCCAAATTTGAAACAAATAGTAGAGTTTTCAGTATTCCTATCAGTACAGAAACCTCATTTAC 1517
Db      ||| 401 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAsnGlnLeuIleTyr 420
Qy      ||| 1518 CTTCAGATTTCTGATCTCAACCCAGAGTTGCTTTCAGTGCATTCCTCAATGGCTTGCC 1577
Db      ||| 421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
Qy      ||| 1578 AGTCTCGAAGCTTTGAAAGATGGCTGGCATTTCTTCCAGGAAACCTTCCAGATATC 1637
Db      ||| 441 SerLeuGlnValIleuLysMetAlaGlyAsnSerPheGlnGlnIuhAsnPheLeuProAspIle 460
Qy      ||| 1638 TTCACAGAGCTGAGAACTTGACCTTCTGAGACCTCTCTGAGTGTCAACTGAGCAGATTG 1697
Db      ||| 461 PheThrGlnLeuArgAsnLeuThrPheLeuAspLeuSerGlnGlnLeuGlnIuhLeu 480
Qy      ||| 1698 TCTCCACAGACATTTAACTCACTCTCCAGTCTTCAGGTAATAATATAGCCACAACAC 1757
Db      ||| 481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
Qy      ||| 1758 TTCCTTTTCATTGATACGTTTCTTATATAGTGTCTGAACCTCCCTCCAGGTTCTTGATTAC 1817
Db      ||| 501 PhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyr 520
Qy      ||| 1818 AGTCTCAATCACTAATAGACTTCCAAAGAACAGAACTACAGACATTTCCAGAGACTA 1877
Db      ||| 521 SerLeuAsnHisIleMetThrSerLysLysGlnIuhLeuGlnHisPheProSerSerLeu 540
Qy      ||| 1878 GCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTATCTTGTGAACACAGAGTTTCCTG 1937
Db      ||| 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
Qy      ||| 1938 CAATGATCAAGACCCAGAGGACGCTTTGGTGAAGTTGAAGCATGGAATGTGCACA 1997
Db      ||| 561 GlnThrPleLysAspGlnArgGlnLeuLeuValGlnValIuhArgMetGlnCysAlaThr 580
Qy      ||| 1998 CTTTCAGATAAGACGGGCGATGCGCTGAGTGAATTCACCTTCAGATGAATTAAG 2057
Db      ||| 581 ProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsnLys 600
Qy      ||| 2058 ACCATCATTTGGTGTGCTGCTCTCAGTGTGCTTGTATCTGTTGAGCAGTTCTGTGC 2117
Db      ||| 601 ThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeuVal 620
Qy      ||| 2118 TATATAGTTCTATTTTCACTGATGCTTCTTGTGCTGCTGATTAAGATGGTAGAGTGA 2177
Db      ||| 621 TyrIlePheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGln 640
Qy      ||| 2178 AATCATCATATATGCTTTTATATCTACTCAAGCCAGATGAGCATGGGTGAAGAAAGAG 2237
Db      ||| 641 AsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspIleValAspAsnGln 660
Qy      ||| 2238 CTAGTAAAGATTTAGAAAGAGGGGCTCTCATTTAGCTTGGCTTCTTCACTACAGAGAC 2297
Db      ||| 661 LeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAsp 680
Qy      ||| 2298 TTTATTTCCGGGTGGCCATTTCTGCGCAACATCATCATGAAGTTTCCATTAAGCCGA 2357
Db      ||| 681 PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSerArg 700
Qy      ||| 2358 AAGGTATTTGTGTGGTCCAGCACTTATCCAGAGCGCGTGTATCTTGAATAT 2417
Db      ||| 701 LysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnTyr 720
Qy      ||| 2418 GAGATTCTCAGACCTGGCAGTTTCTGAGCAGTGTGCTGGTATCATTTCTATGTCCTG 2477

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Db      ||| 721 GluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeu 740
Qy      ||| 2478 CAGAAGGTGAGAGAACCCCTGCTCAGACAGACAGGTGAGCTGTACCGCTTCTCAGACAG 2537
Db      ||| 741 GlnLysValGlnLysThrLeuAsnArgGlnValGlnLeuTyrArgLeuLeuSerArg 760
Qy      ||| 2538 AACCTTACCTGGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGGAGACGATC 2597
Db      ||| 761 AsnThrTyrLeuGlnIuhTrpGlnAspSerValLeuGlyArgHisIlePheThrArgLeu 780
Qy      ||| 2598 AGAAAGCCCTGCTGGATGTGAATATCATGGAATCCGAAGAAACAGTGGGTACAGATGC 2657
Db      ||| 781 ArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGlyCys 800
Qy      ||| 2658 AATTGGCAGGAGCAACATCTATC 2681
Db      ||| 801 AsnTrpGlnIuhAlaThrSerIle 808

RESULT 13
AA06352
ID AA06352 standard; protein; 799 AA.
XX
AC AA06352;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human DNAX toll-1-like receptor DTLR4.
XX
KW DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW Interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN WO9850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98MO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHB ) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
WP1: 1999-059670/05.
XX
DR N-PSDB; AA060666.
XX
PT Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
XX
XX Example; Page 115-117; 171pp; English.
PS
XX The present invention specifically describes human DNAX toll-1-like
XX receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
XX in the present invention. Also described are: (1) a fusion protein
XX comprising a DTLR protein or peptide; (2) a binding compound, preferably
XX an antibody or antibody fragment which specifically binds to a DTLR
XX protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
XX; (4) an expression vector comprising the nucleic acid of (3); and (5) a
XX host cell comprising the vector of (4). The host cell of (5) can be used
XX to produce the DTLR proteins. The DTLR proteins can be used to alter
XX phosphate metabolism, to modulate inflammatory function, innate immunity
XX responses or morphological effects. The DTLR proteins can be used in the
XX treatment of conditions exhibiting abnormal expression of the receptors
XX of their ligands. These abnormalities are typically manifested by
XX immunological disorders
XX
XX Sequence 799 AA;

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Alignment Scores:

Pred. No.: 0 Length: 799
 Score: 4141.00 Matches: 799
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 61.59% Indels: 0
 DB: 2 Gaps: 0

US-09-396-985B-3 (1-3811) x AAW6352 (1-799)

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QY 285 ATGAGAGTGAATTTCTACAAAATCCCGACAACTCCCTTCTCAACCAAGAACTTGGAC 344
DB 1 MetGluLeuAsnPhetYrYsIleProAspAsnLeuProPheSerThrYsAsnLeuAsp 20
QY 345 CTGAGCTTTAATCCCGGAGGACATTTAGGAGCATATGCTTCTTCAGTTTCCGAGAACTG 404
DB 21 LeuSerPheAsnProLeuAlaGHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY 405 CAGGTGCTGGAATTTATCCAGGTGTGAATCCAGACATTTGAGATGGGCGCATATCAGAGC 464
DB 41 GluValLeuAsnProLeuSerArgYsGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
QY 465 CTAGCCACCTCTCTACCTTAATATTGACGGAACCCCATCCAGAGTTTAGCCCTGGGA 524
DB 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY 525 GCGTTTCTGAGCTATCAAGTTTACAGAACTGTGGCTGTGGAGACAAATCTAGCATCT 584
DB 81 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 100
QY 585 CTAGAGAACTTCCCATTTGAGACATCTCAAAACTTTGAGAACTTAATGTGGCTCAAAAT 644
DB 101 LeuGluAsnPhetProIleGlyHisLeuValThrLeuValGlyLeuAsnValAlaHisAsn 120
QY 645 CTTATCCAACTTTTCAAAATTAAGTGAATTTTCTTAATCTGACCAATCTAGGACACTTG 704
DB 121 LeuIleGlnSerPheYsLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 140
QY 705 GACCTTTCAGAAACAAGATTCAAAAGATTATTATTTGACAGACTTGGGGGTTCTACATCAA 764
DB 141 AsnLeuSerSerAsnValIleGlnSerIleTyrCysThrAspLeuValIleAsnValGln 160
QY 765 ATGCCCTTACTCAATCTCTCTTTAGACCTGTGCCCTGAACTTGAACCTTTATCCAAACA 824
DB 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnProIleGlnPro 180
QY 825 GGTGCATTTAAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATAATTTGATAGTTTA 884
DB 181 GlyAlaPheYsGluIleArgLeuHisIleLeuThrLeuArgAsnAsnPheAspSerLeu 200
QY 885 AATGTATATGAAAACCTTGATTTCAAGGCTGGCTGGTTTAGAAGTCAATCGTTTGGTTCTG 944
DB 201 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspGluValLeu 220
QY 945 GGAGAAATTTGAATGAATGAAGAACTTGAAGAAAGTTTGACAAATCTGCTTAGAGGCGCTG 1004
DB 221 GlyGluPheArgGlnGluGlyAsnLeuGluValPheAspYsSerHisAlaGluGluGlyLeu 240
QY 1005 TGCAAATTTGACATTGAAGAAATTCGATTAGCACTTATGACCTAAGCTGATGATATT 1064
DB 241 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspYrTyrLeuAspAspIle 260
QY 1065 AATGACCTTATTTAATGTTTGAACAATGTTTCTTCAATTTCCCTGGAGGTGACATATT 1124
DB 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
QY 1125 GAAAGGGTAAAGACTTTTCTTAATAATTCGATGGCAACATTAGAAATTAGTTAACTGT 1184
DB 281 GluArgValIleAspPheSerTyrAsnPhetGlyTyrGlnHisLeuGluLeuValAsnCys 300
QY 1185 AAATTTGGACAGTTTCCACATTTGAACCTCAATCTCTCAAAAGCTTACTTCACTTCC 1244
  
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DB 301 LysPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrSer 320
QY 1245 AACCAAGGTGGGAATCTTTTTCAGAACTTGATCTACCAAGCTTGAGTTTCTAGATCTC 1304
DB 321 AsnValGlyGlyAsnHisPheSerGluValAspLeuProSerLeuGluLeuLeuAspLeu 340
QY 1305 AGTAGAAATGGCTTGAGTTTCAAGGTTGCTGTCTCAAAAGTGAATTTGGACCAACACAC 1364
DB 341 SerArgAsnGlyLeuSerPheYsGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTAACATAGATTCAAACTTCTGGGC 1424
DB 361 LeuYsTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
QY 1425 TTAGAACACTGAACATCTGGAATTTCCAGCAATTCATTTGAACAAATGAGTAGATT 1484
DB 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuYsGlnMetSerGluPhe 400
QY 1485 TCAGATTTCTTCACTACAGAAACCTCATTTAACCATTTCATTACTCAACACAGA 1544
DB 401 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisArg 420
QY 1545 GTTGCTTTCAATGGCATCTTCAATGGCTGTGTCCAGTCTGGAAGTCTTGAAATGGCTGGC 1604
DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuYsMetAlaGly 440
QY 1605 AATTTCTTCAGAGAAACTTCCCTTCAGATATCTTCAACAGACTGAGAACTTGACCTTC 1664
DB 441 AsnSerPheGlnGluAsnPhetProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
QY 1665 CTGAGACTCTCTCAGTGTCACTGAGACAGCTGTGTCTCAACAGCAATTTAATCACTCTCC 1724
DB 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
QY 1725 AGCTTCAAGTACTAAATATGAGCCACAAACAATCTTTTCAATGGATACGTTTCTTAT 1784
DB 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
QY 1785 AAGTGTGAATCTCCCTCCAGGTTCTTGATTAAGTCTCAATCACTAATGACTTCCAA 1844
DB 501 LysCysLeuAsnSerLeuGlnValLeuAspYrSerLeuAsnHisIleMetThrSerLys 520
QY 1845 AACACAGAACTACAGCAATTTTCCAAAGTACTTCAAGTCTTCTTAATCTTACTCAGATGAC 1904
DB 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY 1905 TTTGCTTGTACTTTGGAACAACAGAGTTTCTGCAATGGATCAAGGACAGGACGCTC 1964
DB 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeu 560
QY 1965 TTGGTGAAGTTGAACGAATGGAATGTGCACACCTTGATTAAGACAGGACATGCTGTG 2024
DB 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspYsGlnIleMetProVal 580
QY 2025 CTGAGTTTGAATATCACTGTGATGAATGAATGAACCATCATTTGATGTGCTGCTCAGT 2084
DB 581 LeuSerLeuAsnIleThrCysGlnMetAsnValSerThrIleIleGlyValSerValLeuSer 600
QY 2085 GTTGCTTGATGATCTGTGTAGCAGTCTGTGCTATTAAGTTCTATTTTCACTGATGCTT 2144
DB 601 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 620
QY 2145 CTTGCTGCTGATTAAGTATGATGTGAGAGTGAACATATATGATGACCTTGTATCTAC 2204
DB 621 LeuAlaGlyCysIleLeuYrTolYrArgGlyLeuAsnIleTyrAspHisPheValIleTyr 640
QY 2205 TCAAGCAGAGATGAGGACTGGGTGAAGGATGAAGCTAGTAAGAAATTTGAAGAGGGGTG 2264
DB 641 SerSerGlnAspGluAspTyrValArgAsnGluLeuValLysAsnLeuGluGluVal 660
QY 2265 CTTCAATTTCAAGCTCTGCTTCACTACAGAGACTTATTTCCGGGTGTGGCCATGCTGTC 2324
DB 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 680
  
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Oy	2325	AACATCATCCATGAAGGTTTCCATTAATTAAGCCGAAAGCGATGTTGGTGTCCACGAC	2384
Db	661	Aenillellehslgulgylphehisllysserraglysvalllevalvalserghmhls	700
Oy	2385	TTTCATCCAGAGCCCGCTGGTGTATCTTTGATATAGATTTGCTCAGACCTGCGAGTTCTG	2444
Db	701	PheilleglnserrargtrpCysillepheeliunrgrluilealaglntmtrtpglNpheu	720
Oy	2445	AGCAGTGTGCTGGTGTATCTTCAATTGTCTCGCAGAAAGGTTGGAGAAAGACCTTGCTCAGG	2504
Db	721	SerserrargalaglyllellepheellevallleuGlnySvalIguylstheleuLmarg	740
Oy	2505	CAGCAGGTGAGCTGTACCGGCTTCTCAGCAGAGAACCTTACCTCGAGGTGAGAGACAGT	2564
Db	741	GlnGlnvalIguIleunrYArgleuleuSerArgantrhYrleuGlntrpGlnpsSer	760
Oy	2565	GTCCTGAGCGGACATCTTGTGAGACGACTCAGAAAAGCCCTGCTGATGTGTAATCA	2624
Db	761	ValleuGlyArgHsllePheHtrpArgArgleuArgylsalaleuLeuAspGlyLysSer	780
Oy	2625	TGGAAATCCAGAAAGAACGCTGGTACGAGATGCATTTGGGCGAGAAAGCAATCTATC	2681
Db	781	TrpsnprProGlnGlyThrValGlyThrGlyCysantrpGlnGlnAlaThrSerlle	799
RESULT 14			
AAE16093			
XX	AAE16093	standard; protein; 799 AA.	
XX	AAE16093;		
XX	26-MAR-2002	(first entry)	
XX	Human DNAX Toll like receptor (DTLR) 4 #1.		
XX	Human; DNAX Toll like receptor; DTLR therapy; immunological disorder;		
KW	interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
XX	Homo sapiens.		
XX	W0200190151-A2.		
XX	29-NOV-2001.		
XX	23-MAY-2001; 2001WO-US016766.		
XX	25-MAY-2000; 2000US-0207558P.		
XX	(SCHE) SCHERING CORP.		
XX	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;		
XX	WPI; 2002-083085/11.		
XX	N-PSDB; AAD26283.		
XX	New DNAX Toll like receptor (DTLR) proteins, useful for treating		
XX	conditions exhibiting abnormal expression of the receptors of their		
XX	ligands, particularly abnormalities manifested by immunological		
XX	disorders.		
XX	Claim 1; Page 35; 297p; English.		
XX	The invention relates to mammalian receptor proteins, e.g., primate,		
XX	human DNAX Toll like receptor (DTLR) protein and their corresponding		
XX	nucleic acids. The DTLR is useful for treating conditions exhibiting		
XX	abnormal expression of the receptors of their ligands. Such abnormality		
XX	is manifested by immunological disorders. In particular, the DTLR is		
XX	useful for treating various disease or disorders associated with abnormal		
XX	expression or abnormal triggering of response to a ligand. The DTLR is		
XX	also useful as an immunogen for the production of antisera or antibodies		
XX	specific, e.g. capable of distinguishing between other interleukin (IL)-1		
XX	receptor family members, for the DTLR or its various fragments. The		
XX	purified DTLR can be used to screen monoclonal antibodies or antigen-		

CC	binding/fragment. The antibodies are useful for screening expression
CC	libraries for particular expression products. These are useful for
CC	detecting or diagnosing various immunological conditions related to
CC	expression of DTLR or cells that express it. The present sequence is
CC	human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX	
80	Sequence 799 AA:
	Alignment Scores:
	Pred. No.: 0 Length: 799
	Score: 4141.00 Matches: 799
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 61.59% Indels: 0
	DB: 5 Gaps: 0
	US-09-396-985B-3 (1-3811) x AAE16093 (1-799)
QY	285 ATGGAGCTGAATTTCTCAAAAATCCCGGACACTCCCTCTTCAACCGAAGACCTGGAC 344
DB	1 MetGluLeuasnPheTyrLysIleProaspasnLeuProPheSerThrLysAsnLeuasp 20
QY	345 CTGAGCTTTAATCCCGGACGACTTTTGGGACGTATAGCTCTTTCAGTTTCCGAGAACTG 404
DB	21 LeuSerPheasnProLeuAsnArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY	405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGCAAAATTGAAGAATGGGGCATTCAGAGC 464
DB	41 GluValLeuAspLeuSerSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
QY	465 CTAGGCCACCTCTCTACCTTAATTTGACAGGAAACCCATCCAGAGTTTACGCTTGGGA 524
DB	61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY	525 GCCTTTTCTGGACTATCAAGTTTACAGAGCTGGGCTGTGAGAGCAAACTTAGCATCT 584
DB	81 AlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGlnThrAsnLeuAlaSer 100
QY	585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAATGTGGCTCACAA 644
DB	101 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
QY	645 CTTATCCAACTTTTCAAAATTAACCTGAGTATTTTCTTAATCTGACCAATCTTAGAGCAT 704
DB	121 LeuIleGlnSerPheLysLeuProGlyTyrPheSerAsnLeuThrAsnLeuGluHisLeu 140
QY	705 GACCTTTCGAGCAACAAGATTCAAAAGTATTATTTGACAGACTGGGGGTTCTACATCA 764
DB	141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuAlaGlyValLeuHisGln 160
QY	765 ATGCCCTTACTCATCTCTCTTTAGACCTTGCCCTGAAACCTTAGTAACTTTATCCAAACA 824
DB	161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY	825 GGTGCACTTTAAGAAATTGAGCTTCATAGCTGACTTTAAGAAATTAATTTGATAGTTTA 884
DB	181 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
QY	885 AACTATTAAGAAAATTTGATTAACAAGCTCGGCTGGTTTGAAGAGCCATCGTTTGCTTG 944
DB	201 AsnAlaMetCysThrCysIleGlnGlyLeuValAlaGlyLeuGluValHisAspLeuValLeu 220
QY	945 GGAAGAAATTGAAGTAAGGAAACTTGGAAGAAATTGACAAATCTGCTTAGAGGGCTTG 1004
DB	221 GlyGluThrArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 240
QY	1005 TGCAATTGACCATTTGAAGAAATTCGATAGCATACTATTGACTATCTTCGATGATATT 1064
DB	241 CysAsnLeuThrThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrGlyLeuAspAspIle 260
QY	1065 ATTGACTTATTTAATGTGTTGACAAAGTTTCTTCATATTTCCCTGGGTGAGGTGACATTT 1124
DB	261 IleAspLeuPhePheAsnLysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280

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 QY 1485 TCAGTATTCCTATCACTCAGAAAACCTCATTTACTTGACATTTCTCATCTCACACAGA 1544
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 DB 461 LeuAspLeuSerGIInCySGIInLeuGIInLeuGIInLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGTCTTCAAGTAAATATATAGCCACACAACTTCTTTTCAATGATGATGTTTCTTAT 1784
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 DB 541 PheAlaCySThrCySGIInhiSLeuInsPheLeuGIInThrIleLysAspGIInArgGIInLeu 560
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 DB 561 LeuValGIInValGIInArgMetGIInCySAlaThrProSerAspLysGIInGlyMetProVal 580
 QY 2025 CTGAGTTTGAATATCACTCTGACAGATGAATGAACCACTCATGCTGTGCTGCTCAGT 2084
 DB 581 LeuSerLeuAsnIleThrCySGIInMetAsnLysThrIleIleGlyValSerValLeuSer 600
 QY 2085 GTGCTGTAGATCTGTGTGAGCAGTTCTGCTATATAGTATTAATTTTCACTGATGCTT 2144
 DB 601 ValLeuValValSerValValAlaValLeuValTyrLysPheThrSLeuMetLeu 620
 QY 2145 CTTGCTGGCTGCATAAAGTATGTAAGGTGAAGAAACATATGATGCTTGTATTTATAC 2204
 DB 621 LeuAlaGlyCySThrLysTyrGIInArgGIInGluAsnIleTyrAspAlaPheValIleTyr 640

QY 2205 TCAGCCAGATAGAGACTGGGTGAAGATGAGTATGAAGATTTAGAAAGGGGTG 2264
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 QY 2265 CCTCCATTTACAGCTTGCCTTCACTACAGAGACTTTATTCGGGGTGGCCATTTGCTGCC 2324
 DB 661 ProProPheGIInLeuCySLeuIleSThrArgAspPheIleProGlyValAlaIleAla 680
 QY 2325 AACATCATCAGAAAGGTTTCCATTAAGACGAAAGGTGATGTTGTGTCGCCAGCAC 2384
 DB 681 AsnIleIleIleGIInGlyPheIleLysSerArgLysValIleValValValSerGIInIle 700
 QY 2385 TTCAATCAGAGCCGCTGTGTATCTTGAATATGAGATTTCTCAGACTGGAGTTTCTG 2444
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 QY 2505 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGAAACACTTACCTGAGTGGAGAGCAGT 2564
 DB 741 GIInGIInValGIInLeuLysArgLeuLeuSerArgAsnThrTyrLeuGIInTrpGIInAspSer 760
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 DB 761 ValLeuGIInArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
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 DB 781 TrpAsnProGIInGlyThrValGIInThrGlyCySAsnTrpGIInAlaThrSerIle 799
 RESULT 15
 ABB83162
 ID ABB83162 standard; protein; 799 AA.
 AC ABB83162;
 XX 09-AUG-2002 (first entry)
 DT
 XX
 XX Human Toll-like receptor-4, Tlr4.
 DE
 XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
 KW cytoleak; immunostimulatory; scavenger receptor; Toll receptor;
 KW respiratory tract infection; Toll-like receptor; Tlr4.
 OS Homo sapiens.
 XX
 XX MO200235236-A1.
 PN
 XX 02-MAY-2002.
 PD
 XX 26-OCT-2001; 2001MO-FR003352.
 PF
 XX 27-OCT-2000; 2000FR-00013883.
 PR
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX Jeanmin P, Magistrelli G, Herbault N, Bonnefoy J;
 PT WPI; 2002-383586/41.
 DR N-PSDB; ABB83318.
 XX
 XX Identifying agent that binds to scavenger receptors and signals through a
 PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
 PT cytotoxic T cell response.
 PS
 XX Disclosure; Page 58-60; 71pp; French.
 XX
 XX The present invention relates to a method for identifying new therapeutic
 CC compounds (1) by selecting molecules that bind to scavenger receptors and
 CC signal through a Toll receptor. The present sequence is the protein
 CC sequence for human Toll-like receptor-4, Tlr4, which was used to

CC illustrate the method of the invention. (1) are useful as carriers and/or
 CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
 CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
 CC tumour cell, especially a pathogen that causes respiratory tract
 CC infection, also more generally for inducing an immune response. (1) can
 CC also be used for specific targeting of active agents (antigens etc.) to
 CC antigen-presenting cells (especially immature dendritic cells), for
 CC subsequent internalisation by these cells

XX Sequence 799 AA:

Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	61.59%	Indels:	0
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US-09-396-985B-3 (1-3811) x ABB83162 (1-799)

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 QY 465 CTAAGCCACTCTTCACTTAATATTTGAACAGAAACCCCATCCAGCTTTAGCCCTGGGA 524
 DB 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
 QY 525 GCCCTTTCTGAGCATATCAAGTTTACAGAGGCTGGCTGGTGGAGCAAACTTACGATCT 584
 DB 81 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 100
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAACTTAAATGGCTCAGCAAT 644
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 QY 645 CTTATCCAACTTTCAATTAACCTGAGTATTTTCTATCTGACCAATCTTAGACACTTG 704
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 DB 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuAspValLeuHisGln 160
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 QY 1965 TTGCTGGAAGTTGAAGAAATGGAATGTGCAACCTTTCAGATTAAGAGGCAAGGCTGTG 2024
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 DB 601 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 620
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Search completed: March 29, 2005, 17:01:15
Job time : 237.22 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 33.481 Seconds
(without alignments)
16993.973 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724

Sequence: 1 acggggcactgtctgtcac.....tctcactgacagagacta 3811

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsm62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4394	65.3	844	US-09-949-016-9438	Sequence 9438, Ap
2	619.5	9.2	661	US-08-514-014-4	Sequence 4, Appl
3	619.5	9.2	661	US-08-833-823-4	Sequence 4, Appl
4	599.5	8.9	784	US-09-982-308B-23	Sequence 23, Appl
5	539	8.0	775	US-09-949-016-8799	Sequence 8799, Ap
6	325	4.8	605	US-09-063-950-5	Sequence 5, Appl
7	306.5	4.6	623	US-09-949-016-10995	Sequence 10995, A
8	306	4.6	605	US-08-190-802A-49	Sequence 49, Appl
9	306	4.6	605	US-08-477-346-49	Sequence 49, Appl
10	306	4.6	605	US-08-473-089-49	Sequence 49, Appl
11	306	4.6	605	US-08-487-072A-49	Sequence 49, Appl
12	306	4.6	605	US-09-538-092-1087	Sequence 1087, Ap

13	298	4.4	603	1	US-08-190-802A-50	Sequence 50, Appl
14	298	4.4	603	3	US-08-477-346-50	Sequence 50, Appl
15	298	4.4	603	3	US-08-473-089-50	Sequence 50, Appl
16	298	4.4	603	4	US-08-487-072A-50	Sequence 50, Appl
17	298	4.4	662	4	US-09-538-092-1325	Sequence 1325, Ap
18	298	4.4	662	4	US-09-949-016-6619	Sequence 6619, Ap
19	298	4.4	665	4	US-09-949-016-10710	Sequence 10710, A
20	295.5	4.4	1525	3	US-09-191-647-2	Sequence 2, Appl
21	295.5	4.4	1525	3	US-09-540-245A-2	Sequence 2, Appl
22	295.5	4.4	1525	3	US-09-540-153-2	Sequence 2, Appl
23	293.5	4.4	907	4	US-09-170-496D-264	Sequence 264, App
24	293.5	4.4	907	4	US-09-170-496D-278	Sequence 278, App
25	293.5	4.4	1529	4	US-09-312-283C-396	Sequence 396, App
26	290	4.3	1112	3	US-09-353-585-3	Sequence 3, Appl
27	286	4.3	1112	3	US-09-353-585-2	Sequence 2, Appl
28	283.5	4.2	1166	4	US-10-101-464A-900	Sequence 900, App
29	281.5	4.2	1523	3	US-09-182-024A-2	Sequence 2, Appl
30	275	4.1	620	4	US-09-907-794A-73	Sequence 73, Appl
31	275	4.1	620	4	US-09-905-125A-73	Sequence 73, Appl
32	275	4.1	620	4	US-09-902-175A-73	Sequence 73, Appl
33	275	4.1	620	4	US-09-906-1700-73	Sequence 73, Appl
34	275	4.1	620	4	US-09-903-603A-73	Sequence 73, Appl
35	275	4.1	620	4	US-09-904-920A-73	Sequence 73, Appl
36	275	4.1	620	4	US-09-905-381A-73	Sequence 73, Appl
37	275	4.1	620	4	US-09-905-618-73	Sequence 73, Appl
38	275	4.1	620	4	US-08-666-271-2	Sequence 2, Appl
39	274.5	4.1	863	2	US-08-666-485-5	Sequence 5, Appl
40	274.5	4.1	1091	3	US-08-986-485-5	Sequence 5, Appl
41	274.5	4.1	1480	3	US-09-191-647-7	Sequence 7, Appl
42	274.5	4.1	1480	3	US-09-540-245A-7	Sequence 7, Appl
43	274.5	4.1	1480	3	US-09-540-153-7	Sequence 7, Appl
44	274.5	4.1	1480	5	PCT-US91-09055-2	Sequence 2, Appl
45	272.5	4.1	1480	3	US-09-182-024A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Alignment Scores:

Pred. No.: 0
Score: 4394.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 65.35%
DB: 4
Length: 844
Matches: 844
Conservative: 844
Mismatch: 0
Indels: 0
Gaps: 0

US-09-396-985B-3 (1-3811) x US-09-949-016-9438 (1-844)

QY 150 ACACACAGAAAGCTGGAGTAAACCCAGAGCTTCAGACTCCGAGAGCTCAGCCCTTC 209

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Db 1 ThrThrGlnbSerTrpHisglnThrGlnSerPheGlnThrProGlnProGlnProPhe 20
QY 210 ACCCGCATTCATGCTTCTTGCTAAATGCTGCCGTTTATTCACGGAGGTGCTCTAAAT 269
Db 21 ThrProIleProIleuLeuAlaLysCysCysArgPheIleThrGlnValValProAsn 40
QY 270 ATTACTTAATCAATGCAATGAGCTGAATTTCTACAAATCCCGACAAACCTCCCTCTCA 329
Db 41 IleThrTyrlGlnCysMetGlnLeuAsnPheTyrlLysIleProAsnAsnLeuProPheSer 60
QY 330 ACCAAGAACCTGGACCTGACCTTTAAATCCCTGAGCATTTAGACACTATAGCTTCTTC 389
Db 61 ThrLysAsnLeuAsnLeuSerPheAsnProLeuAlaArgHisLeuGlnYserTySerPhePhe 80
QY 390 AGTTTCCCGAATCTGACAGGTGCTGATTTATCCAGGTGTGAATTCAGACAAATTGAAGAT 449
Db 81 SerPheProGlnLeuGlnValLeuAsnLeuSerArgCysglnIleGlnThrIleGlnAsp 100
QY 450 GGGGCATATCAGAGCCTTAAGCCATCCTCTACCTTAATATGACGGAACCCCATCCAG 509
Db 101 GlyAlaTyrlGlnSerLeuSerHisLeuSerThrLeuIleuThrGlnAsnProIleGln 120
QY 510 AGTTTAGCCCTGGAGCCTTTTCTGACTATCAAGTTTACAGAACTGTGCTGTGAG 569
Db 121 SerLeuAlaLeuGlnLysAlaPheSerGlnLeuSerSerLeuGlnLysLeuValAlaValGln 140
QY 570 ACAAAATCTAGCATCTCTAGAAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTT 629
Db 141 ThrAsnLeuAlaSerLeuGlnAsnPheProIleGlnHisLeuLysThrLeuLysGlnLeu 160
QY 630 AATGTGCTCAACATCTTAATCCAAATCTTCAATTCCTGAGATTTTCTATCTGACAC 689
Db 161 AsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlnTyzPheSerAsnLeuThr 180
QY 690 AATCTAGACACTTGGACCTTTCCAGCAACAAGATTCAAAAGTATTTATTCACAGACTTG 749
Db 181 AsnLeuGlnHisLeuAsnLeuSerSerAsnLysIleGlnSerIleTyzCysThrAsnLeu 200
QY 750 CGGGTCTACATCAATGCCCCATCTCATCTCTTTAGACCTGTGCCGAAACCTATG 809
Db 201 ArgValLeuHisglnMetProLeuLeuAsnLeuSerLeuAsnProMet 220
QY 810 AACTTATCCAAACAGGTGACTTTAAAGAAATTAGCTTCATAGCTGACTTTAAGAAAT 869
Db 221 AsnPheIleGlnProGlnLysAlaPheLysGlnIleArgLeuHisLysLeuThrLeuAlaGAsn 240
QY 870 AATTTGATAGTTAAATGTAAATGAAAACTTGATTCAGAGTCTGGCTGTGTTTGAAGATC 929
Db 241 AsnPheAsnSerLeuAsnValMetLysThrCysIleGlnGlnLeuAlaGlnLeuGlnVal 260
QY 930 CATCGTTTGGTCTGGAGAAATTTAGAAATGAAGAAACTTGGAAAGTTTGACAAATCT 989
Db 261 HisArgLeuValLeuGlnGlnPheArgAsnGlnGlnLysAsnLeuGlnLysPheAsnLysSer 280
QY 990 GCCTTGAGGGCCGTGCAATTTGACATTTGAAGAATTCGATTAGATCTTAAGACTAC 1049
Db 281 AlaLeuGlnGlnLysLeuCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyzLeuAsnLysTy 300
QY 1050 TACCTCGATGATATTAATGACTTAATTAATTTGTTTGAACAATGTTTCTTATTTCCCTG 1109
Db 301 TyzLeuAsnAsnLysIleIleAsnLeuPheAsnCysLeuThrAsnValSerSerPheSerLeu 320
QY 1110 GTAGGTGTGACTATTTGAAGGGTAAAGACTTTTCTTAATAATTTCCGATGGCAACTTTA 1169
Db 321 ValSerValThrIleGlnArgValLysArgPheSerTyzAsnPheGlnTyzProGlnHisLeu 340
QY 1170 GAATTAAGTAACTGTAATTTGACAGTTTCCCATTTGAAATCTCAAACTCTCAAAAGG 1229
Db 341 GlnLeuValAsnCysLysPheGlnGlnPheProThrLeuLysLeuLysSerLeuLysArg 360
QY 1230 CTTACTTCACTTCCAAACAAGGTGGAGTCTTTTCAGAAAGTTGATTCACCAAGCTT 1289

Db 361 LeuThrPheThrSerAsnLysGlnLysAsnAlaPheSerGlnValAlaAsnLeuProSerLeu 380
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QY 1350 TTTGGGACAAACAGCCTAAAGTATTTAGATCTGACCTTCAATGCTGTTATTAACATGACT 1409
Db 401 PheGlnTyzThrSerLeuLysTyzThrLeuAsnLeuSerPheAsnGlnValIleThrMetSer 420
QY 1410 TCAAACTTCTGGGCTTGAACAACAATACTGAAACTCTGGAATTTCCAGACTTCCAAATTGAAA 1469
Db 421 SerAsnPheLeuGlnLysGlnGlnLeuGlnHisLysAsnPheGlnHisSerAsnLeuLys 440
QY 1470 CAATGAGAGATTTTCAAGTATTCCTATCACTCAGAAACCTGATTTACCTTGACATTTCT 1529
Db 441 GlnMetSerGlnPheSerValPheLeuSerLysLysArgAsnLeuIleTyzLeuAsnLysSer 460
QY 1530 CATACTCACACAGAGATTGCTTCAATGGACATCTTCAATGGCTTGTCCAGTCTCGAAGTC 1589
Db 461 HisThrHisThrArgValAlaPheAsnGlnLysPheAsnGlnLysLeuSerSerLeuGlnVal 480
QY 1590 TTAGAAATGGCTGGCAATCTTTCCAGAAACTTCTCCAGATATCTTCAACAGACTG 1649
Db 481 LeuLysMetAlaGlnLysSerPheGlnGlnAsnPheLeuProAsnLysIlePheThrGlnLeu 500
QY 1650 AGAAACTTGAACCTTCTGGACCTCTCAGTGTCAACTGGACAGTGTCTCCAAACAGCA 1709
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QY 1830 ATTAATGACTCCAAAAAACAGAACTACAGCACTTTTCCAAAGTACGTACTTCTTAAT 1889
Db 561 IleMetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsn 580
QY 1890 CTTACTCAGAAATGACTTTGCTTGATCTTGGAACAACAAGTTCCTGCAATGATGATCAAG 1949
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QY 1950 GACGAGGCAAGCTCTTGCTGGAAGTTGAACGAATGGAATGTGCACAACCTTCAAGTAAG 2009
Db 601 AspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAsnLys 620
QY 2010 CAGGGAGATGCTGTGTGAGTTTGAATATCACCTGTCAAGATTAAGCAATCATTTGGT 2069
Db 621 GlnGlnLysProValLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGln 640
QY 2070 GTGTGCGTCCAGTGTGCTTGAATCTGTGATCTGTGTGACAGTTCTGCTCTAATAGTTCTAT 2129
Db 641 ValSerValLeuSerValLeuValAlaSerValAlaValLeuValTyzLysPheTyz 660
QY 2130 TTTCACTGATGTCTTGTGCTGCTGATTAAGATATGTAAGAGTGAAGAAACATCTAATGAT 2189
Db 661 PheHisLeuMetLeuLeuAlaGlnCysIleLysTyzGlnArgGlnTyzLysAsnIleTyzAsp 680
QY 2190 GCCTTTGTTATCTACCAAGCCAGATGAGAGCTGGGTAAAGAAATGAGTAAAGTAAGTAAT 2249
Db 681 AlaPheValAlaLysTyzSerSerGlnAsnArgLysAsnTrpValArgAsnGlnLeuValLysAsn 700
QY 2250 TTAGAAGAAAGGGTGCCTCATTTGACCTGTGCTTCACTCAAGACACTTATTTCCCGGT 2309
Db 701 LeuGlnGlnGlnLysAlaProProPheGlnLysCysLeuHisTyzArgAsnPheIleProGln 720
QY 2310 GTGGCCATTTGCTGCCAACAATCATCATGAAAGTTTTCATTAAGCCGAAAGGTGATGTT 2369
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QY 2370 GTGGTGTCCAGCACTTTCATCCAGACCGGTGATCTTGAATATGAGATTGCTCAG 2429
 DB 741 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGln 760
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 QY 2490 AAGACCTCTCAGAGAGAGAGGTGAGTGTACCGCTTCTCAGCAGAAACCTTACCTG 2549
 DB 781 LysThrLeuLeuArgGlnGlnIleValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 800
 QY 2550 GAGTGGAGAGACAGATGCTCCTGGGGCGGCAATCTTCTGAGAGCACTCAGAAAAGCCTG 2609
 DB 801 GluTrpGluAspSerValLeuGlyArgHisIlePheThrArgArgLeuArgIysAlaLeu 820
 QY 2610 CTGGATGTAAATCATGAAATCCAGAAAGAGAGGTGATGAGATGCAATTGGCAGAA 2669
 DB 821 LeuAspGlyLysSerTyrPasnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGlu 840
 QY 2670 GCAACATCTATC 2681
 DB 841 AlaThrSerIle 844
 RESULT 2
 US-08-514-014-4
 ; Sequence 4, Application US/08514014
 ; Patent No. 5707829
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McKeough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSER: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514,014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-4
 Alignment Scores:
 Pred. No.: 8.56e-58
 Score: 619.50
 Percent Similarity: 45.45%
 Best Local Similarity: 29.33%
 Length: 661
 Matches: 200
 Conservative: 110
 Mismatches: 277

Query Match: 9.21% Indels: 95
 DB: 1 Gaps: 24
 US-09-396-985b-3 (1-3811) x US-08-514-014-4 (1-661)
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 QY 261 GTTCTTAATATATCTTAATCAATGCAATGAGATGGAATTTCTACAAATCCCGGCAACCTC 320
 DB 32 GluAlaAsnLysThrTyrAsnGlyCysGlnIleLeuSerGlnIleProAspThrLeu 51
 QY 321 CCTCTCAACCAAGAACTGAGCTGATTTATCCCTGAGGCACTTATGAGCACTAT 380
 DB 52 ProAsnThrThrGluPheLeuGlnIlePheSerPheAsnPheLeuProThrIleHisAsnArg 71
 QY 381 AGCTTCTTCAGTTTCCAGAACTGCAAGGTGCTGATTTATCCAGGTGTGAATCCAGACA 440
 DB 72 ThrPheSerArgLeuMetAsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrp 91
 QY 441 ATTGAAGATGGGCAATATCAAGAGCTTAAGCCACTCTCTACTTAATATGACAGAAAC 500
 DB 92 IleHisGluAspThrPheGlnSerHisIleGlnLeuSerThrLeuValLeuThrGlyAsn 111
 QY 501 CCCATCCAGATTTAGCCCTGGGAGCTTTCTGAGATATCAAGTTTACAGAACTGGTG 560
 DB 112 ProLeuIlePheMetAlaGlyThrSerLeuAsnGlyProLysSerLeuIlyHisIlePhe 131
 QY 561 GCTGTGAGACAAATCTAGCATCTGTAGAACTTCCCATTTGACATCTCAAACTTTG 620
 DB 132 LeuIleGlnThrGlyIleSerAsnLeuGlnPheIleProValHisAsnLeuGlnIle 151
 QY 621 AAAGACTTAATGTGGCTTCACATCTTATCCATCTTCAATTAACCTGAGATTTTCT 680
 DB 152 GluSerLeuTyrLeuGlySerAsnHisIleSerSerIleLysPheProLysAspPhePro 171
 QY 681 AATGACCAATCTGAGCACTTGAGCTTTCACACAAAGATCAAGATTAAGTATTATTC 740
 DB 172 ---AlaArgAsnLeuValLeuAspPheGlnAsnAlaIleHisTyrIleSerArg 190
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 DB 191 GluAspMetArgSerLeuGlnGln-----AlaIleAsnLeuSerLeuAsnIly 208
 QY 801 AACCTTAAGACTTATTCACACAGCTGATTTAAGAAATTAAGCTTATAGCTGACT 860
 DB 209 AsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
 QY 861 TTAAGAAATTAATTTGATAGTTTAATGAAGAAACTTGATTAACAAGTGTGCTGCT 920
 DB 228 -----AsnPheGlyGlyThrProAsnLeuSerValIlePheAsnIlyLeuGlnAsn 244
 QY 921 TTAGAAGTCCATCGTTTGTCTGGAGAAATTTAGAAATGAAGAACTTGAAGAAATTT 980
 DB 245 SerThrThrGlnSerLeuThrPheGlnIlyAspAsp---GluAspIle 263
 QY 981 GACAAATCTCTTGAAGGCTGTGCAATTTGACATTAAGCAATGAAGAAATCCGATGACATAC 1040
 DB 264 SerSerAlaMetLeuLysGlyLeuGlyCysGlnMetSerValGluSerLeuAsnIlyGln--- 282
 QY 1041 TTAGACTACTACCTGATGATTTATTAAG---TATTTAATTTGTTGCAAAATGCTCT 1097
 DB 283 ---GluHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGln 301
 QY 1098 TCATTTTCCCTGTGAGTGTGACTATTTGAAGGTTAAAGAACTTTTATTAATTTTCCGA 1157
 DB 302 GluLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSer-----Gly 316
 QY 1158 TGGCAACATTTGAATTAAGTTAAC----- 1181
 DB 317 MetLysGlyLeuAsnLeuLeuLysLysLeuValLeuSerValAsnHisPheAspGlnLeu 336

OY	1182	TGTAATTT-----GGACAGTTTCCCAATGG-----AAATTC	1214
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OY	1215	AAATCTCTCAAAAGGCTTACTTTCACCTTCCAAACAAAGGGGAAATGCTTTTTCAGAAAGTT	1274
Db	357	LybLybLeuH1sLeuGlyValGlyCysbLeuGlybLeuGlybAsn-----	371
OY	1275	GATCTACCAAGACCTTGAAGTTTCTAGATCTCAAGTAAATAATGGCTTGAGTTTCAAAAGTTGC	1334
Db	372	-----LeuGlnThrLeuAspSerH1sAsnAerIleGluAlaSerAspCys	387
OY	1335	TGTTCTCAAGAGATTTTGGGCAACACAGGCTTAAGTATTTAAGATCTGAGCTCAATAGT	1394
Db	388	CysSerLeuGlnLeuLybAsnLeuSerH1sLeuGlnThrLeuAsnLeuSerH1sAsnGly	407
OY	1395	GTTATTACATGAGTTTCAAAAC---TTCTTGGGCTTGAAGACATAAGAACATCTGGATTTC	1451
Db	408	ProLeuGlyLeuGlnSerGlnAlaPheLeuSgIuCsProGlnLeuGlnLeuLeuAspLeu	427
OY	1452	CAG-----CATTCCAAATTGAAACAATGAGTGAAGTTTCA-----GTATTTC	1493
Db	428	AlaPheThrArgLeuH1sIleAsnAlaProGln---SerProPheGlnAsnLeuH1sPhe	446
OY	1494	CTATACATCCAGAAACCTGATTAC-----CTTGACATTTCTGCATCTACACACAGAGATT	1547
Db	447	LeuGlnValLeuAsnLeuThrTyTyrAspPheLeuAspThrSerAsnGlnH1s-----	463
OY	1548	GCTTTCATAGGCATCTCAATAGGCTTGTTCAGAGTCTGAAAGTCTTGAAATAGGCTGGCAAT	1607
Db	464	-----LeuLeuAlaGlyLeuLeuProValLeuAlaGlnH1sLeuAsnLeuLybGlyAsn	479
OY	1608	TCTTTCCAGAAAACCTTCCTT-----CCAGATATCTTCAACAGAGCTGAGAACTTGACC	1661
Db	480	H1sPheGlnAspGlyThrIleThrLybThrAsnLeuGlnThrValGlySerLeuGln	499
OY	1662	TTCCTGCAGACCTCTCTCAAGTGTCAATGGAGACAGTGTCTCCAAACAGATTTAACATCACT	1721
Db	500	ValLeuIleLeuAsnSerCysGlyLeuLeuSerIleAspGlnGlnAlaPheH1sSerLeu	519
OY	1722	TCCAGTCTTCAAGTGTCTAATATATGAGCAACAACACTTCCTT-----TCATTTGAGATACG	1775
Db	520	GlyLybMetSerH1sValAspLeuSerH1sAsnSerLeuThrCysAspSerIleAspSer	539
OY	1776	TTTCTCTTAT-----AAGTGTGAACTCCCTCCAGATTCCTGAT	1814
Db	540	LeuSerH1sLeuLybGlyIleTyTyrLeuAsnLeuAlaIaAsnSerIleAsnIleLeuSer	559
OY	1815	TACAGTCTCAATCAATATATAGACTTCCAAAAACAGAACTACACAGACTTTTCCAAAGTATG	1874
Db	560	ProArgLeuLeuProIleLeu-----SerGln	568
OY	1875	CTAGCTTCTTAAATCTTACTCAGAAATGACTTGTCTGTACTTGTGAACACAGAGTTTC	1934
Db	569	GlnSerThrIleAsnLeuSerH1sAsnProLeuAspCysThrCysSerAsnIleH1sPhe	588
OY	1935	CTGCAATGATCATCAAGACACAGAGGAGCTTGTGTGGAAGTTGAACGAATGGAATGTGCA	1994
Db	589	LeuThrTrpTyTyrGlybAsnLeuH1sLybLeuGlnGlySerGlnGlyThrThrCysAla	608
OY	1995	ACACCTTACAGATACAGAGGACATGCGCTGTGCTGAAGTTGAATATACCTGTCAATGAAAT	2055
Db	609	AsnProProSerLeuArgGlyValLybSerSerAspValLybSerCysGlyIle---	627
OY	2055	AAGACATCATTTGGTGGTGGCTCTCCAGTGTGCTTGAATATCTGTTGTGAGCACTTCG	2114
Db	628	---ThrAlaIleGlyIlePhePheLeuIleValPheLeuLeu---LeuLeuAlaIleLeu	645
OY	2115	GTCTAT	2120
Db	646	LeuPhe	647

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US-08-833-823-4
Sequence 4, Application US/08833823
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Alignment Scores:
Pred. No.:      8,56e-58      Length:      661
Score:          619.50       Matches:     200
Percent Similarity: 45.45%   Conservative: 110
Best Local Similarity: 29.33% Mismatch:      277
Query Match:    9.21%       Indels:      95
DB:             2           Gaps:         24

US-09-396-985B-3 (1-3811) x US-08-833-823-4 (1-661)

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QY      261 GTTCCAAATTAATTACTAATGCATGAGCGCATTTCTACAATAATCCCGACAACTC 320
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Db      32 GluAlaAsnIysThrlYrAsnIySGlulAsnleugIylSeuSrgIulllePdaSPTlleu 51

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Db      52 ProAsnthrlThrcIuhleuIdubheserRheAsnRheIuProPllleIleIAsnIArg 71

QY      381 AGCTTCTTAGITTTCCACAGACTGCAAGTGTGATTTATCSAGGTGTGAATCSAGACA 440
        |||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      72 ThrPhseArYgrIuewMetAsnleuthrRheIuAspleuthrArgCysGlnIleAsnTrp 91

QY      441 ATTGAAGATGGGGCATATGAGGCTTAAGCCACTCTTACCCTTAATTAATTGACAGAAAC 500
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 92 LLehlglnuapRhrpneInserH1sH1sGlnLeuSerThrLeuValLeuThrGlyAsn 111
 QY 501 CCCATCCAGAGTTTACGGCTGGAGCCTTTCTGACATATCAAGTTTACAGAACTGGT 560
 Db 112 ProeuIllePheMetAlaGlnThrSerLeuAsnGlyProLysSerLeuYsH1sLeuPhe 131
 QY 561 GCTGTGAGACAAATATGACATCTAGAGAACTCCCATTTGAGATCTCAAACTTTG 620
 Db 132 LeuIleGlnThrGlyLeuSerAsnLeuGlnPheIleProValH1sAsnLeuGlnAsnLeu 151
 QY 621 AAGAAGCTTAATGTGGCTCAATCTTATCAATCTTTCAATATCTGAGATTTTCT 680
 Db 152 GluSerLeuYrLeuGlySerAsnH1sIleSerSerIleLysPheProLysAspPhePro 171
 QY 681 AATTCACCAATATGAGACCTTGACCTTCCAGCAACAAAGTTCAAGATTTATTTGC 740
 Db 172 ---AlaArgAsnLeuYsValLeuAspPheGlnAsnAsnAlaIleH1sYrIleSerArg 190
 QY 741 ACAGACTGGGGCTTACATCAAAATGCCCCCTACTCATCTCTTTTGAAGCTGCTG 800
 Db 191 GluAspMetArgSerLeuGlnGln-----AlaIleAsnLeuSerLeuAsnPheAsnGly 208
 QY 801 AACCTTATGAATTTATCCACACAGGTGCTTTAAAGAAATTAAGCTTCAATAGCTGACT 860
 Db 209 AsnAsnValIysGlyIleGlnLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
 QY 861 TTAGAATAATTTGATGTTAAATGTAATGAAACTGTATTCAGAGCTGGCTGCTG 920
 Db 228 -----AsnheGlyGlyThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsn 244
 QY 921 TTAGAATCCATGTTTGGTTCTGGAGAAATTTAGAAATGAAAGAACTTGAAGATTT 980
 Db 245 SerThrThrGlnSerLeuThrLeuGlyThrPheGlnAspIleAspAsp---GluAspIle 263
 QY 981 GACAAATCTGCTCTAGAGGCTGTGCAATTTGACATTAAGAAATTCGGATTAAGCATAC 1040
 Db 264 SerSerAlaMetLeuYsGlyLeuYsGluMetSerValGluSerLeuAsnLeuGln--- 282
 QY 1041 TTAGATACACCTGATGATATATTTGAC---TTATTTAATGTTTGAACAATGTTCT 1097
 Db 283 ---GlnH1sArgPheSerAspIleSerSerThrThrPheGlnYsPheThrGlnLeuGln 301
 QY 1098 TCATTTTCCCTGGTGGTGGATGATATTAAGAGGCTTGAAGAACTTTCTATATTTCCGA 1157
 Db 302 GluLeuAspLeuThrAlaThrH1sLeuYsGlyLeuProSer-----Gly 316
 QY 1158 TGGCAACATTTAGAAATTAAGTAAAC----- 1181
 Db 317 MetYsGlyLeuAsnLeuLeuYsYsLeuValLeuSerValAsnH1sPheAspGlnLeu 336
 QY 1182 TGTAAATTT-----GACAGTTTCCCACTTG-----AAATC 1214
 Db 337 CysGlnIleSerAlaAlaAsnProSerLeuThrH1sLeuYrIleArgIleAsnVal 356
 QY 1215 AATCTCTCAAAAAGGCTTACTTCACTTCCAAACAAGTGGAGATCTTTTTCAGAACTT 1274
 Db 357 YsYsLeuH1sLeuGlyValGlyCysYsLeuGlnYsYsLeuGlnAsn----- 371
 QY 1275 GATCTACCAAGCTTGAGTTTCTAGATCTCAAGTAAGATGCTTGAAGTTCAAGGTTGC 1334
 Db 372 -----LeuGlnThrLeuAspLeuSerH1sAsnAspIleGlnAlaSerAspCys 387
 QY 1335 TGTTCCAAGTATTTTGGACAAACACCTTAATATTTAGATCTTGAGCTTCAATGCT 1394
 Db 388 CysSerLeuGlnLeuYsAsnLeuSerH1sLeuGlnThrLeuAsnLeuSerH1sAsnGln 407
 QY 1395 GTTATTCATGAGTTCAAACT---TTCTTGAGCTTGAACAATGAAATCATCTGATTTTC 1451
 Db 408 ProLeuGlyLeuGlnSerGlnAlaPheYsGlyCysProGlnLeuGlnLeuAspLeu 427
 QY 1452 CAG-----CATTCGAATTTGAACAATAATGAGTACTTTCA-----GTATTC 1493
 Db 428 AlaPheThrArgLeuH1sIleAsnAlaProGln---SerProPheGlnAsnLeuH1sPhe 446

QY 1494 CTATCAGTCAAGAACTCATTTAC-----CTTGAACATTTCTCATCTCAGACAGAGTT 1547
 Db 447 LeuGlnValLeuAsnLeuThrYrCysPheLeuAspThrSerAsnGlnH1s----- 463
 QY 1548 GCTTTCAATGAGCATCTTCAATGAGCTTTGTCAGCTTCCAGAGCTTTGAAAGTGGCTGCAN 1607
 Db 464 -----LeuLeuIleGlyLeuProValLeuArgH1sLeuAsnLeuYsGlyAsn 479
 QY 1608 TCTTTCCAGAAAACTCTCTT-----CCAGATATCTTCAACAGCTGAGAACTTGACC 1661
 Db 480 H1sPheGlnAspGlyThrIleYrThrAsnLeuGlnThrValGlySerLeuGln 499
 QY 1662 TTCCTGAGACCTCTCAGGTGTCAGTCAAGAGAGAGCTGTGTCACAAAGCATTTTAACTCATC 1721
 Db 500 ValLeuIleLeuSerSerCysGlyLeuLeuSerIleAspGlnAlaPheH1sSerLeu 519
 QY 1722 TCCAGCTTCAAGATCTAATATATGAGCCACAAACTTCTT-----TCATTTGATAG 1775
 Db 520 GlyYsMetSerH1sValAspLeuSerH1sAsnSerLeuThrCysAspSerIleAspSer 539
 QY 1776 TTTCTTAT-----AAGTGTGAATCTCCCTCCAGTCTTGTAT 1814
 Db 540 LeuSerH1sLeuYsGlyYrIleYrLeuAsnLeuAlaIleAsnSerIleAsnIleSer 559
 QY 1815 TACAGTCTCAATCACAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTACT 1874
 Db 560 ProArgLeuLeuProLeuLeu-----SerGln 568
 QY 1875 CTAGCTTTCTTAATCTTACTCAGATGACTTGTGCTTGTATCTTGACACAGAGTTTC 1934
 Db 569 GlnSerThrIleAsnLeuSerH1sAsnProLeuAspCysThrCysSerAsnIleH1sPhe 588
 QY 1935 CTGCATGATCAAGACCAAGAGGACCTCTTGCTGAGAACTTGAACGAATGCAATGCA 1994
 Db 589 LeuThrTrpYrLeuGlnAsnLeuH1sYsYsLeuGlnGlySerGlnGlnThrCysAla 608
 QY 1995 ACACCTTGAGTAAGAGGAGCATGCTGCTGCTGATGATATATCACTGATGAGAT 2054
 Db 609 AsnProProSerLeuArgIleValYsLeuSerAspValYsLeuSerCysGlyIle--- 627
 QY 2055 AAGACCATCATGCTGTGTGCTGCTCCTCAGTGTCTGTAGTATCTGTGTGACAGTTCTG 2114
 Db 628 ---ThrAlaIleGlyIlePhePheLeuIleValPheLeuLeu---LeuLeuAlaIleLeu 645
 QY 2115 GTCTAT 2120
 Db 646 LeuPhe 647
 RESULT 4
 US-09-982-308B-23
 / Sequence 23, Application US/09982308B
 / Patent No. 6531290
 / GENERAL INFORMATION:
 / APPLICANT: Dalie, Barbara
 / APPLICANT: Fan, Xuedong
 / APPLICANT: Lundell, Daniel
 / APPLICANT: Lunn, Charles A.
 / APPLICANT: Tan, Jimmy C.
 / APPLICANT: Zavadny, Paul J.
 / TITLE OF INVENTION: Mammalian TNF-alpha Convertases
 / FILE REFERENCE: J06010C
 / CURRENT APPLICATION NUMBER: US/09/982,308B
 / CURRENT FILING DATE: 2001-10-17
 / PRIOR APPLICATION NUMBER: 09/156,163
 / PRIOR FILING DATE: 1998-09-17
 / PRIOR APPLICATION NUMBER: 08/889,909
 / PRIOR FILING DATE: 1997-07-10
 / PRIOR APPLICATION NUMBER: 60/021,710
 / PRIOR FILING DATE: 1996-07-12
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 23


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/ LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.: 1,46e-55 Length: 784
Score: 599.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.92% Indels: 219
DB: 4 Gaps: 38

US-09-396-985B-3 (1-3811) x US-09-982-308B-23 (1-784)

QY 306 ATCCCGGAGAACCTCCCTTCACACGAACTGACCTTAATCCCTGAGG 365
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Db 46 IleProSerGlyLeuThrGluAlaValLysSerLeuAspLeuSerAsnAsnArgIleThr 65
   :::::
QY 366 CATTAGGAGCATAGCTTCTTCAGTTCCCGAGATCGAGTGCATTTATCCAG 425
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Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
   :::::
QY 426 TGTGAATCCAGACAAATTGAAGATGGGACATATCAGAGCTTAAGCCACTTCTACCTTA 485
   |||||
Db 86 AsnGlyIleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGluHisIleu 105
   :::::
QY 486 AATTGACAGAAACCCCATCCAGAGTTTACCCCTGGAGCCTTTTCTGACATCAACT 545
   |||||
Db 106 AspLeuSerLysAsnTyrLeuSerAsnLeuSerSerTyrPheLysProLeuSerSer 125
   :::::
QY 546 TTACAGAACTG-----GTGCTGTGAG 569
   |||||
Db 126 LeuThrPheLeuAsnLeuLeuGlnLysProTyrTyrLeuGlyGluThrSerLeuPhe 145
   :::::
QY 570 ACAAACTGACATCTCTAGAAACTTCCCATTTGACATCTCAAACT----- 617
   |||||
Db 146 SerHisLeuThrTyrLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
   :::::
QY 618 -----TTGAAAGAACTTATGTGCTCACAATCTT 647
   |||||
Db 166 GlnAlaGlyAspPheAlaGlyLeuThrPheLeuGlnIleuGlnIleAspAlaSerAsp 185
   :::::
QY 648 ATCCAACTTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGACCTTGAC 707
   |||||
Db 186 LeuGlnSerTyrGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisIleu 204
   :::::
QY 708 CTTTCAGAACAAAG-----ATTCAAACTATT 734
   |||||
Db 205 LeuHisMetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerVal 224
   :::::
QY 735 TATTCAGACAGCTTGGGGGTTCATCAATGCCCTACTCAATCTCTTTAGACCTG 794
   |||||
Db 225 GlnCysLeuGluIleuLysG-----AspThr 232
   |||||
QY 795 TCCCTTAACCCCTATGAAGTTT-----ATCCAAACAGAGTCATTAAAGAAATAGAGCTT 848
   |||||
Db 233 AspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---Ile 251
   :::::
QY 849 CATTAAGCTGATTAAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAA 896
   |||||
Db 252 LysLysPheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLys 271
   :::::
QY 897 ACTGTG-----ATTCAAGGTCTGGCTGCTTTGAAGTCATGTTGGTCTG----- 944
   |||||
Db 272 LeuLeuAsnGlnIleSerGlyLeuLeuGluIleuGlnPheAspAspCysThrLeuAsnGly 291
   :::::
QY 945 ----GGAGAAATTGAATGAATGAAGAACTTGGAAAAGTTTGACAAATCTGCTAGAGGGC 1001
   |||||
Db 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGln--- 310
   :::::
QY 1002 CTGTGCAATTGACCAATTGAAGAATTCGATTAGCA-----TACTTAGACTACTACCTC 1055
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Db 311 -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
QY 1056 GATGATATATATGACTTATTTAATGTTTGACAAATGTTTCTATTTCCCTGGTAGT 1115
   |||||
Db 327 ---AspLeuSerThrLeuTyrSerLeuThrGluArgValLys-----Arg 340
   :::::
QY 1116 GTGACTATTTGAAGGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTTAGAAATTA 1175
   |||||
Db 341 IleThrValGluAsnSerLysValPhe-----Leu 350
   :::::
QY 1176 GTTAACTGTAAATTTGGACAGTTTCCCATTTGAATCAATCTCTCAAAAAGCTTACT 1235
   |||||
Db 351 ValProCysLeuLeuSerGln----- 357
   :::::
QY 1236 TTCACCTTCCAAAGTGGGAATGCTTTTCAGAAATGTGATCTACAGCCTTGAGTTT 1295
   |||||
Db 358 -----HisLeuLysSerLeuIuTyr 364
   :::::
QY 1296 CTGATCTCAGTAGAAAT-----GGCTTGAAGTTTCAAGGTGCTGTCT 1340
   |||||
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 382
   :::::
QY 1341 CAAAGTATTTGGACAAACAGCCTTAAAGTATTTGATCTGAGCCTTCAATGCTTATTT 1400
   |||||
Db 383 -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
   :::::
QY 1401 ACCATGAGTTCAAACTTCTGGGCTTAGAACAACATCTGAGATTTCCAGACATTCC 1460
   |||||
Db 398 -----HisLeu-----Ala 400
   :::::
QY 1461 AATTGAAACAATGATGATGATTTTCAGTATTCCTATGACTCAGAACTCATTTACCTT 1520
   |||||
Db 401 SerLeuGluLysThrGlyGlu-----ThrLeuLeuThrLeuLysLeuThrAsnIle 418
   :::::
QY 1521 GACATTTCTCATATCTCACACCAAGAGTCTTTCAATGGCATTTCAATGGCTGTTCAGT 1580
   |||||
Db 419 AspIleSerLys----- 422
   :::::
QY 1581 CTGGAAGCTTGAAGAAATGGCTGGCAATTCCTTCCAGAAAACCTCCTCAGATATCTTC 1640
   |||||
Db 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
   :::::
QY 1641 ACAGAGCTGAGAACTGACCTTCTCGGACCTCTCTCAGTGTCAACTGAGACAGTTGCT 1700
   |||||
Db 433 GlnTyrProGluLysMetLysTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
   :::::
QY 1701 -----CACAACGACTTAACTCACTCTTCAGTCTTCAGTACTTAATATGAGCCAC 1751
   |||||
Db 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
   :::::
QY 1752 AAC-----AAGCTTTTCAATTGAT----- 1772
   |||||
Db 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrIleSerArg 486
   :::::
QY 1773 -----ACGTTTCT---TATAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAC 1817
   |||||
Db 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuPheMetLeuLeuValLeuLysIle 506
   :::::
QY 1818 AGCTCAATCACATATATGACTTCCAAAACAGAACTTACAGCAATTTTCCAAAGTACTTA 1877
   |||||
Db 507 SerArgAsnAlaIleThrThrPheSerLysGlnLeuAspSerPhe---HisThrLeu 525
   :::::
QY 1878 GCTTTCTTAAATCTTACAGAAATGACTTGTGTTACTGTGGAACACAGAGTTTCCG 1937
   |||||
Db 526 LysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
   :::::
QY 1938 CAATGATCAAGACAGAGCACTCTTGCTGAGATT-----GAACGA 1982
   |||||
Db 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 561
   :::::
QY 1983 ATGGAATGTGAACACTTTCAGATTAAGCAGGCGATGCTGTGCTGATTTGAATATCAC 2042
   |||||
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
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OY	2043	-----TGCAGATGAATAAGAACCATTTGGTGTGGCTCCGACGTGGCTTTGA	2093
Db	582	ValSerGluCysHisArgIleAlaLeuValSerGlyMetCysValAlaLeuPheLeu	601
OY	2094	GTATCTGTTGTGACAGTTTGTGCTATAGAATTCTAT-----TTTCACTGATGCTTTCT	2147
Db	602	IleLeuLeuThrGlyValLeuCysHisArgPheHisGlyLeuThrPheMetCysMet	621
OY	2148	GCTGGCTGCATTAAGATGATGTA-----GTTAAAAATCT--TAT	2186
Db	622	TPAlaIlePheGlnAlaIleAlaLysArgLysProArgLysAlaProSerArgPheHisCysTyr	641
OY	2187	GATGCGCTTTGTTATCTACTCAAGCCGAGATGAGAGATGGGGTAAAGATGAGTAAAG	2246
Db	642	AspAlaPheValSerTyrSerGluArgAspAlaTyrTyrValGluPheMetValGln	661
OY	2247	AATTAGAAAGAGGGGTGCTCCATTTCCATTTCACTTGTGCTTCACTACAGAGATTATATCC	2306
Db	662	GluLeuGluAsnPheAsnProPheLysLeuCysLeuHisLysArgAspPheIlePro	681
OY	2307	GGTGTGGCCATTGCTGCGCCAACTCATCTCAATGAAGTTTCCATTAAGCCGAAGGTGAT	2366
Db	682	GlyLysTrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisLysThrVal	700
OY	2367	GTGTGGTGTCCAGACACTTCATCCAGAGCCGGTGGTGTATCTTTGAATATGATTTGCT	2426
Db	701	PheValIleLeuSerGluAsnPheValLysSerGluTrpCysLysTrpGluAsnProSer	720
OY	2427	CAGACCTGGCAGTTTCTGAGCAAGTCGTGTGTATCATCTTCATTGTCTGCAAGAGTG	2486
Db	721	HisPheArgLysLeuPheAspGluAsnAsnAspAlaAlaIleLeuHisLeuLeuGluProIle	740
OY	2487	GAGAAGACCTCTCTCAGGCAAGCAG--GTGAGCTGTACCGCTTCTCAGAGGAACACT	2543
Db	741	GlyLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr	760
OY	2544	TACTGAGTGGGAGAGACAGTGTCTCGGGGGCGGACATCTTTGAGAGACGACTCAGAAA	2603
Db	761	TyrLeuGluIleTrpPrometAspGluAlaGlnArgGluGlyPheThrValAsnLeuArgAla	780
OY	2604	GCCCTG 2609	
Db	781	AlaIle 782	

RESULT 5

US-09-949-016-8799

Sequence 8799, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8799

LENGTH: 775

TYPE: PRT

ORGANISM: Human

US-09-949-016-8799

Alignment Scores:

Pred. No.:	5,63e-49	Length:	775
Score:	539.00	Matches:	218

[illegible]

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Db      386  ValProCyLeuLeuSerGln----- 392
Qy      1236 TTCACCTTCCAAAGAGTGGGAATGCTTTTTCAGAGTGTATCTACCAAGCCTTGAGTTT 1295
Db      393  -----HisLeuLySerLeuGluTyr 399
Qy      1296 CTAGATCTCAGTGAAT-----GGCTTGAGTTTCAAGGTTGCTTCT 1340
Db      400  LeuAspLeuSerGluYasnLeuMetValGluGluTyrLeuLyAsnSerAlaCys----- 417
Qy      1341 CAAAGTGATTTTGGGACACAGCCCTAAAGTATTAGATCTGAGCTTCAATGGTGTATT 1400
Db      418  -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 432
Qy      1401 ACCATGAGTTCAAACTTCTGGGCTTGAAGAACTGAACATCGATTTCCAGACTCC 1460
Db      433  -----HisLeu-----Ala 435
Qy      1461 AATTGAAACAAATGAGTGAATTTTCAGATTCTATCACTGACAAACCTCATTTAAGCTT 1520
Db      436  SerLeuGluTyrThrGlyGlu-----ThrLeuLeuThrLeuYasnLeuThrAsnIle 453
Qy      1521 GACATTCTCATACTGACACACAGAGTTGGTTCAATGGCATTTCAATGGCTTGCCACT 1580
Db      454  AspIleSerLy----- 457
Qy      1581 CTGGAAGTGTGAAATGGCTGGCAATCTTTCAGAAACCTCTCCAGATATCTTC 1640
Db      458  -----AsnSerPheHisSer-----MetProGluThrCys 467
Qy      1641 ACAAGACTGAAAATTGACCTTCTGACACTCTCTCAGTGTCACTGAGACAGTTGTCT 1700
Db      468  GlnTyrProGluYasnMetLysTyrLeuAsnLeuSerThrArgIleHisSerValThr 487
Qy      1701 -----CSAAGCATTTAACTGACTCTGAGCTTCAGGTACTAAATGAGCCAC 1751
Db      488  GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 501
Qy      1752 AAC-----AACTCTTTTCATTGAT----- 1772
Db      502  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuYasnLeuTyrIleSerArg 521
Qy      1773 -----ACGTTTCTCT--TATTAAGTGTGAACTCCCTCAGGTTCTTGATTAAC 1817
Db      522  AsnLyLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuYsnIle 541
Qy      1818 AGTCTCAATCAGATATGACTTCCAAAAACAGAACTACAGACTTTCCAGTACTCTTA 1877
Db      542  SerArgAsnAlaIleThrThrPheSerLyGluGlnLeuAspSerPhe--HisThrLeu 560
Qy      1878 GCTTTCTAAATCTTCACTGACAGTGTGCTTGTGATTTGTAACACAGAGTTTCTGT 1937
Db      561  LysThrLeuGlnAlaLeuLyGlnAsnAsnPheIleCysSerCysLeuIuhLeuSerPheThr 580
Qy      1938 CAATGATGAAGGACCAAGAGCCTTGGTGGAAATT-----GAACA 1982
Db      581  Gln-----GluGlnGlnAlaLeuAlaLyValLeuIleAspTyrProAlaAsn 596
Qy      1983 ATGGAATGTGAACAACTTCAGATTAAGCAGGCGATCCCTGGTGTGATTTGAATATCAC 2042
Db      597  TyrLeuCysAspSerProSerGlnValArgGlyGlnGlnAlaGlnAspValArgLeuSer 616
Qy      2043 -----TGTCAATGATAAGACATCATGATGATGATGATGATGATGATGATGATGAT 2093
Db      617  ValSerGluCysGlnHisArgThrAlaLeuValSerGlyMetCysGlyAlaLeuPheLeuLeu 636
Qy      2094 GATATCTGTTGAGACAGTTCTGGTCTATTAAGTTCTAT-----TTTCACTGATGCTTTCT 2147
Db      637  IleLeuLeuThrGlyAlaLeuCysHisArgPheGlnGlyLeuTyrTyrMetLysMetMet 656

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Qy      2148 GCTGGCTGATTAAGTATGTAGA-----GGTGAACATC---TAT 2186
Db      657  TrpAlaTyrPheGlnAlaLysArgTyrProArgValaProSerArgAsnIleCysTyr 676
Qy      2187 GATGCTTTGTTATCTACTCAAGCCAGATGAGACCTGGTGAAGATGAGCTAGTAAAG 2246
Db      677  AspAlaPheValSerTyrSerGluTyrGlnAlaTyrTrpValGluAsnLeuMetValGln 696
Qy      2247 AATTGAAAGAGGGGTGCTCCATTTGAGCTCTGCTTCACTAAGACCTTATTCCTCC 2306
Db      697  GluLeuGluAsnPheAsnProPheLeuYasnLeuCysLeuHisLyAspAspPheIlePro 716
Qy      2307 GGTGGGCAATTCCTGCCAACATCATCCAGTAAGGTTTCCATTAAGCCGAAAGGTGATT 2366
Db      717  GlyLysTrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrVal 735
Qy      2367 GTTGTGTGTCCAGACACTTCAATCCAGACGCGTGGTATCTTTGAATATGAGATTGCT 2426
Db      736  PheValLeuSerGluAsnPheValLysSerGluTyrCysLysTyrGluLeuAspPheSer 755
Qy      2427 CAGACCTGGCACTTCTTGACAGCTGTGCTGTATCATCTTCACTGTCTCGAAGAGTG 2486
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RESULT 6
US-09-063-950-5
/ Sequence 5, Application US/09063950C
/ Patent No. 6225085
/ GENERAL INFORMATION:
/ APPLICANT: Holzman, Douglas A.
/ TITLE OF INVENTION: NOVEL LRG6 PROTEIN AND NUCLEIC ACID MOLECULES AND USES
/ TITLE OF INVENTION: THEREFOR
/ FILE REFERENCE: MEI-019
/ CURRENT APPLICATION NUMBER: US/09/063,950C
/ CURRENT FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 605
/ TYPE: PRT
/ ORGANISM: Papio hamadryas
US-09-063-950-5

Alignment Scores:
Pred. No.: 9 716-26
Score: 325.00 Length: 605
Percent Similarity: 38.83% Matches: 163
Best Local Similarity: 24.44% Mismatches: 96
Query Match: 4.83% Indels: 254
DB: 3 Gaps: 24

US-09-396-985B-3 (1-3811) x US-09-063-950-5 (1-605)
Qy      201 CAGCCCTTCAACCCCG-----ATTCCATTGCTTCTGTAATGCTGCCGTTT 248
Db      29  GlnProGluThrProGluGlnAlaGluGlyProAlaCysProAlaThrCysAlaCysSer 48
Qy      249 ATCAAGAGAGGTGCTCTAATATTAATTAATCAATGAGTGAAGCTAATTTCTCAAAATC 308
Db      49  TyrAspAspGluValaLysGlnIleLeuSerValPheCysSerSerArgAsnLeuThrArgLeu 68
Qy      309 CCGCAACCTCCCTCTTCACACCAAGAACTGACCTGAGCTTTTAATCCCTGAGGCAT 368
Db      69  ProAspGlyLeuProGlyGlyThrGlnAlaLeuTyrLeuAspSerArgAsnLeuSer 88
Qy      369 TTAGCAGCTAATAGCTTTCAGTTTCCAGAACTGACAGTGAAGTGAATTTATCCAGTGT 428
Db      89  IleProProAlaAlaPheArgAsnLeuSerSerLeuAlaPheLeuAsnLeuGlnGly 108
Qy      429 GAATTCGACAAATTTGAAGATGGGCGATATGACAGCTTAAGCCCACTCTTAATATA 488
Db      109  GlnLeuGlySerLeuGlnProGlnAlaLeuLeuGluGlyLeuGluAsnLeuCysHis 128

```

QY 489 TTGACAGAAACCCCATCCAGATTAGCCCTGGAGCCTTTC----- 533
 DB 129 LeuGIuArgAsnGIuLeuArgSerIeuAlaValGIuThrPheAlaIArgThrProAlaLeu 148
 QY 534 -----GGA 536
 DB 149 AlaLeuGIuLysSerAsnAsnArgLeuSerArgLeuGIuAspGIuLysLeuPheGIuLys 168
 QY 537 CTATCAAGTTTACAGAGCTGGCTGGTGAGACAAATCTAGCATCTCTAGAGAACTTC 596
 DB 169 LeuGIuAsnLeuTrpAspLeuAsnLeuGIuYTrpAsnSerIeuAlaValLeuProAspAla 188
 QY 597 CCCATTGGACATCTCAAAACTTTGAAAGAACTTAATGGCTCAGACATCTTCAATCT 656
 DB 189 AlaPheArgGIuLeuGIuLysArgGIuLeuValIeuAlaGIuAsnArgLeu--Ala 207
 QY 657 TTCAAATTACCTGAGATTCTTCTATCTGACCAATCTAGACACTTGACCTTTCACG 716
 DB 208 TyrLeuGIuProAlaLeuPheSerGIuLeuAlaGIuLeuArgGIuLeuAspLeuSerArg 227
 QY 717 AACGAATTCAAAAGTATTATTATTCACAGACTTGGGCTTCTACATCAATGCCCTACTC 776
 DB 228 AsnAlaLeuArgAlaIle-----LysAlaAsnValPheAlaGIuLeuProArgLeu 244
 QY 777 AATCTCTCTTGGACCTGCTCCGTAACCTATGACTTATCCAACTGAGTGCATTAA 836
 DB 245 GIu--LysLeuTrpLeuAspArgAsnLeuIleAlaValAlaProGIuAlaPheLeu 263
 QY 837 GAAATTAGG---CTTCATAGCTGACTTATAGAAATATTTGATAGTTAATGTAAAG 893
 DB 264 GIuLeuLysAlaLeuArgTrpLeuAspLeuSerHisAsn--ArgAlaAlaGIuLeuLeu 282
 QY 894 AAACTTGATTCAGAGCTGCTGGCTGTTTAAAGATCCATCGTTGCTTGGAGAAATT 953
 DB 283 GIuAspTrpPheProGIuLeuLeuGIuLysArgValIeuArgLeu----- 297
 QY 954 AGAATGGAAGAACTTGAAAAAGTTGACAAATCTGCTAGAGGCGCTGGCAATTG 1013
 DB 298 -----SerHisAsnAlaIleAlaSerLeuArgProArg 308
 QY 1014 ACCATTGAAGAAATCCGATTAGCATCTAGACTTACCTGATATTTATGACTTA 1073
 DB 309 ThrPheGIuAspLeu-----HisPheLeuGIuLeu----- 319
 QY 1074 TTTAATTGTTGACAAATGTTCTTCAATTTCCCTGGTAGGTGACATAAGAGGTA 1133
 DB 320 -----GlnLeuGIuYHisAsnArgIleArgGIuLeu 329
 QY 1134 AAAAGCTTTCTTATAATTGCGATGGCAACATTTAGATTAGTTAACTGTAATTGGA 1193
 DB 330 AlaGIuArgSerPheGIu--GIuLeuGIuGIuLeuGIuValLeuThrLeuAspHisAsn 348
 QY 1194 CAGTTTCCACATTTGAACATCTCTCAAAAAGCTTACTTCACTTCC-----AAC 1247
 DB 349 GlnLeuGIuGIuValIeuValGIuAlaPheLeuGIuLeuThrAsnValAlaValMetAsn 368
 QY 1248 AAGGTGGAATGCTTTTCAAGAGTTGATCTACCAAGCCTTGAGTTCTAATCTCACT 1307
 DB 369 LeuSerGIuAsnCysLeuArg-----AsnLeuProGIuGIuValPheArgGIuLeuGIu 386
 QY 1308 AAG---AATGGCTTGAGTTTCAAAAGTTGCTGT-----TCTCAAACTGAT 1349
 DB 387 LysLeuHisSerIeuHisLeuGIuGIuLysSerCysLeuGIuArgIleArgProHisTrpPhe 406
 QY 1350 TTTGGACACACAGCTTAAGTATTATAGATCTGAGCTTCAATGGTGTATTAACATGAGT 1409
 DB 407 AlaGIuLysSerGIuLeuArgLeuPheLeuLysAspAsnGIuLeuValGIuLysGIu 426
 QY 1410 TCAAACTTCTTG--GGCTTAGAACACTTAGAACTCTGAGATTCCAGCAATTCATTTG 1466
 DB 427 GIuGIuSerLeuTrpGIuLeuAlaGIuLeuGIuLeuAspLeuThrSerArgGIuLeu 446

QY 1467 AAACAATGAGTAGTTTCAGTATTCCTATCTACAGAAACCTCATTTACCTTGACATT 1526
 DB 446 ----- 446
 QY 1527 TCTCATCTACACACAGACTTCTTCAATGCAATCTTCAATGCTTGTCCAGTCTGCA 1586
 DB 447 -----ThrHisLeuPro-----HisGlnLeuPheGIuGIuLysLeuGIu 461
 QY 1587 GCTTGAANAATGGCTGGCAATCTTTCAGAGAAACCTTCCTGCA---GATATCTTCA 1643
 DB 462 TyrLeuLeuLeuSerHisAsnArgLeuAlaGIu-----LeuProAlaAspAlaLeuGIu 479
 QY 1644 GAGCTGAGAACTTGAACCTTCCCTGAGACCTTCTCAGTGTCACTGAGAGCTTGTCTCA 1703
 DB 480 ProLeuGIuArgAlaPheTrpLeuAspValSerHisAsnArgLeuGIuAlaLeuProGIu 499
 QY 1704 ACAGCAATTTAATCACTCTCCAGTCTTCAAGGTACTTAATATGACCAACAACTTCTT 1763
 DB 500 SerLeuLeuAlaSerLeuGIuYArgLeuArgTrpLeuAsnLeuArgAsnAsn----- 516
 QY 1764 TCATGATAGCTTCCCTTATAGTGTCTGAACCTCCCTCAGGTTCTTATACAGTCTC 1823
 DB 517 SerLeuArgTrpPheTrpProGIu----- 524
 QY 1824 AATCATATATGACTTCCAAAAACAGAACTACAGACTTTTCCAAAGTAGTCACTTTC 1883
 DB 525 -----ProProGIuLeuGIuArg 530
 QY 1884 TTAATCTTACTCAGAAATGACTTGTGCTTACTTGTGAACACCAAGT----- 1931
 DB 531 LeuTrpLeuGIuGIuYAsnProTrpAspCysSerCysProLeuLysAlaLeuArgAspPhe 550
 QY 1932 -----TTCGCGAATGATC-----AAGGAC 1952
 DB 551 AlaLeuGIuAsnProSerAlaValProArgPheValGIuAlaIleCysGIuLysAsp 570
 QY 1953 CAGAGCAGACTTGTGATGAGTTGACAGATGATGATGATGATGATGATGATGATGATG 2012
 DB 571 CysGIuProProValYTrpThrYAsnAsnIleThrCysAlaSerProProGIuValAla 590
 QY 2013 GGCATGCTGTGCTGAGTTTG 2033
 DB 591 GIuLeuAspLeuArgAspLeu 597

RESULT 7
 US-09-949-016-10995
 ; Sequence 10995, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH TYPE 2 DIABETES MELLITUS
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 10995
 ; LENGTH: 623
 ; TYPE: PRN
 ; ORGANISM: Human
 ; US-09-949-016-10995

Alignment Scores:
 Pred. No.: 1,03e-23 Length: 623
 Score: 306.50 Matches: 175
 Percent Similarity: 38.17% Conservative: 96

Best Local Similarity: 24.65% Mismatches: 279
 Query Match: 4.56% Indels: 160
 DB: 4 Gaps: 27

US-09-396-985B-3 (1-3811) x US-09-949-016-10995 (1-623)

95 CCTCTCCGCTGAGACAGAAAGCTGGAGCCCTGCGAGACTTTGGCCCTAAACAC 154
 15 ProAlaCyArgMetAlaLeuArglyGlyLeuAla-----LeuAlaLeuLeu 32
 155 ACAGAAAGCTGGCAGTAAACCCAGACTTTCAAGCTCCGAGCCCTTACACCC 214
 3 LeuSerTrpValAlaLeuGlyProArg--SerLeuGlyAla-AspProGlyThrPr 51
 215 G-----ATTCCATTGCTTCTTAATGCTCCGCTTATACAGGAGGTGCT 262
 51 oclYgluaIagIugIyProAlaCyArgProAlaAlaCyValCySerTyArgPrAspAl 71
 263 TCCTAATATTACTTATCAATGATGAGCTGAATTTCTACAAATCCCGACAACTCC 322
 71 aAspGluLeuSerValPheCySerSerArgAsnLeuThrArgLeuProAspGlyAlaPr 91
 323 CTCTTCAACCAAGAACCTGAGCTTAAATCCCTGAGGCAATTTAGGCACTTAAG 382
 91 oclYglYthrGlnAlaLeuTrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAl 111
 383 CTCTTCACTTTCCCGAACTGAGCTGCTGATTTATCCAGGTGGAATCCAGACAT 442
 111 aPheGlnAsnLeuSerSerLeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLe 131
 443 TGAAGATGGGCAATATCAGAGCTTAAGCCACTCTTACCTTAATATTCAGAAACCC 502
 131 uclYpProGlnAlaLeuLeuGlyLeuGlyAsnLeuCyHisLeuHisLeuGlnAlaArgAsnG 151
 503 CATCCAGATTAGCCCTGAGAGCTTTCT----- 533
 151 nLeuArgSerLeuAlaLeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLe 171
 534 -----GAGCTATCAAGTTTACA 550
 171 uSerAsnAsnArgLeuSerArgLeuGlnAlaAspGlyLeuPheGlnGlyLeuGlySerLeuTr 191
 551 GAAGCTGTGCTGTGAGACAAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCT 610
 191 pAspLeuAsnLeuGlyTrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLe 211
 611 CAAACTTTGAAAAGACTTAATGTGCTCAAACTTTATCCAACTTTTCAAAATTACCTGA 670
 211 uclYSerLeuArgGlnLeuValLeuAlaGlyAsnArgLeu--AlaTyLeuGlnProAl 230
 671 GTATTTTTCTAATCTGACCAATCTAGACACTTGGACCTTCCAGAGCAACAAGTTCAAG 730
 230 aLeuPheSerGlyLeuAlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAl 250
 731 TATTTTTTCACAGACTTCCGGGTCTTACATCAAAATGCCCTACTCAATCTCTCTTAA 790
 250 aIle-----LysAlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTy 266
 791 CCTGTCCCTGAACCTTAGAACTTTATCCAAACGAGTGCATTTAAAGAAATTAGG---CT 847
 266 rLeuAspArgAsnLeuIleAlaAlaValAlaProGlyAlaPheLeuGlyLeuTyValaIle 286
 848 TCATAAGCTGACTTAAAGAAATTAATTTGATAGTTAAATGTAAATGAAATCTGTATTC 907
 286 uArgTrpLeuAspLeuSerHisAsn--ArgValAlaGlyLeuLeuGlnAlaAspThrPhePr 305
 908 AGCTGTGCTGGTGTGAAGTCAATGCTTTGTTTGGGAAATTAGAAATGAAAGAA 967
 305 oclYLeuLeuGlyLeuAlaArgValLeuArgLeu----- 315
 968 CTTGAAAAGTTTGACAAATCTGCTCTAGAGGCTGTGCATTTGACCAATTGAAAGATT 1027
 316 -----SerHisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLe 331

1028 CCGATTAGCAATCTTAGACTTACTACCTGATGATTAATTTAGCTATTATTTGTTGAC 1087
 331 u-----HisPheLeuGlnGlyLeu----- 337
 1088 AAATGTTTCTTCAATTTCCCTGGTAGTGATGATTTGAAAGGTAAGAACTTTCTTA 1147
 338 -----GlnLeuGlnHisAsnArgIleArgGlnLeuAlaGlnArgSerPr 352
 1148 TAAATTCGAGTGGCAACTTTAGATTTAGATTTAACTGTAAATTTGACAGTTTCCACAT 1207
 352 eclY--GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnVala 371
 1208 GAAACTCAAACTCTCAAAAAGCTTACTTCACTCC-----AACAAAGTGGAGATGC 1261
 371 llyAlaGlyAlaPheLeuGlyLeuThrAsnValAlaValaMetAsnLeuSerGlyAsnCy 391
 1262 TTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTCAGTAGA--AATGCTT 1318
 391 vLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGlyLysLeuHisSerLe 409
 1319 GAGTTTCAAAAGTTCTGT-----TCTAAAGTGAATTTGGACAAACAG 1363
 409 uHisLeuGlnGlySerCyvLeuGlyArgIleArgProHisThrPheThrGlyLeuSerG 429
 1364 CCTAAAGTATTAGATCTGAGCTTCAATGCTGTATTTACATGAGTTCAAACTTCTG-- 1421
 429 yLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGlnGlnGlnSerLeuTr 449
 1422 -GGCTTAGAAACAATAGAACATCTGATTTCCAGACTTCCAAATTTGAAACAAATGATGA 1480
 449 pclYLeuAlaGlnLeuLeuGlnLeuAspLeuThrSerAsnGlnLeu----- 464
 1481 GTTTTCAGATTCTTATCACTCAAGAAACCTGATTTACTTGACATTTCTCAATCTCACAC 1540
 465 -----ThnHisLe 467
 1541 CAGAGTGTCTTCAATGCGATCTTCAATGCTTGTGCTGCAAGTCTTGAATGAGC 1600
 467 uPro-----HisArgLeuPheGlnGlyLeuGlyLysLeuGlnTyTyLeuLeuLeuSe 484
 1601 TGGCAATCTTCTTCAGAAAACCTTCTTCA--GATATCTTCAACAGCTGAGAACTT 1657
 484 rArgAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeuGlnAlaG 502
 1658 GACCTTCTGAGACCTCTCTCACTGTCACATGAGAGATGTTCTCCAAAGCACTTTAACTC 1717
 502 aPheTrpLeuAspValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaPr 522
 1718 ACTTCCAGTCTTTCAGTAACTAAATATGAGCCACAACAATCTTTCATTTGATGATGCT 1777
 522 oclYArgLeuAlaGlyTyLeuSerLeuArgAsnHis-----SerLeuArgThrPh 539
 1778 TCCTTAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAACGTCAATCACAATATGAC 1837
 539 eThrProGln----- 542
 1838 TTCCAAAAAACAGAACTACAGCAATTTTCCAAAGTGTCTAGCTTTCTTAAATCTTACTCA 1897
 543 -----ProProGlyLeuGlnArgLeuTrpLeuGlnG 553
 1898 GAATGACTTGTGCTTGAATCTTGAACACACAGATTTCCTGCAATGAGTCAAGAC----- 1952
 553 yAsnProTrpAspCyvGlyCyvPro-----LeuTyValaLeuAlaArgAspPheAl 569
 1953 -----CAGAGGAGCTTGTGTGAAGTTGAACGATGCAATG 1990
 569 aLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCyvGlnGlyAspAspTy 589
 1991 TGCAAACCTTTCAGATTAAGCAGGCACTGCTGTGCTGATTTGAATGATCACTGTCAAGT 2050
 589 eclYProProAlaTyTyThrTyAsn-----AsnIleThrCyAlaLeSe 603

QY 2051 GAATAGACCATCATGTTGTGTGCGTC 2078
Db 603 rProProgluValValGlyLeuAepLeu 612

RESULT 8

US-08-190-802A-49
Sequence 49, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Alignment Scores:

Pred. No.: 1.14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.25% Conservative: 94
Best Local Similarity: 24.10% Mismatches: 258
Query Match: 4.55% Indels: 152
DB: 1 Gaps: 24

US-09-396-985b-3 (1-3811) x US-08-190-802A-49 (1-605)

QY 219 CCATTCCTCTTCTTAATGCTCCGTTTATCAGGAGGTGCTTCTAATATTACTTAT 278
Db 39 ProAlaCyProAlaAlaCyValCySerTyrAspAspAlaAspGluLeuSerVal 58
QY 279 CAATGATGAGGTGAATTTCTCAAAATCCCGACAACCTCCCTTTCACCAAGAAC 338
Db 59 PheCysSerSerArgLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78
QY 339 CTGACCTGAGCTTATATCCCTGAGGACATTAGGACGATAGCTTTCTTCACTTCCCA 398
Db 79 LeuTyrLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98
QY 399 GAATCAGAGTGTGATTATTCAGGTGTGAATCCAGACAATTGAATGGGGCATAT 458

Db 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGluProGlnAlaLeu 118
QY 459 CAGAGCCTAAGCCACCTCTCTACCTTAATATTGACAGAAACCCATCCAGAGTTTAAACC 518
Db 119 LeuGlyLeuGluAsnLeuCyHisLeuHisLeuGluValArgAsnGlnLeuArgSerLeuAla 138
QY 519 CTGGAGACCTTTCT----- 533
Db 139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
QY 534 -----GACATATCAAGTTTACAGAGCTGGCTGTG 566
Db 159 SerArgLeuGluAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGly 178
QY 567 GAGACAATCTAGCATCTTAGAGACCTTCCCATTTGACATCTCAAACTTGAAGAA 626
Db 179 TyrAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlu 198
QY 627 CTTAATGTGAGCTCACAATCTTAATCCAAATCTTTCAATTAACCTGAGATTTTCTAATCTG 686
Db 199 LeuValLeuAlaGlyAsnArgLeu---AlaTyrLeuGlnProAlaLeuPheSerGlyLeu 217
QY 687 ACCAATCTAGAGCACTTGACCTTTCCAGCAACAGATTCAAGATTAATTGACACAGAC 746
Db 218 AlaGluLeuArgGlyLeuAspLeuSerSerArgAsnAlaLeuArgAlaLeu-----Lys 234
QY 747 TTGGGGGTTCTACATCAATATGCCCTTACATCTCTCTTTAGACCTGTGCCGACCT 806
Db 235 AlaAsnValPheValGlnLeuProArgLeuGln---LysLeuTyrLeuAspArgAsnLeu 253
QY 807 ATGAATCTTATCCACAGGTGATTTAAGAAATTAGG---CTTCATAAGCTGACTTTA 863
Db 254 IleAlaAlaValAlaProGlyAlaPheLeuGlyLeuAlaLeuArgTrpLeuAspLeu 273
QY 864 AGAATATATTTGATGATTTAATGTAATGAAACCTTGATTCAGAGCTGTGGCTGTTA 923
Db 274 SerHisAsn---ArgValAlaGlyLeuLeuGluAspThrPheProGlyLeuLeuGlyLeu 292
QY 924 GAATCCATCGTTTGTGTTCTGGAGAAATTAGAAATGAAGAAACCTTGAAAAATTGAC 963
Db 293 ArgValLeuArgLeu-----Ser 298
QY 984 AATATGCTGTAGAGGCGCTGTGCAATTTGACCATTTGAAGAAATTCGATTAAGCATCTTA 1043
Db 299 HisAsnAlaIleAlaSerLeuArgProArgGlnPheLeuAspLeu----- 313
QY 1044 GACTATACCTCGATGATATTTATTTGACTTAATTTGTCGAATGTTCTTCATTT 1103
Db 314 ---HisPheLeuGluLeuLeu----- 319
QY 1104 TCCCTGTGATGATGTGACTTTTGAAGGGTAAAGACTTTTCTATATTTGATGGAGCA 1163
Db 320 GlnLeuGlyHisAsnArgIleArgGlnLeuAlaGluValSerPheLeu---GlyLeuGly 338
QY 1164 CATTTAGATTTGTTAATCTGTAATTTGACAGTTTCCACATTTGAATCAAAATCTTC 1223
Db 339 GlnLeuGluValLeuThrLeuAspHisAsnGlnLeuGlnValAlaGlyAlaPhe 358
QY 1224 AAAAGCTTACTTTCACTTCC-----AACAAAGGTGGAAATGCTTTTCAGAAATTGAT 1277
Db 359 LeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnCyLeuArg-----Asn 376
QY 1278 CTACCAAGCCTTGAGTTTCTAATCTGACGTAG--AATGGCTTGAGTTTCAAGGTTCG 1334
Db 377 LeuProGluGlnValPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGluGlySer 396
QY 1335 TGT-----TCTGAAGTGAATTTTGGAGCAACCAAGCTTAAGATTAGAT 1379
Db 397 CysLeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPhe 416
QY 1380 CTGAGCTTCAATGTGTATTTACCATGAGTTCAAACTTCTTG---GGCTTAACAACTTA 1436

Db 417 LeuLYAspAsnGlyLeuValGlyIleGluGlnSerLeuTrpGlyLeuAlaGluLeu 436
QY 1437 GAACATCTGATTTCCAGATTCACAAATTGAAACAAATGAGTGGATTTTCAGTATCTCA 1496
Db 437 LeuGluLeuAspLeuThrSerAsnGlnLeu----- 446
QY 1497 TCACAGAAACCTCATTTACCTTGAACATTTCTCACTACACAGAGTGGCTTCAAT 1556
Db 447 -----ThrHisLeuPro-----His 451
QY 1557 GGCATCTTCAGATGGCTTGTCCAGCTTCGAAGCTTGAAATGGCTGGCAATTTCTCCAG 1616
Db 452 ArgLeuPheGlnIleGlyLeuGlyIleGluGlnLeuSerArgAsnArgLeuAla 471
QY 1617 GAAAGCTTCTTCA-----GATATCTTCACAGAGTGAAAGTGAACCTTCCTGAGCTCG 1673
Db 472 Gln-----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspVal 489
QY 1674 TCTCAGTGTCACTGAGAGCAGTGTCTCCACAGACATTTAACTCACTCTCCAGCTTCAG 1733
Db 490 SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArg 509
QY 1734 GTACTAAATAGACCAACAACTCTTTCACTTGATACGTTCTCTTAAGTGTCTG 1793
Db 510 TyrLeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
QY 1794 AACTCCCTCCAGGTTCTTGATTACAGTCACTCAATATGACTTCCAAAAACAGAA 1853
Db 524 ----- 524
QY 1854 CTACAGCATTTTCCAGTACGATCTTCTTAATCTTACAGAAATGACTTGTCTGT 1913
Db 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCys 540
QY 1914 ACTTGTGACACACAGAGTTCTCTGCAATGATGATCAAGAC----- 1952
Db 541 GlyCysPro-----LeuLYAlaLeuArgAspPheAlaLeuGlnAsnProSer 556
QY 1953 -----CAGAGCAGCTCTGTGTGAAGTGAAGATGGAATGGAACACCTTCAGAT 2006
Db 557 AlaValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaTyr 576
QY 2007 AAGCAGGAGCATGCTGTGTGATGATTGAATATCACTCTGAGATGAATAAGACCATAT 2066
Db 577 ThrTyrAsn-----AsnIleThrCysAlaSerProProGluValVal 590
QY 2067 GGTGTGTGGTTC 2078
Db 591 GlyLeuAspLeu 594
RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49
Alignment Scores:
Pred. No.: 1,14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.258 Conservative: 94
Best Local Similarity: 24.10# Mismatches: 258
Query Match: 4.55# Indels: 152
DB: 3 Gaps: 24
US-09-396-985b-3 (1-3811) x US-08-477-346-49 (1-605)
QY 219 CCATTGCTTCTTGCTAAATGCTGCCGCTTTTATCAGCAGAGTGAGTTCCTAATATTACTTAT 278
Db 39 ProAlaCysProAlaIalaCysValCysSerTyrAspAspAlaAspGlnLeuSerVal 58
QY 279 CAATGATGAGAGTGAATTTCTAACAATCCCGACACCTCCCTTCCAAACCAAGAAC 338
Db 59 PheCysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyIleGlnAla 78
QY 339 CTGGACCTGAGCTTTAATCCCTGAGGACATTTAGGACGATATGACTTCTTCAGTTTCCCA 398
Db 79 LeuTrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98
QY 399 GAATGACAGTGTGATTTATTCAGAGTGTGAATCCAGACAAATTGAAGATGGGCGATAT 458
Db 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
QY 459 CAGAGCTTAAGCACCCTCTCTACCTTAATATTTGACAGAGAAACCCATCCAGATTAGCC 518
Db 119 LeuGlyLeuGlnAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAla 138
QY 519 CTGGAGCCTTTTCT----- 533
Db 139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
QY 534 -----GGACTATCAAGTTTACAGAAAGCTGTGCTGTG 566
Db 159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuTrpAspLeuAsnLeuGly 178
QY 567 GAGACAAATCTAGCATCTTAGAGAACTTCCCATTTGAGCATCTCAAACTTTGAAAGAA 626
Db 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGln 198
QY 627 CTTAATGAGCTCACCACTTATCCAACTTTCAAAATTACCGAGATTTTCTATATCG 686
Db 199 LeuValLeuAlaGlyAsnArgLeu--AlaTyrLeuGlnProAlaLeuPheSerGlyLeu 217
QY 687 ACCAATCTAGAGCACTTGACCTTTCAGCAACAAGATTCAAGATTTATTGACAGAC 746

Pred. No.:	1.14e-23	length:	605
Score:	306.0%	Matches:	160
Percent Similarity:	38.25%	Conservative:	94
Best Local Similarity:	24.10%	Mismatches:	256
Query Match:	4.55%	Indels:	152
DB:	3	Gaps:	24


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QY      1497 TCACAGAAACCTCATTTACCTTGACATTTCTCATCTCAGACAGAGTTGCTTCAT 1556
Db      447 -----ThrlsleuPro-----His 451
QY      1557 GGCATCTTCAATGGCTTGTCCAGCTCGAAGCTTGTAATAAGCTGGCAATCTTTCAG 1616
Db      452 ArgLeuPheGlnGlyLeuGlyLeuGlyLeuLeuLeuSerArgSerArgLeuAla 471
QY      1617 GAAAATCTCTTCCA---GATATCTTCAAGAGCTGAGAAATCTTGACCTTCTGACCTC 1673
Db      472 Gln-----LeuProAlaSerAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspVal 489
QY      1674 TCTCAGTGTCAACTGGAGAGGTTGCTCCAAAGCAATTAATCACTCATCTCCAGTCTTCA 1733
Db      490 SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArg 509
QY      1734 GACTAATATATGAGCCAAACAATCTTTTCATTTGATACGTTTCTTATATAGTGTCTG 1793
Db      510 TyrLeuSerLeuArgSerAsn-----SerLeuArgThrPheThrProGln----- 524
QY      1794 AACTCCCTCAGGTCTTGTATTAAGTCTCATCTCATCATATATGACTTCCAAAAACAGAA 1853
Db      524 ----- 524
QY      1854 CTACAGCATTTTCCAGTAGTCTAGCTTCTTAATCTTACTGAGATGACTTGTGCTGT 1913
Db      525 -----ProProGlyLeuGlnArgLeuThrLeuGlnArgProThrAspCys 540
QY      1914 ACTGTGAACACCAAGATTTCTGCAATGATGATCAGAC----- 1952
Db      541 GlyCysPro-----LeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSer 556
QY      1953 -----CAGAGGAGCTCTTGTGTGGAAGTTGAACGATGATGTGCAACCTTCAAT 2006
Db      557 AlaValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProAlaTyr 576
QY      2007 AAGCAGGAGATGCTGTGCTGATTTGATATATCAGCTGAGATGATGATTAAGACATCAT 2066
Db      577 ThrTyrAsn-----AsnIleThrCysAlaSerProGlnValVal 590
QY      2067 GGTGTGTCGGTC 2078
Db      591 GlyLeuAspLeu 594

RESULT 12
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1087
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087
Alignment Scores:

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Pred. No.: 1,14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.25% Conservative: 94
Best Local Similarity: 24.10% Mismatches: 258
Query Match: 4.55% Indels: 152
DB: 4 Gaps: 24

US-09-396-985B-3 (1-3811) x US-09-538-092-1087 (1-605)
QY      219 CCATGCTTCTTCTTAATGCTGCCGTTTATCAGAGAGTGCTTCTTAATTAATTA 278
Db      39 ProAlaCysProAlaAlaCysValCysSerTyrAspAspAlaAspGlnLeuSerVal 58
QY      279 CAATGATGAGCTGATTAATTTACAAATCCCAACCAATCCCTTCTTCAACAAGAAC 338
Db      59 PheCysSerSerArgSerArgSerLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78
QY      339 CTGACCTGAGCTTAAATCCCTGAGGCAATTTAGCAGCTATAGCTTCTTCAAGTTCCCA 398
Db      79 LeuThrLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98
QY      399 GAATGACAGTGTGATTTATCCAGGTGTGAATCCCAATTCAGATTAAGATGGGCAAT 458
Db      99 SerLeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
QY      459 CAGAGCTGAGCAACCTCTCTACCTTAATATTTAGCAGAAACCCATCCAGATTTAGCC 518
Db      119 LeuGlyLeuGlnAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAla 138
QY      519 CTGGAGACCTTTCT----- 533
Db      139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
QY      534 -----GACTATCAAGTTTACAGAAAGTGTGCTGTG 566
Db      159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGly 178
QY      567 GAGCAAAATCTGACATCTCTAGAGAACTTCCCATTTGAGCATCTCAAACTTTGAAAGAA 626
Db      179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuAlaGln 198
QY      627 CTTAATGTGGCTCACAAATCTTATCCAACTTCTTCAATTAACCTGATTTTCTAATCTG 686
Db      199 LeuValLeuAlaGlyAsnArgLeu--AlaTyrLeuGlnProAlaLeuPheSerGlyLeu 217
QY      687 ACCAATCTAGACACTTGACCTTTCCAGCAACAAATTCAAAGTTATTTATGACACAGAC 746
Db      218 AlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaIle-----Lys 234
QY      747 TTGGGGTTCTACATCAATGCCCCCTACTCAATCTCTTTGAGCCTGTCCCTGAACCTT 806
Db      235 AlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTyrLeuAspArgAsnLeu 253
QY      807 ATGAATTTATCCAAACAGGTCAATTAAGAATTAAGG--CTTCATAGCTGACTTTA 863
Db      254 IleAlaAlaValAlaProGlyAlaPheLeuGlyLeuLysAlaLeuArgTrpLeuAspLeu 273
QY      864 AGAAATATTTGATAGTTAAATGTAATGAAAACCTGTATTCAGAGTCTGTGCTGTTTA 923
Db      274 SerHisAsn--ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeu 292
QY      924 GAAGTCATGCTTTGGTTCTGGGAGAAATTTAGAAATGAAGAAACTTGGAAAAGTTTGAC 983
Db      293 ArgValLeuArgLeu-----Ser 298
QY      984 AATGTGCTTAGAGGCTGTGCAATTTGACCAATTTGCAATTTGCAATTAAGCATTA 1043
Db      299 HisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu----- 313
QY      1044 GACTACTACCTGATGATATTAATTGACTTAATTTATTTGACAAATGTTCTTCAATT 1103
Db      314 ---HisPheLeuGlnGlnLeu----- 319

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OY	1104	TCCTCGTAGAGTGACATCTTAAAGGGGAAAAAGCTTTTCTTAATATTTGGATGGGACA	1163
Db	320	GlnLeuGlyHisAsnArg11LeuArg11LeuAlaGlySerPheGlu--GlyLeuGly	338
OY	1164	CATTAGATTTAGTTAACTGTAAATTTGGACAGTTTCCACATTTAACTGAATCTCTC	1223
Db	339	GlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValValAlaGlyAlaPhe	358
OY	1224	AAAAGCTTACTTTCACCTTCC-----AACAAAGGTGGGAATGCTTTTCAGAAAGTTGAT	1277
Db	359	LeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----Asn	376
OY	1278	CTACCAAGCGCTGAGTCTTCTAGATCTGAGTGA---AATGGCTTGAGTTCAAAAGTTGC	1334
Db	377	LeuProGlnGlnValPheArgGlyLeuGlyLeuHisSerLeuHisLeuGlnGlySer	396
OY	1335	TGT-----TCTCAAAAGTATTTTGGACAAACAGCGCTTAAAGATTTAGAT	1379
Db	397	CysLeuGlyArg11LeuArgProHisSerThrPheThrGlyLeuSerGlyLeuArgArgLeuPhe	416
OY	1380	CTGAGCTTCATATGTTGTTATTCATCCATGAGTTCAAACTTCTTG--GGCTTAGAACACTA	1438
Db	417	LeuTyrAspAsnGlyLeuValGlyLeuGlnGlnSerLeuThrGlyLeuAlaGlyLeu	436
OY	1437	GAACATCTGGAATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATTTTCAGTATCTCTA	1486
Db	437	LeuGlnLeuAspLeuThrSerAsnGlnLeu-----	446
OY	1497	TCACTCAGAAACCTCATTTTACTTGACATTTCTCATCTCACACAGAGTTGCTTTCAT	1556
Db	447	-----ThrHisLeuPro-----His	451
OY	1557	GGCATCTTCAATGGCTGTCTCCAGTCTCGAAGCTTTGAAATGGCTGCAATTTCTTCCAG	1616
Db	452	ArgLeuPheGlnGlyLeuGlyLeuGlnGlyLeuLeuLeuSerArgAsnArgLeuAla	471
OY	1617	GAAGAACTTCTTCCA---GATATCTTCCACAGAGCTGAGAAACTTGAACCTTCTCTGACCTC	1673
Db	472	Glu-----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspVal	489
OY	1674	TCTCAGTGTCACTGAGAGAGTGTCTCCAAACAGACTTTAACTCATCTCTCCAGTCTTCAG	1733
Db	480	SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuAlaProLeuGlyArgLeuArg	509
OY	1734	GTACTTAATATGAGCCACACAACTTCTTTCATTTGATGAGTTTCTTATTAAGTGTCTG	1793
Db	510	TyrLeuSerLeuArgAsnAsn-----SerLeuAlaGlyThrPheThrProGln-----	524
OY	1794	AACCTCCCTCCAGGTTCTGATTACAGTCTCAATCATCATATGACTTCCAAAAACAGGAA	1853
Db	524	-----	524
OY	1854	CTACAGCATTTTCCAGATAGTCTACTTCTTAAATCTTACTCAGAAATGACTTGTCTGT	1913
Db	525	-----ProProGlyLeuGlnArgLeuThrLeuGlnGlyAsnProTyrAspCys	540
OY	1914	ACTTGTGAACACAGAGTTTCTCCGTCAATGATGATCAAGAC-----	1952
Db	541	GlyCysPro-----LeuTyrAlaLeuArgAspPheHisAlaLeuGlnAsnProSer	556
OY	1953	-----CAGAGCGAGCTCTTGGTGGAGTTGAACGAATGAGATGTGCAACCTTCAGAT	2006
Db	557	AlaValProArgPheValGlnAlaLeuLeuCysGlnGlyAspArgCysGlnProProAlaTyr	576
OY	2007	AAGCAGGGGCAATGCTGTGCTGATGTTGAATATTCACCTCTCAGATGAAATAAACATCATTT	2066
Db	577	ThrTyrAsn-----AsnIleThrCysAlaSerProProGlnValVal	590
OY	2067	GATGTGTGCGTTC	2078
Db	591	GlyLeuAspLeu	594

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US-08-190-802A-50
/ Sequence 50. Application US/08190802A
/ Patent No. 5519003
/ GENERAL INFORMATION:
/ APPLICANT: Mochly-Rosen, Daria
/ APPLICANT: Ron, Dorit
/ TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
/ TITLE OF INVENTION: Thereof
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/190,802A
/ FILING DATE: 01-FEB-1994
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 8600-0139
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 50:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 603 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHEITICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
/ INDIVIDUAL ISOLATE: pro. complex-fac, Fig. 33
US-08-190-802A-50

Alignment Scores:
Pred. No.:      8,46e-23      Length:      603
Score:          298.00       Matches:     163
Percent Similarity: 37.11%   Conservative: 89
Best Local Similarity: 24.01% Mismatches:    260
Query Match:     4.43%      Indels:      167
DB:              1         Gaps:        26

US-09-336-985B-3 (1-3811) x US-08-190-802A-50 (1-603)
QY      TCAGACTCCGAGCCTCA-----GCCCTTACCCCGATTGCATGTCTTTGGTAATG 238
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      28 ThrAspProclAlaSerIlelaSphlaIguglProglncysprovalAlaCys-Thrcy 47
      CTGCGCGTTTATTCACGAGGTGGTTCTCATATTTACTTATCATGATGAGTGGAATTT 298
QY      |
Db      47 sserHis-----AspAspIyrThrAspGluleuservalPheCysSerSerIylsaAle 65
      299 CTGCAAAATCCCGACAACCTCCCTTTCMAACCAAGAAGACTGAGCTTATATCC 358
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      65 vthrlslsluProAspAepIlePrivalSetThraIgaIaleutrypleuasplYaas 85
      CCTGAGCATTATGAGCAGCTATAGCTTTCTTCAgTTTTCCAGAACCTGACAGGTGATTT 418
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      85 nleusSerSerIleProSerAlalaIahPhcGlnaslneusSererleuasnPhelenuAle 105
      419 ATCCAGGTGTGAATTCACAGACATTGGAAGATGGGCGCATATTCAGAGCTTAAGCACTCTC 478
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 105 uGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeuGlyLeuGlnAsnLeuTrp 125
 QY 479 TACCTTAATATGACAGAAACCCCATCCAGATTAGCCCTGGAGCCCTTTCGTGACT 538
 Db 125 rTyTrLeuH1sLeuGlnArgAsnTrpGlnArgAsnLeuAlaValGlyLeuPheThrH1sTrh 145
 QY 539 ATCAAGTTTACAGAAAGCTGGTGGCTGGAGCAAAATCTAGCATCTCTAGAGAACTTCC 598
 Db 145 rProSerLeuAlaSerLeuSerLeuSerAsnLeuLeuGlyArgLeuGlnGlnGlnGlyLe 165
 QY 599 CATGGACATCTCAAAACTTTGAAGAACTTAATGGCTCTCTCTCTCTCTCTCTCTCTCT 638
 Db 165 uPheGlnGlyLeuSerH1sLeuTrpAsnLeuLeuGlyTrpAsnSerLeuValValLe 185
 QY 639 -----GCAATCTTATTC-----GCAATCTTATTC----- 650
 Db 185 uProAsnTrpValPheGlnGlyLeuGlnValAsnLeuH1sGlnLeuValLeuAlaGlyAsn 205
 QY 651 -CAATCTTCAAAATGACGATTTTCTAATCTGACCAATCTTACAGCACTTGGACCT 709
 Db 205 sLeuThrTrpTrpLeuGlnProAlaLeuPheCysGlyLeuGlnGlyLeuArgGlyLeuAsp 225
 QY 710 TTCAGCAACAAAGATTCAAGATTTATTTGACAGACTTGGGGTTCTACATCAAAATGCC 769
 Db 225 uSerArgAsnAlaLeuArgSerVal-----LysAlaAsnValPheValH1sLeuPr 242
 QY 770 CCTACTCAATCTCTTTTGAACCTGTCCCTGAAACCTATGAACTTTATCCAAAGCTGC 829
 Db 242 oArgLeuGln--LysLeuTrpLeuAsnArgAsnLeuLeuLeuAlaValAlaProGlyAl 261
 QY 830 ATTAAAGAAATTTAGG---CTTCATTAAGCTGATTTAAGAAATATTTGATGATTTTAA 886
 Db 261 aPheLeuGlyMetLeuAlaLeuArgTrpLeuAsnLeuSerH1sAsn--ArgValAlaG 280
 QY 887 TGTATGAAATCTGTATTCAGAGTCTGGCTGTGTTGAAGTCCATCGTTGGTT----- 941
 Db 280 uLeuMetGlnAsnTrpPheProGlyLeuLeuGlnGlyLeuH1sValLeuArgLeuH1sVal 300
 QY 942 -----CTGGAGAAATTTAG 955
 Db 300 nAlaLeuAlaSerLeuArgProArgTrpPheLysAsnLeuH1sPheLeuGlnGlnGlyLeu 320
 QY 956 A--AAATGAAGAACTTGGAAAGATTTGACAAATCTGCTCTAGAGAGCCCTGTGCAATTT 1012
 Db 320 nLeuGlnH1sAsnArgGlyLeuGlnLeuGlnGlyLeuArgTrpPheGlnGlyLeuGlnGly 340
 QY 1013 GACCATTTGAAGAAATTCGATTTAGCATGATTAAGTCACTACCTGATGATTT--ATTGA 1069
 Db 340 uGlnVal-----LeuThrLeuAsnAsnArgGlnH1sLeuGlnValArgValG 356
 QY 1070 CTATTTAATGTTTGAACAATGTTTCTTCAATTTCCCTGGTGAAGTGACTATT----- 1124
 Db 356 yAlaPheSerGlyLeuPheAsnValAlaValMetAsnLeuSerGlyAsnCysValLeuArgSe 376
 QY 1125 -----GAAAGGGTA-----AAAACATTTTCTTATATTTGGATGGCAACATTT 1168
 Db 376 rLeuProGlnArgValPheGlnGlyLeuAsnArgLysLeuH1sSerLeuH1sLeuGlnH1sSe 396
 QY 1169 AGAATTAAGTAACTGTAATTTGACAGATTTCCCACTGAAATCTCAAAATCTTCAAAAG 1228
 Db 396 rCysLeuGlnH1sValArgLeuH1sTrpPhe-----AlaGlyLeuSerGlyLeuArgTr 414
 QY 1229 GCTTACTTTCACTTCCAAAGAGTGGGATGCTTTTTCGAAGTTGAT----- 1277
 Db 414 gLeuPheLeuArgAsp-----AsnSerH1sSerSerH1sLeuGlnGlnGlnGlnGlnGln 430
 QY 1278 -----CTACAAAGCCTTGAGTTTCTAGATCTCAGTAAGAAATGCTGATTTCAAAAG 1330
 Db 430 uAlaGlyLeuSerGlyLeuLeuGlnGlyLeuAsnArgLeuThrH1sAsnArgLeuH1sTrh 448
 QY 1331 TTGCTGTTTCAAAAGTATTTTGGAGCAACAGCTAAATATTTAGATCTGAGCTTCAA 1390
 Db 449 -LeuProArgGlnLeuPheGlnGlyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 468

QY 1391 TGTGTATTACCATGATGTTCAAACTTCTTGGGCTTAGAACAATAGAAATCTGGAATTT 1450
 Db 468 nGlnLeuThrTrpLeuSerH1sGlnValLeuGly----- 479
 QY 1451 CCAGATTTCCAAATTTGAAAACAAATAGTGAATTTTCAATATCTTATCACTCAGAAACCT 1510
 Db 480 -----ProLeuGlnArgAl 484
 QY 1511 CATTTACTTGAACATTTTCTCATCTCACACAGAGTTGCTTCATGGCATTTCAATGG 1570
 Db 484 aPheTrpLeuAsnTrpH1sSerH1sAsnH1sLeuGlnThrLeuAlaGlnGlyLeuPheSerSe 504
 QY 1571 CTGTGTCAGCTCTGAAAGCTTGAATAAGCTGGCAATTTCTTCCAGAAACCTTCTTCC 1630
 Db 504 rLeuGlyArgValArgTrpLeuSerLeuArgAsnAsnSerLeuGln--ThrPheSerTr 523
 QY 1631 AGATATCTTTCACAGAGCTGAGAAACTTGAACCTTCTGACCTCTCTCAGTGTCAACTGA 1690
 Db 523 o-----GlnProGlyLeuGln 528
 QY 1691 GCAATTTGTCCAAACAGCATTTTAAGTCACTCTCAGCTCTTCAAGTACTTAATATGAGCA 1750
 Db 528 uArgLeu----- 530
 QY 1751 CAACAACCTTCTTTCATTTGATACGTTTCTTATTAAGTGTGAACTCCCTCCAGGTTCT 1810
 Db 531 -----TrpLeuAsnPrAlaAsnProTrpAsnProCysSerCysProLeuValAlaLe 546
 QY 1811 T--GATTACAGTCTTCATCACAATAAGACTTCCAAAAACAGAACTACAGCATTTTCC 1867
 Db 546 uArgAsnPheAlaLeuGlnGlnAsn-----ValCysGln-----Pr 554
 QY 1868 AAGTACTGACGTTTCTTAACTTAACTCAGAAATGACTTGGTGTGACTTGTGAACACA 1927
 Db 554 oGlyValValProArgPheValGlnThr-----ValCysGln----- 566
 QY 1928 GAGTTTCTGCAATGATGATCAAGACCAAGAGAGCTCTTGGTGAAGTTGAAGCAATGGA 1987
 Db 567 -----GlyAsnAsnProCysGlnProValTrpThrTrpAsnAsnLeuH 580
 QY 1988 ATGTGCAACCTTTCAGATTAAGCAGGCAATGCTGTGCTGATTTGAATATGACC 2042
 Db 580 rCysAlaGlyProAlaAsnValSerGlyLeuAsnArgValSerGlyuThr 598
 RESULT 14
 US-08-477-346-50
 ; Sequence 50, Application US/08477346
 ; Patent No. 6262023
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/487,072

Db 356 yAlaPheSerGlyLeuPheAsnValAlaValMetAsnLeuSerGlyAsnCysLeuArgSe 376
QY 1125 -----GAAAGGTA-----AAAGCTTTCTTAATAATTCGATGGCAACATTT 1168
Db 376 rLeuProGlnArgValPheGlnGlyLeuAspLysLeuHisSerLeuHisLeuGlnHisSe 396
QY 1169 AGAATTAGTTAACTGTAATTTGGACAGATTTCCACATTTGAACTCAATCTCAAAAG 1228
Db 396 rCysLeuGlyHisValArgLeuHisThrPhe-----AlaGlyLeuSerGlyLeuArgAr 414
QY 1229 GCTTACTTTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAGTTGAT----- 1277
Db 414 gLeuPheLeuArgAsp-----AsnSerHisSerSerHisLeuGlnGlnInsertle 430
QY 1278 -----CTACCAAGCTTTGATTTCTAGATCTCAGTAAAGTGGCTTGAGTTCAAGG 1330
Db 430 uAlaGlyLeuSerGlyLeuLeuGlnLeuAspLeuThrThrAsnArgLeuThrHis----- 448
QY 1331 TTGCTGTTCTCAAAAGTATTTTGGACCAACAGCCTTAAGATTTAGATCTGAGCTTCAA 1390
Db 449 -LeuProArgGlnLeuPheGlnGlyLeuGlnHisLeuGlnHisLeuLeuLeuSerTyrAs 468
QY 1391 TGGTGTATTAACCAAGTCAAGTTCAACTTCTTGAGCTTAGAACAACTAGAACATCTGATTT 1450
Db 468 ngInLeuThrThrLeuSerAlaGluValLeuGly----- 479
QY 1451 CCAGCATTCCAATTTGAAACAAATGAGTGAATTTTCAGTATTCCTATCACTCAGAAACCT 1510
Db 480 -----ProLeuGlnArgAl 484
QY 1511 CATTACCTTGACATTTCTCATACTCAACACAGATTTGCTTCAATGGCATCTTCAATGG 1570
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QY 1571 CTGTCAGCTCTCGAAGCTTTGAAATGGCTGGCAATTTCTTCCAGGAAAACTTCTTCC 1630
Db 504 rLeuGlyArgValArgTyrLeuSerLeuArgAsnAsnSerLeuGln---ThrPheSerPr 523
QY 1631 AGATATCTTCACAGAGCTGAGAAACTTGACCTTCTGACCTCTCTCAGTGTCACTGGA 1690
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QY 1691 GCAGTTGTCTCAACAGACATTTAATCTCATCTCCAGTCTTCAGGTACTAATATAGCCA 1750
Db 528 uArgLeu----- 530
QY 1751 CAACAACTTCTTTTTCATTGGATACGTTTCCTTATAGTGTGAATCCCTCCAGTTTCT 1810
Db 531 -----TripleuAspAlaAsnProTyrAspCysSerCysProLeuHisAlaLe 546
QY 1811 T--GATTACAGTCTCAATCATATATGACTTCCAAAAACAGGAACCTACAGCATTTTCC 1867
Db 546 uArgAspPheAlaLeuGlnAsn-----Pr 554
QY 1868 AAGTAGCTAGCTTTCTTAATCTTACTCAGAAATGACTTGTGTTACTGTGAACACA 1927
Db 554 oGlyValValProArgPheValGlnThr-----ValCysGln----- 566
QY 1928 GAGTTTCTCGAATGATCAAGACAGGACAGGACCTTGTGGAGATTGAACGATGGA 1987
Db 567 -----GlyAspAspCysGlnProValTyrThrTyrAsnAsnHisLeu 580
QY 1988 ATGTGCACAACTTCAGATTAAGACAGGACATGCTGTGCTGATTTGAATATACCC 2042
Db 580 rCysAlaGlyProAlaAsnValSerGlyLeuAspLeuArgAspValSerGlnThr 598

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nzp model

Run on: March 29, 2005, 11:51:33 ; Search time 39.6953 Seconds

(without alignments)
18474.848 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724
Sequence: 1 acagggccactgcgtccac.....tccactgacagagaacta 3811

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+npz model -DEV=xlh
-Q=/cgmt_1/USPTO.spool/US09396985/runat_28032005_155743_21159/app_query.fasta_1.85098
-DB=PIR_79 -QFMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=prc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CCN 1.1_1164 @runat_28032005_155743_21159 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656.5	9.8	661	2	156258
2	474	7.0	786	2	108664
3	454	6.8	1097	2	A29943
4	433	6.4	1389	2	T13852
5	421	6.3	1385	2	T13887
6	404	5.0	1066	2	T15864
7	333.5	6.0	1134	1	A29944
8	325	4.8	605	2	JC5239
9	317.5	4.7	853	2	T17461
10	306	4.6	605	2	A41915
11	299.5	4.5	855	2	T17460
12	299	4.4	603	2	T24315
13	298	4.4	603	2	JC1282
14	298	4.4	662	2	S42799

15	298	4.4	1531	2	T42218	slit-1 protein hom
16	296.5	4.4	994	2	H96510	probable disease r
17	295	4.4	845	2	T07039	Hcr9-0 protein - c
18	293.5	4.4	907	2	JB0176	orphan G protein-c
19	293	4.4	603	2	JC6128	insulin-like growt
20	292	4.3	907	2	JG0193	G protein-coupled
21	291	4.3	855	2	T07015	Cf-4A protein - to
22	290	4.3	1112	2	T10504	disease resistance
23	285	4.2	622	2	JC7973	synleutin - human
24	285	4.2	1134	2	T04587	hypothetical prote
25	282.5	4.2	1019	2	T06519	probable disease r
26	282	4.2	1027	2	B85089	receptor protein k
27	280	4.2	890	2	T00800	disease resistance
28	276.5	4.1	768	2	T17462	MEG5 protein - ra
29	276.5	4.1	1523	2	T13953	probable disease r
30	276	4.1	983	2	G84524	Cf-9 protein membran
31	274.5	4.1	863	2	A55173	glial cell membran
32	274.5	4.1	1091	2	A58532	slit protein 2 pre
33	274.5	4.1	1469	2	B36665	slit protein 1 pre
34	274.5	4.1	1480	2	A36665	hypothetical prote
35	272.5	4.1	766	2	T01817	receptor-like prot
36	272.5	4.1	1109	2	T18536	hypothetical prote
37	271	4.0	1143	2	T10636	probable disease r
38	268	4.0	910	2	G84648	hypothetical prote
39	266.5	4.0	1784	2	C96615	probable protein k
40	263.5	3.9	1064	2	B86465	hypothetical prote
41	262.5	3.9	967	2	T48210	gpi50 protein - fr
42	262.5	3.9	1051	2	T13174	protein kinase hom
43	259	3.9	1029	2	T00712	hypothetical prote
44	259	3.9	1232	2	T05322	hypothetical prote
45	257	3.8	738	2	T19938	hypothetical prote

ALIGNMENTS

RESULT 1
156258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: 156258; PMID:95204928; PMID:7897216
A/Accession: 156258
A/Status: preliminary; translated from GB/EWBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g76171

Alignment Scores:

Pred. No.: 2.63e-41
Score: 656.50
Percent Similarity: 45.31%
Best Local Similarity: 28.72%
Query Match: 9.76%
DB: 2
Gaps: 17

US-09-396-985B-3 (1-3811) x 156258 (1-661)
QY 192 CCGAGCCCTCAGCCCTTACCCGATTCATTGCTTCAATAGTCGCGCTTTATC 251
DB 3 ProAspIleSerCysPheLeuValAlaLeuPheLeuAlaSer--CysAgaAlaThr 21
QY 252 ACG-----GAGTGTGTTCTTAATATTAATTAATCATGATCATGAG 290
DB 22 ThSeSerAspGlnIlyCysIleGluYsgIValAsnIlyThrIenYsgIValen 41
QY 291 CTGAATTTCTACAAATATCCCGACCAACCTCCCTTCAACCAAGAACTGACGACG 350
DB 42 LeuGIyLeuAsnIlyLeuProGIyThrLeuProAsnSerThrIcIyCysLeuGIyPheSer 61

QY 351 TTTAATCCCTGAGGAGATTAGGACGATAGCTTCTTCAGTTTCCAGAACTGACAGT 410
 ||||| ||||| : : : : : |||||
 Db PheAsnValLeuSerProthrIleGlnAsnThrPheSerArgLeuIleAsnLeuThrPhe 81
 QY 411 CTGGATTATTCAGGCTGTAATTCAGACAAATTGAGATGGGCGATTCAGACCTTAGC 470
 ||||| ||||| : : : : : |||||
 Db LeuAspLeuThrArgCysGlnIleTyrTrpIleHisIleGlnAspThrPheGlnSerGlnHis 101
 QY 471 CACCTCTCCTTAATATATGACAGAAACCCGATCCAGAGTTTAGCGCTGGAGGCTTT 530
 ||||| ||||| : : : : : |||||
 Db ArgLeuAspThrLeuValLeuThrAlaAsnProLeuIlePheMetAlaGluThrAlaLeu 121
 QY 531 TCTGAGCTATCAGATTACAGAGCTGCTGCTGAGAGACAAATCTAGCTCTAGAG 590
 ||||| ||||| : : : : : |||||
 Db SerGlyProIleValLeuIleHisIlePhePheIleGlnThrGlyIleSerSerIleLeu 141
 QY 591 AACTCCCATTCGACATCTCAAAACTTTGAAAGAACTTAATGCTGCTCAAACTTTATC 650
 ||||| ||||| : : : : : |||||
 Db PheIleProIleHisIleGlnIleTyrThrLeuGlnSerLeuTyrLeuGlySerAsnHisIle 161
 QY 651 CAATCTTTCAATATCCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTGACCTT 710
 ||||| ||||| : : : : : |||||
 Db SerSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 180
 QY 711 TCCAGCAACAAGATTCAAGATATTATTCAGACACTTCGCGGTTCTACATCAAAATGCC 770
 ||||| ||||| : : : : : |||||
 Db GlnAsnAsnAlaIleHisTyrIleIleSerIleGlnAspMetSerSerIleGlnGln----- 198
 QY 771 CTACTCAATCTCTTTAGACTCTGCTCCCTGACCCCTTAGAATTTTATTCACCAAGCTGCA 830
 ||||| ||||| : : : : : |||||
 Db AlaThrAsnLeuSerLeuLeuAsnGlyAsnAspIleAlaGlyIleGluProGlyAla 218
 QY 831 TTTAAGAATTTAGGCTTCAATAGCTGACTTAAGAAATAATTTAGTACTTTAATTTGA 890
 ||||| ||||| : : : : : |||||
 Db PheAspSerAlaValPheGlnSerLeu-----AsnPheGlyIleThrGlnAsn 234
 QY 891 ATGAAACCTGTATTCAGGCTCTGCTGCTGTTTGAAGTCCATGCTTGTCTGGAGAA 950
 ||||| ||||| : : : : : |||||
 Db LeuLeuValIlePheIleGlyLeuIleIleAsnThrIleGlnSerLeuTrpLeuGlyThr 254
 QY 951 TTTTGAATATGAGAACTTGGAAAGTTTGACAAATCTGCTCTAGAGGCTCTGCTCAT 1010
 ||||| ||||| : : : : : |||||
 Db PheGlnAspMetAspAsp---GlnAspIleSerProAlaValPheGlnGlyLeuCysGln 273
 QY 1011 TTGACCACTTGAAGATTCGATTAGACATCTTAGACATCACTCCATGATATTATTATG 1070
 ||||| ||||| : : : : : |||||
 Db MetSerValGlnSerIleAsnLeu---GlnHisIleTyrPhePheAsnIleSerSerAsn 292
 QY 1071 TTATTTAATGTTTGAACAAATGTTTCTTCATTTCCCTGCTGAGTGTGACTATTGAAG 1130
 ||||| ||||| : : : : : |||||
 Db ThrPheIleCysPheSer----- 298
 QY 1131 GTTAAAGACTTTTCTTATTAATTCGATGCGCAATTGAAATTTAGTTAACTGTAATTT 1190
 ||||| ||||| : : : : : |||||
 Db GlyLeuGlnIleLeuAspLeuThrAlaThrHisLeu 310
 QY 1191 GGAAGATTTCGACA-----TTGAAACCTCAATCTGCAAGGCTTACTTTCACATCC 1244
 ||||| ||||| : : : : : |||||
 Db SerGlnLeuProSerGlyLeuValGlyLeuSerThrLeuIleValLeuSerAla 330
 QY 1245 AACAAAGTGGGAAT-----GCTTTTTCAGAAATTGATCTACCAAGCTTGAAGTTT--- 1295
 ||||| ||||| : : : : : |||||
 Db AsnIlePheGlnAsnLeuCysGlnIleSerIleSerAsnThrProSerLeuThrHisLeu 350
 QY 1295 ----- 1295
 Db SerIleIleGlyAsnThrIleArgLeuGlyLeuGlyThrGlyCysLeuGlnAsnLeuGlu 370
 QY 1296 -----CTAAGTCTCAGTAAAGATGCGCTGAGTTTCAAGGTTCTGCTTCGAA 1343
 ||||| ||||| : : : : : |||||
 Db AsnLeuArgGlnLeuLeuSerLeuHisAspAspIleGlnThrSerAspCysAsnLeu 390
 QY 1344 AGTGAATTTGGCAACACGCTAAAGATATTAGATCTGAGTTCAATGCTGTTATATAC 1403

Db 391 GlnLeuArgAsnLeuSerHisIleGlnIleSerLeuAsnLeuSerTyrAsnGluProLeuSer 410
 : : : : : ||||| : : : : : |||||
 QY 1404 ATGAGTTCAAC-----TTCTTGGGCTTAGAAACAATGAAACATCTGATTTCCAGACTTCC 1460
 : : : : : ||||| : : : : : |||||
 Db LeuIleThrGlnAlaPheLeuGlyCysProGlnIleGlnLeuLeuAspLeuAlaPheThr 430
 QY 1461 AATTGAAACAATGAGTAGTAGTTTTCAGTATCTCTATCACTGACAGAAACCTCAATTTACTT 1520
 ||||| ||||| : : : : : |||||
 Db ArgLeuIleValIleAspAlaGlnSerProPheGlnAsnLeuHisIleLeuIleValLeu 450
 QY 1521 GACATTTCTCATCTACACACAGAGTCTTCAATGACATCTTCAATGAGCTTTCAGT 1580
 ||||| ||||| : : : : : |||||
 Db AsnLeuSerHisIleSerLeuLeuAspIleSerSerGlnIleLeuPheAspIleLeuProAla 470
 QY 1581 CTGCAAGCTTGAATAATGCTGCGCAATTTCTTCCAGAAACTCTT-----CCAGAT 1634
 ||||| ||||| : : : : : |||||
 Db LeuGlnHisIleLeuAsnLeuGlnIleGlnHisIlePheProIleGlyAsnIleGlnIleThrAsn 490
 QY 1635 ATCTTCACAGAGCTGAGAACTTGACCTTCTGAGACCTCTCAGTGTCACTGAGAGAG 1694
 ||||| ||||| : : : : : |||||
 Db SerLeuGlnThrLeuGlyArgLeuGluIleLeuValLeuSerPheCysAspLeuSerSer 510
 QY 1695 TTGCTTCCAAACAGATTTAATCACTCTCAGCTCTTCAAGTACTAATATGACCCCAAC 1754
 ||||| ||||| : : : : : |||||
 Db IleAspGlnHisAlaPheThrSerLeuIleIleIleIleIleIleIleIleIleIleIleIle 530
 QY 1755 AACTTTTCTTCAATGGATACGTTCTCTTAAAGTGTCTGAACCTCCCTCCAG-----GTT 1808
 ||||| ||||| : : : : : |||||
 Db Arg-----LeuHisSerSerSerIleGlnAlaLeuSerHisIleLeuIleGlyIleTyr 547
 QY 1809 CTGATTAACAGTCTCAATCACTAATGACTTCCAAAAAACAGAACTACAGACTTTTCA 1868
 ||||| ||||| : : : : : |||||
 Db LeuAsnLeuAlaSerAsnHisIleSerIleIle-----LeuPro 560
 QY 1869 AGTAGTCTAGCTTTCTTA-----AATCTTACTCAGAAATGACTTTGCT 1910
 ||||| ||||| : : : : : |||||
 Db SerLeuLeuProIleLeuSerGlnGlnArgThrIleAsnLeuArgGlnAsnProLeuAsp 580
 QY 1911 TGTACTTGGAAACACAGAGTTTCTGCAATGATGATCAAGACAGACAGAGCTTTGGTG 1970
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 Db CysThrCysSerAsnIleTyrPheLeuIleTyrTyrGlyAsnMetGlnIleIleGln 600
 QY 1971 GAAGTTGAACGAAATGGAATGTGCAACACTTCCAGATTAACAGAGGACGCTGTGCTGAGT 2030
 ||||| ||||| : : : : : |||||
 Db AspThrGlnAspThrLeuIleCysGlnAsnProProLeuLeuArgGlyValArgLeuSerAsp 620
 QY 2031 TTGAATATGACCTGTCCAGATGAATAGACCATCATTTGATGTGCTGCTCAGTGTCTT 2090
 ||||| ||||| : : : : : |||||
 Db ValThrLeuSerCysSerMetAlaAlaValGlyIlePhePheLeuIleValPheLeuLeu 640
 QY 2091 GTTAGTATCTGTGTAGCACTTCTGCTCTAAGTCTAT 2129
 ||||| ||||| : : : : : |||||
 Db ValPheAlaIleLeuLeuIlePheAlaValIleTyrPhe 653

RESULT 2
 208664
 Toll protein-like receptor DKFZp547I0610.1 - human
 C/Species: Homo sapiens (man)
 C/Date: 11-Jun-1999 #sequence__revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T08664
 R/Pousterka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A/Reference number: Z16466
 A/Accession: T08664
 A/Molecule type: mRNA
 A/Residues: 1-786 <POU>
 A/Cross-references: UNIPROT:O15399; EMBL:AL050262
 A/Experimental source: fetal brain; clone DKFZp547I0610
 A/Note: DKFZp547I0610.1
 Alignment Scores:

Pred. No.:	1.56e-27	Length:	786
Score:	474.00	Matches:	204
Percent Similarity:	41.80%	Conservative:	130
Best Local Similarity:	25.53%	Mismatches:	303
Query Match:	7.05%	Indels:	162
DB:	2	Gaps:	32

US-09-396-985B-3 (1-3811) X T08664 (1-786)

QY	531	TCGGACATATGAAGTTTACAGAAAGCTGGCTGGTGAGACAAATCTGCATCTGAC	590
Db	34	AsnGlyLeuIleHisValProIyAspLeuSerGlnIyThrIleLeuAsnIleSer	53
QY	591	AAC TTC C C C A T T G G A C A T C T C A A A C T	626
Db	54	GlnAsnTyrlIleSerGlnLeuThrPhrSerAspIleLeuSerLeuSerIyLeuArgIle	73
QY	627	CTTAATGGGCTCACATCTTATCCAAATCTTCAATTAACCTGAGTATTTTCTATCTG	686
Db	74	LeuIleIleSerHisAsnArgIleGlnTyrlLeuAspIleSerValPheIyAspAsn---	92
QY	687	ACCAATCTAGACCTTGGACCTTTCCAGACAAAGATTAAGATTTATTTGGACAGAC	746
Db	93	GlnGlnLeuGlnTyrlLeuAspLeuSerHisAsnIySbLeuValIyIleSerCys----	110
QY	747	TTGGCGGGTTCTACATCCAAATGCCCTTCAATCTCTCT--TTAGACTGGTCCCTGAC	803
Db	111	-----HisProthrIleAsnLeuIyHisIleAspLeuSerPheAsn	124
QY	804	CCATAAGACTTTATC-----CAACCGAGTGCATTTAAAGAAATTAGCGTTCAAT	851
Db	125	AlaPheAspAlaLeuProIleCysIySbGlnPheGlnAsnMetSerGlnLeuIyPheLeu	144
QY	852	AAGCTGACTTAAAGAAATAATTGATAGTTTAATGAATGAAGAAACCTTGATCAAGCT	911
Db	145	GlyLeuSer-----ThrThrHisLeuGlnIySbSerValIleuPro	158
QY	912	CTGGCTGGTTAGAACTGCATCGTTGGTCTG-----GAGAAATTT	953
Db	159	IleAlaHisIleuAsnIleSerIyValLeuLeuValIleuGlnTyrlTyrlGlnIyIyS	178
QY	954	AGAAATGAGAAACTTGGAAAGTTTGACAAATGCTCTTGAAGAGGCTTGCAATTTG	1013
Db	179	GlnAspProGlnTyrlLeuGlnAspPheAsnThrGlnSerLeuHisIleValPheProthr	198
QY	1014	ACCAATGAGAAATTCGACTTAGACACTTAACTACTACTGCTGCATGATTAATTGACTTA	1073
Db	199	AsnIySbGln-----	201
QY	1074	TTTATATGTTGACAAATGTTTCTTCAATTTCCCTGAGAGTGAGTACATTGAAGGCTA	1133
Db	202	PheHisPheIleLeuAspValSerValIyThrValAlaAsnLeuGlnLeuSerAsnIle	221
QY	1134	AAAGACTTTTCTTAATTTTGGATGGACAACTTGAATTAAGTTAACTGTAATTTGGA	1193
Db	222	LysCysValIleuGlnAspSerIyCysSerTyrlPheLeuSerIleLeuAlaIyLeuGln	241
QY	1194	CAGTTTCCCACTTGAAGAACTGAAATCTCTCAAAAGCTTACTTTCACTTCCAACAA--	1256
Db	242	ThrAsnProIySbLeuSerSerLeuThrLeuAsnAsnIleGlnTyrlThrIyPAspSerPhe	261
QY	1251	-----GGTGGGAATGCTTTTTCGAAAGTT	1274
Db	262	IleArgIleLeuGlnLeuValIyThrHisThrIyValTyrlPyrSerSerIleSerAsnVal	281
QY	1275	GATTTACCA--AGCCTTGAGTTTCTAGATCTCAGTAGAAATGCGCTTGATTTCAAGGT	1331
Db	282	LysLeuGlnGlnIyGlnLeuAspPheArgAspPheAspTyrlSerGlnTyrlSerLeuIyAla	301
QY	1332	TGCGTTCTCAA-----AGGAT-----	1349
Db	302	LeuSerIleHisGlnValValSerAsnAspAlaPheGlnPheProGlnSerTyrlIeTyrlGln	321

OY	1350	---	TTTGGGACAACAGCCTTAAG-----	1370
			
Db	322	IlPheSerAsnMetValIeLysAspPheThrValSerGlyThrArgMetValHisMet	341	
OY	1371	-----	TATTAGATCTGAGCTTCATGGTGTTATT-----	1400
Db	342	LeuGlyAspProSerGlyIleSerProPheLeuHisIleuAspPheSerAsnAsnLeuLeuThr	361	
OY	1401	---ACATGAGTCAAACTTCTTGAGCTTTAGAACAACTAAGAACATCGAGATTTCACAGCAT	1457	
Db	362	AspThrValPheGluAsnGlyGlyHisIleuThrGluLeuGluThrLeuIleLeuGluHisMet	381	
OY	1458	TTCCAAATTGGAACAAATGAGAGGAGTTTCA---CTATTCTCATACCTCAGAAACCTCATTT	1514	
Db	382	AsnGluLeuGlyGluLeuSerLysIleAlaGluMetThrThrGluMetLysSerLeuGlu	401	
OY	1515	TACCTTGACATTTCTCATCTACACACAGAGTTGCTTTCAT-----GGCATCTTC	1565	
Db	402	GluLeuAspIleSer-----GlnAsnSerValSerGlyTrpAspGlyValGlyGlyAspGly	419	
OY	1566	AATGAGCTTGTCACAGCTTCGAACTTTGAAAAATGGCTGGCAATTTCTTCACAGAAACTTC	1625	
Db	420	SerThrThrLysSerLeuLeuSerLeuAsnMetSerSerAsnIleLeuThrAspThrIle	439	
OY	1626	-----CTCCAGATATCTTCACAGAGCTGAAGAAACTTGACCTTCCTGACACTCTCT	1676	
Db	440	PheArgCysLeuProPro-----ArgIleLysValIleAspLeuHis	453	
OY	1677	CAGTGTCACTCGAGAGAGTGTGTCACAAAGCATTTAACTCAGCTCCAGCTTCAGAGTA	1736	
Db	454	SerAsnLysIleLysSerIle--ProLysGlnValIalLysLysLeuGluAlaLeuGluGlu	472	
OY	1737	CTAAATATGAGCCCAACAACTTCTTTTCATGTGATACGTTTCT-----TAT	1784	
Db	473	LeuAsnValAlaPheAsn-----SerLeuThrAspLeuProGlyCysGlySerPhe	489	
OY	1785	AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTATACAGTCTCATCTCAATCAATTAAGTACTCCAA	1844	
Db	490	SerSerLeuSerValIleuIleIleAspHisAsnSerValSerHisProSerAlaAspPhe	509	
OY	1845	AAACAGGAACCTACAGCATTTTCCAAAGATGCTAGCTTTCTTAAATCTTACTCAGAAATGAC	1904	
Db	510	PheGlnSerCysGlnLysMetArgSer-----IleLysAlaGlyAspAsnPro	525	
OY	1905	TTTGCCTTGTACTTGTGTAACACACAGAGTTTCTTCGATAGATGATACAGACACAGAGCAGCTC	1964	
Db	526	PheGlnCysThrCysGluLeuGluGlyIlePhe-----ValLysAsnIleAspGlnVal	542	
OY	1965	TTTGTGTGAAGTT-----GAACGAATGGAATGTGCACACCTTCAGATTAAG	2009	
Db	543	SerSerGluValLeuGluGlyLysProAspSerGlyCysAspGlyLysProGluSerGly	562	
OY	2010	CAGGGC-----ATGCTGTGCTGAGTTTGAATATACCTGTGAC	2048	
Db	563	ArgGlyIleThrLeuLeuLysAspPheHisIleMetSerGluLeuSerCysAsnIleThrLeuLeu	582	
OY	2049	ATGATATTAAGACCATTTGGTGTGCTGCTGCTCAGTGTGCTTGGATGATCTGTTGTAGCA	2108	
Db	583	IleValThrIleValAlaThrMetLeuValIleuAlaValThrValThrSerLeuCysIle	602	
OY	2109	GTTTGTGTCTAATAGTTCTAATTTTTCACCTGATGCTTCTTGCTGGCTGCATTAAGATATGAT	2168	
Db	603	TyrLeuAspLeuProThrPyrLysLeuArg--MetValCysGlnTrpThrGlnThrArgArg	621	
OY	2169	AGAGGTAAAAATCTC-----TATGATGCTTTGTT	2198	
Db	622	ArgAlaArgAsnIleProLeuGluGluLeuGlnArgAsnLeuGlnPheHisAlaPheIle	641	
OY	2199	ATCTACTCAAGCCAGATGAGAGTGGGTGAAGAAATAGCTAGTAAAGAAATTTAGAA--	2255	
Db	642	SerTyrSerIleGlyHisAspSerPheIleThrValLysAsnIleuLeuProAsnLeuGluLys	661	
OY	2256	GAAGGGGTGCTTCATTTACGCTTCGCTTCACTACAGACATTTATTTCCGGGTGTGGCC	2315	

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Db      662  GlnGlyMet-----GlnIleCysLeuHISgluAAsnBheValProGlyLysSer 678
QY      2316  ATTTGCGCCCAATCATTCATGAAGTTTCCATTAAGCCGAAGGATGTTGTTGGG 2375
Db      679  ILevalGluSnhIlelle---ThrCysIleGluLysSerTrpLysSerIlePheVal 697
QY      2376  TCCCAACACTTCATCCAGAGCCCGTGTATCTTGAATATGATGATGCTGACACTG 2435
Db      698  SerProAsnBheValGlnSerGlnuTrpCysHISetydIleuLyrPheAlaHISnAsn 717
QY      2436  CAGTTTTCAGACAGCTGCTGTGATTCATCTTATGTTCTGTCGAGAAGTG---GAGA 2492
Db      718  LeuPheHISgluLysSerAsnSerLeuIleLeuIleLeuGlnProIleProGlnLyr 737
QY      2493  ACCCTGCTACGAGACAGCTGAGCTGTATCCGCTTCTGACGAGAACCTTACCTGAG 2552
Db      738  SerIleProSerSerTrpHISLysLysSerLeuMetAlaArgHISThrLyrLeuGln 757
QY      2553  TGGAGAGACAGTGTCTGTGGGCGCACATCTTCTGAGACGACTCGAAGAACCTTG 2609
Db      758  TrpProLysgluLysSerLysArgLysLeuPheTrpAlaAsnLeuArgAlaIle 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A29943
C/Hashmoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A/Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, is
A/Reference number: A29943; PMID:88135760; PMID:2449285
A/Accession: A29943
A/Molecule type: DNA
A/Residues: 1-1097 <HAS>
A/Cross-references: UNIPROT:P08953; GB:M1969; GB:J02682; NID:G158640; P1DN:AAA28941.1;
C/Genetics:
A/Gene: FLYBase:Fl
A/Cross-references: FLYBase:FBgn0003717
C/Keywords: Transmembrane protein
F/1-17/Domain: signal sequence #status predicted <SIG>
F/18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 5 37e-26 Length: 1097
Score: 454.00 Matches: 219
Percent Similarity: 38.97% Conservative: 129
Best Local Similarity: 24.52% Mismatches: 291
Query Match: 6.75% Indels: 254
DB: 2 Gaps: 43

US-09-396-985b-3 (1-3811) x A29943 (1-1097)
QY      267  AATATTACTTATCATGATGAGCTGATTTCTACAAA---ATCCCGCAACCTTCCC 323
Db      270  AsnValThrAspIleAsnLeuSerAlaAsnLeuPheArgSerLeuProGlnGlyLeuPhe 289
QY      324  TTCTCAACCAAGACTGAC-----CTGAGCTTTAAT-----CCCTGAGGCAT 368
Db      290  AspHISAsnLysHISLeuAsnGlnValArgLeuMetAsnAsnArgValProLeuAlaThr 309
QY      369  TTGAGGAGCTATAGCTTCTTCCAGATTCGAGACGTGAGCTGAGCTTATTCAGGTG 428
Db      310  LeuProSerArgLeuPheAlaAsnGlnProGlnLeuGlnIleLeuArgLeu---ArgAla 328
QY      429  GAATCCAGACATTTGAAGATGGGCGCATATCAGAGCTTAAGCCACTTCTACCTTAATA 488
Db      329  GluLeuGlnSerLeuProGlyAspLeuPheGlnHISerThrGlnIleThrAsnIleSer 348
QY      489  TTGACAGAAACCCCATCCAGAGTTTACCCCTGGAGACCTTTTCTGACATCAAGTTTA 548
Db      349  LeuGlyAspAsnLeuLeuLysThrLeuProAlaThrLeuGlnHISGlnValAsnLeu 368

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QY      549  CAGAACTGCTGCTGTGAGACAATATGACATCTTAGAAGACTTCCCATTTGACAT 608
Db      369  LeuSerLeuAspLeuSerAsnAsnArgLeuThrHISLeuProAspSerLeuHeAlaHIS 388
QY      609  CTCAAAACCTTGAAGAACTTAATGTGGCTCAAACTTTATTCAACTTTTCAAAATTA 668
Db      389  ThrThrAsnLeuThrAspLeuArgLeuAspAsnLeuLeuThrGlyLysSer---Gly 407
QY      669  GAGTATTTTTCATTCGACCAATCTAGACACTTGACCTTTCAGACCAAGAAATTTCA 728
Db      408  AspIlePheSerAsnLeuLysAsnLeuValThrLeuValMetSerArgAsnArgLeuArg 427
QY      729  AGATT-----TATTCACAGACTTGGCGGTTCTACAT----- 761
Db      428  ThrIleAspSerArgAlaPheValSerThrAsnGlyLeuArgHISLeuHISLeuAspHIS 447
QY      762  -----CAAAATGCCCTTACAAATCTCTTTTACACCTGCTCCGTAAC--- 803
Db      448  AsnAspIleAspLeuGlnInProLeuAspIleMetLeuGlnThrGlnIleAsnSer 467
QY      804  CCTATGAACTTATTCACACAGTGCACTTAAGAATTAAGCTTCATAGCTGACTTTA 863
Db      468  ProPheGlyLyrMetHIS-----GlyLeuLeuThrLeuAsnLeu 480
QY      864  AAGAAATATTTGATGATGTTAATGTAAGAAACTTGATTCAGAGCTGCTGGTTTA 923
Db      481  ArgAsnAsn-----SerIlelle----- 486
QY      924  GAATTCATCGTTTGTTGTTCTGAGAAATTTGACAAATGAAGAAACTTGAGAAATTTG 983
Db      487  -----PheValLyrAsnAspTrpLysAsn----- 494
QY      984  AATTCGCTTAGAGGCGCTGTGCAATTTGACACTTGAAGAAATTCGATAGACTTTA 1043
Db      495  -----ThreLeuGlnLeuArgGlnLeuAspLeuSerLyr--- 506
QY      1044  GACTACTACCTGATGATGATTAATGACTTATTAATTTGACAAATGTTTCTTCATTT 1103
Db      507  -----  AsnAsnIleSerSerLeu 512
QY      1104  TCCCTG-----GTGAGCTGACATTTGAA 1127
Db      513  GlyLyrGluAspLeuAlaPheLeuSerGlnAsnArgLeuHISValAlaAsnMetThrHISAsn 532
QY      1128  AGGTTAAAGACTTTTCT-----TATATTTCCGA 1157
Db      533  LysIleArgArgIleAlaLeuProGluAspValHISLeuGlyGlnGlyLyrAsnAsnAsn 552
QY      1158  TGGCAACATTTGAATTA-----GTTAACTGTAAATTTTGACAGTTT 1199
Db      553  LeuValHISValAspLeuAsnAspAsnProLeuValCysAspCysThrIleLeuTrpPhe 572
QY      1200  CCCCACTTG-----AAACTCAAACT 1220
Db      573  ILeuGlnLeuValArgGlyValHISLysProGlnLyrSerArgLysPheLysLeuArgThr 592
QY      1221  CTCAAAAGCTTACTTCACTTCCAAC---AAAGTGGGAAGCTTTTTCAGAACTGAT 1277
Db      593  AspArgLeuValCysSerGlnProAsnValLeuGlnGlyLyrThrProValArgGlnIleGln 612
QY      1278  -----CTACCAAGCTTGAGTTCTAGACTTCAGTGAAGAAATGGCTTGAGTTTC 1325
Db      613  ProGlnThrLeuIleLysProLeuAspPheSerAspAspProArgLysLysCysPro 632
QY      1326  AAGGTTGC---TGTTCTCAAGATGATTTTGGACACACAGCTTAAGTATTTAGATCTG 1382
Db      633  ArgGlyCysAsnCysHISValArgThrLyrAsp-----LysAlaLeuValIle 648
QY      1383  AGCTTCAATGCGTTTATTCATGACTTCAAACTTTGGGCTTGAACAACATGAAACAT 1442
Db      649  AsnCysHIS-----SerGlyAsnLeuThrHISValProArgLeuProAsn 663

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QY 1443 CTGATTTCCAGCATTCCTCAATTTGAAACAAATGAGTGGATTTTCAGTATTCCTATTCATC
DB 664 Leu-----HisLysAsnMetGlnLeuMetGlu-----LeuHisLeu 675
QY 1503 AGAAACCTCATTTTACATTTCTGACATTTCTACACCCAGAGTTCCTTCAATGGACATC
DB 676 GluAsnAsnThrLeuLeuArgLeuProSerAlaAsnThr----- 688
QY 1563 TTCATGGCTTGTTCCTGCAAGTCTGCAAAATGGCTGGCAATTCCTTCCAGGAAAC
DB 689 ---ProGlyTyrGluSerValThrSerLeuHisLeuAlaGlyAsn----- 702
QY 1623 TTCCTTCCAGATATCTTCCAGAGCTGAGAAATCTTGACCTTCCAGACTCTCCAGTGT
DB 703 -----AsnLeuThrSerIleAspValAspGlnLeu 712
QY 1683 CAATGGAGCATGTTGTCTCCAAACGATTTAACTACTCTCCAGCTTCCAGTACTTAAAT
DB 713 -----ProThr-----Asn 715
QY 1743 ATGAGCCCAACAACCTTCTTTTCACTGGATACGTTTCTTATAAGTGTGAACTCCCTC
DB 716 LeuThrHis----- 718
QY 1803 CAGGTTCTGTATTACAGTCTCAATCATATATGACTTCCAAAAACAGAACTACAGCAT
DB 719 -----LeuAspIleSerThrAsnHisLeu-----GlnMetLeuAsn--- 730
QY 1863 TTTCCAAGTACGTACGTTTCTTAAAT-
DB 731 ---AlaThrValLeuGlyPheLeuAsnArgThrMetLysThrArgSerValLysLeuSer 749
QY 1896 CAGATGACTTTGCTGTACTGTGACACACAGAGTTCTCTGCAATGATCAAGACAGCAG
DB 750 GlyAsnProThrMetCysAspCysThrAlaLysProLeuLeuLeuPheThrGlnAspAsn 759
QY 1956 AGGACAGCTTGTGTGAGTGAAGTGAACGAAATGTCACACCTTCAGATTAAGCAGGCG
DB 770 PheGlnArgIleGlyAspArgAsnGlnMetCysValAsnAlaGlnMetProThrArg 789
QY 2016 ATGCTCTGCTGAGTTGAAATATCATCCTGTCAATGAAATAGAACCATC--ATTGGTGTG
DB 790 MetValGlnLeuSerThrAsnAspIleCysProAlaGlnLysGlyValPheIleAlaLeu 809
QY 2073 TCGGTC-----CTCAGTGTGCTGTAGTATCTGTGTAGAGTTCGTGCTTAAG
DB 810 AlaValValIleAlaLeuThrGlnGlyLeuLeuAlaGlyPheThrAlaAlaLeuTyrLys 829
QY 2124 TTC-----TATTTTCACCTGATGCTTCTTGTGCTGCTGCATG
DB 830 PheGlnThrGlnIleLysIleTyrPheLysAlaHisAsnLeuLeu----- 845
QY 2160 AAGTAGTAGAGGTGAAACATC-----TATGATGCTTTGTATATC
DB 846 TrpPheValThrGlnGlnAspLeuAspLysAspLysPheAspAlaPheIleSerTyr 865
QY 2205 TCAAGCAGATGAGAGCTGGTGAAGAAATGAGTATGAAATTTAAGAAAGAGGCTG
DB 866 SerHisLysAspGlnSerPheIleGlnAspLysLeuValProGlnLeuGlnHisGlyPro 885
QY 2265 CTTCAATTTGAGTCTGCTTCACTACAGAGACTTTATTCCTCCGCTGCGCATTTGCTGC
DB 886 GlnLysPheGlnLeuCysValHisGlnLysArgSerThrLeuValGlnGlyHisIleProGln 905
QY 2325 AACATCATCATGAAAGTTTCAATAAAAGCGAAAGGTGATGTTGTGTGTCCTCCAGAC
DB 906 AsnIleMet---ArgSerValAlaAspSerArgArgThrIleIleValLeuSerGlnAsn 924
QY 2385 TTGATCCAGAGCCGCTGTATCTTGTGATATGAGATTTGCTCAGACTGGCAGTTTCTG
DB 925 PheIleLysSerGlnTyrAlaArgLeuGlnPheArgAlaAlaHisArgSerAlaLeuAsn 944
QY 2445 AGCAGTGTGCTGTATCATCTTCAATGTC-----CTGCAGAAAGTGAGAAAGAC

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DB 945 GlnGlyArgSerArgIleIleValIleIleTyrSerAspIleGlyAspValGlnLys--- 963
QY 2496 CTGCTCAGCAGAGAGGTGAGCTGTACCGCTTCTCAGCAGGAAACCTTACCTGGAGTGG
DB 964 ---LeuAspGlnGlnLeuLysValAlaTyr-----LeuLysMetAsnThrTyrLeuLysTrp 980
QY 2556 GAGACAGTGTCTCTGGGCGGCACATCTTCTGAGACGACTCAGAAAGCCCTGTGGAT
DB 981 GlyAspPro-----TrpPheThrAspLysLeuArgPheAlaLeuProHis 995
QY 2616 GGTAAATCATGAAATCCAGAGGACAGTGGTACAGA
DB 996 ArgArg-----ProValGlnAsnIleGlyAsnGly 1005

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_rev1sion 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13852
R/Eidom, E.: Kooyer, S.; D'everlym, D.; Duman, M.; Lawinger, P.; Bocas, J.; Belien, H.
Development 120, 885-899, 1994
A/Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simi
A/Reference number: Z17796; PMID:95324375; PMID:760965
A/Accession: T13852
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-1389 <ELD>
A/Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:9415682; PID:G1019104; PID:AAA792
A/Genetic:
A/Genes: wheeler
A/Cross-references: FlyBase:FBgn0004364

Alignment Scores:
Pred. No.: 2,16e-24 Length: 1389
Score: 433.00 Matches: 217
Percent Similarity: 39.93% Conservative: 138
Best Local Similarity: 24.41% Mismatches: 356
Query Match: 6.44% Indels: 178
DB: 2 Gaps: 34

US-09-396-985b-3 (1-3811) x T13852 (1-1389)
QY 339 CTGAGACTGAGCTTATATCCCTGAGGACATTTAGCAGCATTTGAGTGGATTTCCCA
DB 338 LeuAsnLeuSerAsnAsnAlaLeuThrArgIleGlySerThrPheLysGlnLeuTyr 357
QY 339 GAAGTCAAGTGTGATTTATCCAGGTGGAATCCAGACATTTGAAGATGGAGCATAT
DB 358 PheLeuGlnIleLeuAspMetArgAsnAsnSerIleGlyHisIleGlnGlnGlyAlaPhe 377
QY 459 CAGAGCTTAAGCCACTCTTCACTTATATTTGACAGAAACCCCATCCAGAGTTAGCC
DB 378 LeuProLeuTyrAsnLeuHisThrLeuAsnLeuAlaGlnAsnArgLeuHisThrLeuAsp 397
QY 519 CTGGAGACTTTTCTGACTATATCAAGTTTACAGAACTGTGCTGTGAGACAAATCTA
DB 398 AsnArgIlePheAsnIleLeuTyrValLeuThrLysLeu---ThrLysAsnAsnLeu 416
QY 579 GCATCTCTA---GAGAACTTCCCATTTGAGACATCTCAAACTTGAAGAACTTAATGTG
DB 417 ValSerIleValGlnSerGlnAlaPheArgAsnCysSerAspLeuLysGlnLeuAspLeu 436
QY 636 GCTCACAATCTTAATCCAACTTTCAATTAACCTGACTATTTTCTAATGTGACCAATCTA
DB 437 SerSerAsn-----GlnLeuThrGlnValProGlnAlaValGlnAspLeuSerMetLeu 454
QY 696 GAGCACTTGGACCTTTTCCAGCAACAAGATTTCAAGATTTATTTGACACAGACTGGCGGT
DB 455 LysThrLeuAspLeuGlnLysGlnIleSerGlnPheLysAsnAsnThrPheArgAsn 474
QY 756 CTACATCAATGACCCCTACTCAATCTC-----CTGCAGAAAGTGAGAAAGAC

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Db	475	Leu	ang	in	Leu	thr	Gly	Leu	arg	Leu	1	ea	s	a	n	h	arg	1	le	Gly	as	n	1	le	th	r	Val	Gly	494							
		::: :::																																		
Oy	783	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	815								
		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::										
Db	495	Met	phe	g	in	a	le	Pro	leu	Pro	h	arg	Leu	ser	Val	Leu	a	n	Leu	Ala	Val	s	a	n	h	arg	1	le	Gln	ser	514					
Oy	816	ATC	CA	CA	CA	CG	GT	CA	TT	---AA	GAA	AT	T	AG	CT	TC	TA	AG	CT	TA	AG	CT	TA	TA	AG	CT	TA	TA	AG	CT	872					
		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::								
Db	515	I	le	g	in	arg	Gly	Ala	a	phe	a	sp	Leu	s	er	Thr	Glu	1	le	G	lu	Ala	1	le	arg	Leu	a	sp	Leu	Pro	534					
Oy	873	TTG	TA	TA	CT	TA	AA	T	GT	A	TA	GA	AA	CT	GT	TA	TC	AA	GG	CT	GC	GG	CT	TA	GA	AG	TC	AT	932							
Db	535	Phe	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	548								
Oy	933	CGT	T	T	GC	CT	CG	G	A	AT	T	T	A	GA	AT	T	T	A	GA	AT	T	T	A	GA	AT	T	T	A	GA	AT	962					
Db	549	Leu	e	u	t	r	P	leu	a	n	Leu	s	e	r	G	lu	s	a	n	h	1	s	e	u	Val	T	r	P	he	a	sp	Leu	Pro	568		
Oy	963	GGA	A	CT	T	G	A	A	A	AG	TT	GC	-----	AA	A	T	CG	CT	CA	AG	G	GG	CG	CT	GC	CA	AT	T	G	-----	1013					
		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::						
Db	569	Ser	a	n	Leu	e	u	l	s	t	r	P	leu	a	sp	1	e	h	1	s	e	Gly	a	n	T	r	1	e	G	lu	Ala	Leu	Gly	Asn	Tyr	588
Oy	1014	---	ACC	AT	T	GA	AGA	AT	T	CC	GA	T	T	CA	CT	T	TA	CA	CT	T	TA	CA	CT	T	TA	CA	CT	T	TA	CA	CT	1070				
		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::		::: :::				
Db	589	Lys	e	u	G	in	G	lu	G	lu	1	le	arg	Val	Thr	Thr	Leu	a	sp	Ala	Ser	h	1	s	a	n	h	1	e	th	Glu	608				
Oy	1071	TTA	T	T	A	T	T	A	T	T	GT	T	A	TA	GA	AT	T	GT	CT	CA	T	T	T	CC	CG	G	AG	CG	T							

Db	824	AsnAlaSerIleuMetThrIleuGlnAsnGlySer-----	835
Qy	1629	CSAGATATCTTTCACAGAGCTGAGAACTTGAACCTTCCGAGACCTTCTCAGTGTCAAC	1688
Db	836	-----LeuAlaGlnIleuValAsnIleuAlaArgValIleuHisIleuGlnIleuAsnIleu	852
Qy	1669	GAGCAGTTGTCTCCAAACAGACTTTAACTGCTCCAGTCTTTCAGAGTAACTTAAATAGAC	1748
Db	853	ThrAlaIleuGlnGlyThrGlnPheArgSerIleuGlyIleuLeuArgGlyIleuTyrIleuHis	872
Qy	1749	CACAACAACCTCTTTTCATGGATGATACGTTTCCCTTAATAGTCTGAACCTCCCTCCAGTT	1808
Db	873	AsnMetIleuThrHisIleSerAsnAlaThrPheIleuProIleuValSerIleuGlnVal	892
Qy	1809	CTTGATTAACAGTCAACTCAATCAATATGACTTCCAAAAACAGAACTACAGACTTTTCCA	1868
Db	893	LeuArgIleuAsnAsnArgIleuSerSerIleuProHisIleuGlnTyrArgHis-----	910
Qy	1869	AGTAGTCTAGCTTTCTTAACTTTACTCAGAAATGACTTTGCTGTACTTGTAAAC--	1925
Db	911	--SerIleuGlnGlyIleuThrIleuGlyAlaArgAsnAlaTrpSerCysArgCysGlnGlnIleu	929
Qy	1926	CAGAGTTTCCCGCAATGAGATGCAACAGACAGGACGAGCTTTGGTGAAGTTGAACGAT	1985
Db	930	ArgIleuIleuAlaGlnPheValSerAspAsnAlaMetValValaArgAspAlaHisAspIle	949
Qy	1986	GAATGTGCACACCTTTCAGATTAAGCAGGCGCATGCTGTGTG-----	2027
Db	950	TyrCysIleuAspAlaGlyIleIleYArgGlnIleuIleuIleGlyAsnIleuAlaAsnGly	969
Qy	2028	-----AGTTGAATATCACCTGTCAATGATTAAG	2057
Db	970	ProAspCysSerAspIleuLeuAspAlaSerAlaSerAsnIleSerSerGlnAspIleu	989
Qy	2058	ACC---ATCATTTGTT-----GTGCGGCTCCACTGTGCTTTGATGA	2096
Db	990	AlaGlyAlaIleGlyCysProCysTrpProAlaValIleuValIleuIlePheIleuValVal	1009
Qy	2097	TCTGTGTAGACAGTTTCGTGCTTAAAGTCTTATTTTCACTGATGCTTCTTGCTGCTGC	2156
Db	1010	ValIleuIleIleValPheValPheArgGlnSerValaArgMetTrpIleuPheAla-----	1027
Qy	2157	ATTAAGTATGTT-----AGAGGTGAAC-----ATTATGAT	2189
Db	1028	--HisTyrGlyValaArgValCysGlnProArgPheGlnIleuAspAlaGlyIleuTyrAsp	1046
Qy	2190	GCGTTTGTATCTACTACAGCCAGAGATGAGACCTGGGTAAGATGAGCTAAGTAAAGAT	2249
Db	1047	AlaIleIleIleuHisSerGlnValAspTyrGlnPheValCysArgAsnIleAlaIleGln	1066
Qy	2250	TTAGAAGAAGGGGGCTCCACTTTCACCTGCGCTTCACTACAGACTTTATATCCCGGT	2309
Db	1067	LeuGlnHisGlyAlaArgProPheArgIleuCysIleGlnGlnArgAsp---LeuProPro	1085
Qy	2310	GTGGCCATTTGTGGCCAACTATCATCATGAAGGTTTCCATAAAACCGAAAGGTATGTT	2369
Db	1086	GlnAlaSerHisIleuGlnIleuVal--GlnGlyAlaArgAlaSerArgIleIleIleu	1104
Qy	2370	GTGGTGTCCCAAGCACTTATCATCAAGACCGCTGTGTATCTTTGAATATGAGATTGCTCAG	2429
Db	1105	ValIleuThrArgAsnIleuIleAlaThrGlnTyrAsnArgIleGlnPheArgAsnAla--	1123
Qy	2430	ACCTGGCAGTTTCTGAGCAGATCGTGCTGTATCATTTCAATTGCTCGCAGAG--	2483
Db	1124	-----PheHisGlySerIleuArgGlyIleu-----AlaGlnIleuVal	1136
Qy	2484	---GTGAGAGAACCTCTGCTCAGGCAGCAGCTGAGCTGTACCGCTTCTCAGCAGAAC	2540
Db	1137	IleIleGlnGlnThrIleSerValSerAlaGlnAlaGlnIleuAspValAlaGlnIleuSer-----	1154
Qy	2541	ACTTACTGTGAGTGGAGAGACAGTGTCTGTGGGGCGGACATC-----	2582
Db	1155	ProTyrIleuIleuS-----SerValProSerAsnArgIleuIleuThrCysAspArgTyr	1171

Qy	2583	TTCTGAGACGACTCAGAAAAAGCCCTG	2609
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Db	1172	PheTrpGlnLysLeuArgTyrAlaIle	1180

RESULT 5

t:Clr protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13887
 R:Chiang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contributes to the formation of the posterior compartment in the *Drosophila* embryo
 A:Reference number: Z17805; MUID:95151581; PMID:7848870
 A:Accession: T13887
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AA8333863
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0004364
 A:Note: tlr

Alignment Scores:	
Pred. No.:	1,73e-23
Score:	421.00
Percent Similarity:	39.60%
Best Local Similarity:	23.96%
Query Match:	6.26%
DB:	2
MS-09-396-985B-3 (1-3811) x T13887 (1-1385)	
	Length: 1385
	Matches: 210
	Conservative: 139
	Mismatches: 359
	Indels: 178
	Gaps: 33

QY 339 CTGAGCCTGAGCTTTAATCCCTGAGGATCTTAGGACGTTAAGCTCTTCAGTTGCCA 398
 Db 338 LeuAenleuAenSerAenAenAlaLeuThrArgIleGlySerIleThrPheValGluLeuTrp 357
 QY 399 GAATCGAGGCTGCTGATTTATCCAGGCTGTGAATCCAGAAATTGAAGATGGGCAATAT 458
 Db 358 PheLeuGlnIleLeuAenPheMetArgAenAenSerIleGlyHisIleGluGluGlyAlaPhe 377
 QY 459 CAGAGCCTTAAGCCACCTCTCTTAACCTATATATGACAGAAACCCCATCCAGATTAGCC 518
 Db 378 LeuProLeuTrpAlaLeuAenLeuHisThrLeuAenLeuAlaGluAenArgLeuHisThrLeuAsp 397
 QY 519 CTGGAGACCTTTTCTGACATCATCAAGTTACAGAAAGCTGGTGGCTGTGGAGACAAATCTA 578
 Db 398 AsnArgIlePheAenGlyLeuTrpValLeuThrIleLeu--ThrLeuAenAenAenLeu 416
 QY 579 GCATCTCTTA--GAGAACTTCCCATGAGACATCTCAAAACTTGAAGAAGACTTAATGTG 635
 Db 417 ValSerIleValGluSerGlnAlaPheArgAenCysSerAenPheLeuValGluLeuAspLeu 436
 QY 636 GCTCAACATCTTATTCACATCTTTCAAAATTCAGTAGTAATTTCTMACTGACCAATCTA 695
 Db 437 SerSerAen-----GlnLeuThrGluValProGluAlaIleGlnAenPheSerMetLeu 454
 QY 696 GAGCAGCTTGACCTTTCCAGCAACAGATTCAAAGTATTTATTTGCACAGACTTCGGGATT 755
 Db 455 LysThrLeuAenPheGluGlyIleAenGlnIleSerGluPheLysAenAenThrPheArgAen 474
 QY 756 CTACATCAAAATGCCCCCTACTCAATCTC----- 782
 Db 475 LeuAenGlnLeuThrGlyLeuArgLeuIleAenAenArgIleGlyAenIleThrValGly 494
 QY 783 -----TCTTGAACCTGTCCCTGAAACCCATGAACTTT 815
 Db 495 MetPheGlnAenPheProArgLeuSerValLeuAenAenLeuAlaLysAenArgIleGlnSer 514
 QY 816 ATCCAAACCAAGTGCATTT--AAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATAT 872
 Db 515 IleGluArgGlyAlaPheAenPheLysAenThrGluIleGluAlaIleValGluLeuAenPheLys 534

873	TTTGATAGTTAAATGTAAATGAATACTGTATTCAGAGCTCGGCTTGTTGAATCCAT	932
QY		
Db	535 Phe-----LeuThrAspIleAsnGlyIlePheAlaThrLeuAlaSer	548
QY	CGTTTGCTTCGGGAGAAATTTAGAAATGA-----	962
Db	933 LeuLeuTrpLeuAsnLeuSerGluAsnHisLeuValTrpPheAspTyrAlaPheIlePro	568
QY	633 GGAACCTTGGAAGAGTTTGAC-----AAATCTGCTTAGAGGGCTTGCAATTTG---	1013
Db	569 SerAsnLeuSerTrpLeuAspIleHisGlyAsnTyrIleGluAlaLeuGlyAsnTyrTrp	588
QY	1014 ---ACCAATTGAAGAAATCCGATTGTGGCAATCACTAGTACTATCCCTGCAGATATTTATGAC	1076
Db	589 LysLeuGlnGluGluIleArgValThrThrLeuAspAlaSerHisAsnArgIleThrGlu	608
QY	1071 TTAATTATATGTTGGTCCAAATGTTTCTTCAATTTTCCCTGATGATGACTATTTGAAGG	1133
Db	609 Ile---GlyAlaMetSerValProAsnSerIleGluLeuLeuPheIleAsnAsnIle	627
QY	1131 GTAAAGACCTTTCTTATAT-----TTCCGATGGCAACATTAGAAATTAGTAACTGT	1184
Db	628 IleGlyGlnIleGlnAlaAsnThrPheValAspLysThrArgLeuAlaArgValAspLeu	647
QY	1185 AAATTGTGACAGTTTCCACATTTGAATCTAAATCTGCAGAAAGGCTTACTTCACTTCC	1244
Db	648 TyrAlaAsnValLeuSerLysIleSerLeuAsnAlaLeuArgValAlaProValSerAla	667
QY	1245 AACAAA-----GGTGGAGATGCTTTTCA-----	1266
Db	668 GluIysProValProGluPheTyrLeuGlyGlyAsnProPheGluCysAspCysSerMet	687
QY	1269 -----GAACTGATCTA	1280
Db	688 GluTrpLeuGlnArgIleAsnAsnLeuThrThrArgGlnHisProHisValValAspLeu	707
QY	1281 CCAAGCCCTGATGTTCTTA-----GAT	1301
Db	708 GlyAsnIleGluCysLeuMetProHisSerArgSerAlaProLeuArgProLeuAlaSer	727
QY	1302 CTCAGTAGAAATGAGCTTGAGTTTCA-----GGTTGC	1334
Db	728 LeuSerAlaSerArgPheValCysLysTrpGluSerHisCysProProThrCysHisCys	747
QY	1335 TGTTTCTCAAAATGATTTTGGGACAACAACCTTAAGATTTAGATCTGAGCTTCAATGCT	1394
Db	748 CysGluTyrGluGlnCysGlyCysGluValIleCysProGluAsnCysSerCysPheHis	767
QY	1395 GTTTATTCACATGATTCAAACTTTTG-----GGCTTAGAACAACTTAGAACATCTGGAT	1444
Db	768 AspAlaThrTrpAlaThrAsnIleValAspCysGlyArgGlnAspLeuAlaIleLeu---	786
QY	1449 TTCACAGATTCCTTGTGAAACAAATAGAGATGTTTCCAGATTTCTATCACTACAGAAAC	1508
Db	787 -----ProAsnArgIleProGlnAspValSerAspLeuTyrLeuAspGlyAsnAsn	803
QY	1509 CTCATTTACTTGAACATTTTCTCATATCTACACACAGAGTTGCTTTCATAGGACATTTCAAT	1568
Db	804 MetProGluLeuGluValGlyHisLeuThrGlyArgArgAsnLeuArgAlaLeuTyrLeu	823
QY	1569 GGCCTTGTCCAGTCCGAAAGTCTTGAAAATGGCTGGCAATCTTTCCAGGAAAACCTCTT	1628
Db	824 AsnAlaSerAsnLeuMetThrLeuGlnAsnGlySer-----	835
QY	1629 CCAAGATTTCTTCAACAGAGCTGAGAAATTTGACCTTCTGACACTCTGCAGTGTCAATG	1688
Db	836 -----LeuIleGlnLeuValAsnLeuArgValLeuHisLysLeuGlnAsnAsnLysLeu	852
QY	1689 GAGCAGTTTGTCTCCACAGACATTTAACTCACTCTCCAGTCTTCAAGGTACTAATATAGAC	1748
Db	853 ThrAlaLeuGlnGluGlnTrpGluPheArgSerLeuGluLeuLeuArgGluLeuTyrLeuHis	872

[illegible]

RESULT 6
T15864
hypocholesteral protein C56B6.6 - *Caenorhabditis elegans*
CISpecies: *Caenorhabditis elegans*
CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15864
R:Pulton, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C56B6.
A:Reference number: S69019
A:Accession: T15864
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1066 <Full>
A:Cross-references: UNIPROT:Q18902; EMBL:U03996; NID:g1055114; PID:g1055120; PIDN:AAA61C
C:Genetic8:
A:Gene: CESP:C56B6.6
A:Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 922/3; 952/3; 1000/3
Alignment Scores:
Pred. No.: 3.14e-22
Score: 404.00
Percent Similarity: 41.17%
Best Local Similarity: 25.21%
Query Match: 6.01%
DB: 2
Length: 1066
Matches: 177
Conservative: 112
Mismatches: 268
Indels: 145
Gaps: 29

US-09-396-985B-3 (1-3811) X T15864 (1-1066)

QY	44	GATGATGTCGCTCGCGCTGGCTGGACCTGTATCCAGCAAGGCTCTCCCTGCTG	103
Db	11	AspAsnLeuSerValIleProThrTrrpAlaLeuThrTyrlleuHisSerIeuGlnIleLeu	30
QY	104	CGT---GAGACAGAAAGCTGGAGCCCTGCGTGA-	136
Db	31	HisLeuGlnAsnAsnArgIleAspValLeuThrSerAsnThrPheAspGluThrGlnLeu	50
QY	137	-----GACTTGCC	145
Db	51	AsnAsnLeuGlnPheLeuTyrlleuAspAsnAsnGlnLeuArgIleIleProAsnLeuAla	70
QY	146	CTAAACAC-----ACAGAAAGCTGGCATGAAACCA	178
Db	71	PheAsnHisIleuArgIleuValValLeuMetLeuAlaAsnAsnArgIleThr-GluIleG	90
QY	179	GAGCTTTACAGACTCGGAGCCTCAGCCCTTC-----ACCC	214
Db	90	nllyrMetSerIeuProGlnThrIleuLysPheLeuValLeuArgAsnAsnLeuLeuThrG	110
QY	215	GATTTCATTGCTTCTT-----GCTAAATGCTGCGCTTTATCAGGAGGTGTTCC	265
Db	110	nlleProTyrlleValAlaLeuAsnAspIleuLysThrIleuGlnSerIleAspLeuGlnGlyAs	130
QY	266	TAAATTAATCTATACATGATGATGAGACTGAATTTCTACAAATATCCCGACAACCTCCCTT	325
Db	130	nlAsnIleIleThrHis--LeuMetAspThrAsnGlnValThrPheGlnSerIleuMetLysVa	149
QY	326	CTGACCAACGAACCTGGAAGCTGAGCTTTAATCCCTGAGGAGATTTAGGACAGCTAAGCTT	385
Db	149	IleIleLeuArgAsn-----AsnLysValArgIleuAspLysPheHisSerP	164
QY	386	CTTCAGTTTCCCAAGACTGACAGTCTGCTGATTTATCCAGGTGTAATCCAGACATTTGA	445
Db	164	eArgSerPheArgLysIleArgIleuLeuAspIleSerTyrlleAsnGlnIleGlnThrValG	184
QY	446	AGATGGGGCATATCAAGAGCTTAAGCCACTCTCTACCTAATATATGACAGAAACCCCAT	505
Db	184	uAspSerSerPheGlnThrValGlyHisMetGlnSerIleuAspLeuSerTyrlleAsnArgI	204
QY	506	CCAGAGTTTAGCCCTGGAGAGCTTTTCGAACTATCAAGTTTACAGAAAGCTGGGCTGT	565
Db	204	eAlaTyrlleuProArgGly-----	210
QY	566	GGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGA	625
Db	211	-----MetLeuLysAsnPhe-----AlaLysThrIleuLysThr	221
QY	626	ACTTAATGTGGCTCACACATCTTATCCATCTTTCAATTAATCTGAGTATTTTCTTAATCT	685

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Db      221  rLeuLybLeuLaIuInMeC1LeH1sAla-----ThrProGluLaLeuArgAspLe 239
Oy      686  GACCAATCTAGAGCACTTGACCTTCCAGCAACAATCTTTCATGGATCGTTCC 1780
Db      239  uArgAsnLeuHrH1sLeuInLeuAnGlyAsnLybLeuAnArgL1LeAspLyAspVa 259
Oy      735  -----TATTGCACAGACTTCCGGCTTCTACATCAATGCGCCCTACTCAATCTCTGTT 787
Db      259  lLeuLygLyCysThrAspThrLeuVal-----GluLe 270
Oy      788  AGACCTGCTCCCTGAGCCCTATGAATTTATTCACCAAGGTCATTTAAAGAAATGAGCT 847
Db      270  uPheL1eAlAsnAsnLyR1eugL1uH1e1leProH1eGlyValLeuSerGlyMetLys-- 289
Oy      848  TCATTAACCTGACTTAAAGAAATATTTGATAGTTTAAATGATGAAATCTGATATCA 907
Db      290  -----GlnLeuGluH1sLeuAspL1eSerLysAsnLyS1leMe 302
Oy      908  AGGCTGAGCTGTTTAGAAGTCATCGTTGGTCTGGAGAAATTTGAAATGAAGAA 967
Db      302  tSerLeu-----LysLysProThrSe 309
Oy      968  CTTCGAAAAGTTTGACAAATCTGCTTAGAGCGCTGTCGAATTTGACATTTGAAGAAT 1027
Db      309  rLeuLeuSerL1eHrLySgluGluThrSerThValArgArgLeuInLeuAlaGlyAs 329
Oy      1028  CCGATTGACACTACTAAGCTACTACTCGATGATATTTATGACTTATTTATTTGAC 1087
Db      329  nArgL1eAsnAsnMetSerAspLyR1eU-----L1ePheGluH1sMetProLeuLeuTh 347
Oy      1088  AAAATGTTCT--TCATTTCCCTCGTGAGTGAGTGACTATTTGAAGGGTAAAGACTTTC 1144
Db      347  rTyRValAspValSerPheAsnAspGlyLeArgPheL1eSerProArgValPheGluLysLe 367
Oy      1145  TTATATATTTGGATGGACATTTAGATTTAGTTAACTGTAAATTTGACAGCTTCCAC 1204
Db      367  uLyAsnLeu-----GlnSerLeuPheLeuGlnAsnAsnGlnLeuAlaH1sPheProSe 385
Oy      1205  ATTC--AAACTCAAACTCTCAAAAAGCTTACTTCACTTCCAA-----AAGG 1252
Db      385  rLeuPheArgLeuAspLysLeuAspGlyH1sLeuMetLeuAspAsnAsnGlnL1eGlnLyS1 405
Oy      1253  TGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTGTAGATCTAGTAA 1312
Db      405  eAspAsn--PheSerLeuAlaAspLeuProLySLeuGlnH1sLeuSerLeuAlaGlyAs 424
Oy      1313  TGGCTTGAGTTTCAAGAGTTGCTGTTCTCAAGATTTTGGCAACAACG----- 1364
Db      424  nGlnLeuAspL1e-----L1eThrGluAsnMetPheGlySerSerSerSerG1 441
Oy      1365  -CTTAAGATTTTATGATCTGACCTTCAATGGTGTATTATTCATGATTC--AACTTCTT 1420
Db      441  uLyS1eSerLeuAsnLeuAlaH1sAsnLyS1leH1sSerL1eSerSerArgSerPheSe 461
Oy      1421  GGGCTTGACACTAGATCAATCTGAGTTTCCAGATTTCCAAATTTGAAACAATGATGA 1480
Db      461  rAspLeuAspAsnLeuGlnGlnLeuArgLeuSerH1sAspAsnL1eArgHrL1eThrSe 481
Oy      1481  GTTTTCAGATTTCTCATCTACAGAAACTCATTTACCTTGCATTTCTCATCTACAC 1540
Db      481  rMetThr--PheSerAsnLeuArgAsnLeuArgLyLeuAspLeuSerH1sAsnArgL1 500
Oy      1541  CAGAGTTGCTTTCAATGACATCTTCAATGGCTTGTCAGATCTGCAAGCTTGAAGATGC 1600
Db      500  e1leLyS1leuProSerAlaLeuLyR1eGlnLeuProAlaLeuAspValLeuH1sLeuAs 520
Oy      1601  TGGCAATCTTTCCAGAAAACCTTCCTCCAGATATCTTCACAGAGTGAAGAACTGCAC 1660
Db      520  pH1sAsnAsnLeuAsnGln--L1eAspArgAspAlaPheArgSerPheSerAspLeuG1 539
Oy      1661  CTTCCTGAGCTTCTCAAGTGTCAACTGAGCACTTGTCTTCCAAACAGATTTAATCTCACT 1720

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Db      539  nSerLeuLySLeuSerH1sAsnAlaPheArgArgPheSerCysGlnPheLeuGlySerL1 559
Oy      1721  CTCAGATCTTCCAGTACTTAATATGAGCCACCAACTTCTTTTCATGGATCGTTCC 1780
Db      559  eSerGlnValH1eGlnLeuAspLeuSerSerArgGlnL1eAsnGluL1eAspL1ePhe-- 578
Oy      1781  TTATTAAGTCTG--AACTCCCTCAGGTTCTTGAATTCAGTCTCAATCAATGATGAC 1837
Db      579  -----CysL1eAlaArgGlyL1eArgLySLeuSerLeuAlaSerAsnSerValGluLy 596
Oy      1838  TTCAAAAAAGAGAACTACGACTTTCCAGTACTTGCTTTCTTAAATCTTACTCA 1897
Db      596  s1leAsnArgLyLeuLeuGlnAsp--AlaHrGluLeuThrSerL1eAspL1eSerH1 615
Oy      1898  GAAT-----GACTTGGTTCGACTTGTGAACACAGCTTCC 1936
Db      615  sAsnGlyL1eL1eAspValAspSerAspAlaPheCysGluCysArgLySLeuSerH1sL1 635
Oy      1937  GCAA 1940
Db      635  eLyS 636

RESULT 7
A29944
chaotIn precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: photoreceptor cell-specific membrane protein
C/Species: Drosophila melanogaster
C/Date: 15-Dec-1988 #sequence, revision 15-Dec-1988 #text_change 09-Jul-2004
R/Accession: A29944; A21123
R/Reinke, R.; Krant, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A>Title: ChaotIn, a cell surface glycoprotein required for Drosophila photoreceptor ce
A/Reference number: A29944; PMID:88135762; PMID:3124963
A/Accession: A29944
A/Molecule type: DNA
A/Residues: 1-1134 <REI>
A/Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M190
R/Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A>Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecu
A/Reference number: A21123; PMID:84106810; PMID:6420071
A/Accession: A21123
A/Molecule type: protein
A/Residues: 31-43, 'HX', 46-49, 'H' <ZIP>
C/Genetics:
A/Gene: FlyBase:chp
A/Cross-references: FlyBase:FBgn0000313
A/Intons: 1/3 80/3, 318/3, 377/2 422/2, 702/1 745/3, 831/2, 998/2
C/Superfamily: chaotIn; leucine-rich alpha-2-glycoprotein repeat homology
C/Keywords: cell adhesion; glycoprotein; membrane protein
F/129/Domain: signal sequence #status predicted <SIG>
F/30-1134/Product: chaotIn #status predicted <MAX>
F/80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
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F/351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F/502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F/527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F/551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F/577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>

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QY	1668	TAACCTCTCTCACTGTCAACTGTGAGACAGTGTCTTCCAAAGACATTTAACTCACTCTCCAGT	1727
Db	884	AspIleSerTyrAsnTyrLeuLeuArgIleAspAspAlaValPheAlaIleMetProIlys	903
QY	1728	CTTCAGTACTAAATATGAGCCACCAAC	1763
Db	904	LeuAlaValLeuAspLeuSerHisAsnArgAspLeuIysValMetAspLysSerPheMet	923
QY	1764	-----TCATTGGAATGCTTTCT	1781
Db	924	GlyLeuGluAsnSerLeuIleLysLeuGlyLeuGluAsnValSerLeuSerThrValPro	943
QY	1782	TATAAGTCTCGAATCCCTCCAGTCTTGATTATCACTCTCAACATATATGACTTCC	1841
Db	944	GluIleArgLysTyrTyrLeuArgGluIleArgLeuGlyTyrAsnGlu--LeuProSer	962
QY	1842	AAAAACACGAACTACACACTTTTCCAGTAGTACGTCTTCAATCTTACTACAGAT	1901
Db	963	IleProGlnGluLeuAlaHisAsnMetSerAsnLeuArgMetLeuAspLeuSerAsnAsn	982
QY	1902	GACTTTGCTTGTACTTGTGAACACCAAGATTTCTGCAATGAGATCAAGACCAAGGCGAG	1961
Db	983	Asp-----	983
QY	1962	CTCTTGTGTGAAGTTGAACGAATGGAATGTGCAACCTTACAGATTAAGACG-----	2012
Db	984	--LeuThrAsnValProLeuMetSerHisAlaLeuProHisLeuArgGluMetLeu	1002
QY	2013	---GGCATGCGCTGTAGTGTGAATATCACTGTGAGATGAATTAAGACCATGATTGGT	2069
Db	1003	SerGlyAsnProIleThrSerLeuAsn-----AsnAsnSerPheAspLys	1017
QY	2070	GTTGCGAGTC---CTCAGTGTGTGTGTAGATATCTGTGTAGACAGTCTTGCTATATAGTTC	2126
Db	1018	ValAsnGluAspLeuGluMetLeuAspLysIleSerAsnPheArgLeuHisTyrPheGluTyr	1037
QY	2127	TATTTTACCTGATGCTCTTCTGTGCGCTGCATATA	2159
Db	1038	-----GlyCysIleu	1040

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RESULT 8
JC5239
insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A>Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: JC5239; MUID:97040714; PMID:886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605 <DEL>
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

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Alignment Scores:			
Pred. No.:	2,52e-16	Length:	605
Score:	325.00	Matches:	163
Percent Similarity:	38.83%	Conservative:	96
Best Local Similarity:	24.44%	Mismatches:	254
Query Match:	4.83%	Indels:	154
DB:	2	Gaps:	24
US-09-396-985B-3 (1-3811) x UC5239 (1-605)			
QY	201	CAGCCCTTCACCCCG-----ATTCCATGGCTTCTGCTAAAGCTGCGGTTTT	248
	:::		
DBD	29	GIHFPGIYThrProGlyIuaIaGluGlyProIaIaCysProIaThrCysIaCysSer	48
	:::		
QY	249	ATTCACGAGAGTGGTCTCTTAATATTACTTATTCATGCATGAGCGTGATTTCTTACAATC	308
	:::		
DBD	49	TYrAspAspGluIuaIaengIuIaSerSeValPheCysSerSerArgIaenLeuThrArgIeu	68
	:::		

QY	309	CCGCAACA	CTCCCTCTTCAACCAAGAACTGGACCTTAAATCCCTGAGGAT	368
Db	69	ProAspGlyIleProGlyIleThiGlnAlaLeuTrpLeuAspSerAsnLeuSerSer	88	
QY	369	TTAGACAGCTTAAGCTCTTCAAGTTTCCAGAACTGACGGCTGAGATTTATCCAGGCTG	428	
Db	89	IleProProAlaIleAspAspAsnLeuSerSerLeuAlaPheLeuAsnLeuGlnGlyIle	108	
QY	429	GAATTCAGCAAACTTGAAGATGGGAGATATCAAGACCTTAAGCAACCTCTTAACCTTAATA	488	
Db	109	GlnLeuGlySerLeuGlnProGlnAlaLeuLeuGlyLeuGlnAsnLeuCysHnIleHnIs	128	
QY	489	TTGACAGGAAACCCCATCCAGAGTTTAGCCCTGGAGACCTTTTCT	533	
Db	129	LeuGluArgAsnGlnLeuArgSerLeuAlaValGlyThrPheAlaTyThrProAlaLeu	148	
QY	534	-----GGA	536	
Db	149	AlaLeuLeuGlyLeuSerAsnAsnArgLeuSerArgLeuGluAspGlyLeuPheGluGlyIle	168	
QY	537	CTATCAAGTTTCAAGACGCTGGCTGGAGACAATCTAGACCTCTCTAGAGAACTTC	596	
Db	169	LeuGlyAsnLeuTrpAspLeuAsnLeuGlyTrpAsnSerLeuAlaValLeuProAspAla	188	
QY	597	CCCATTTGACACTGCAAACTTGAAAGACTTAATGCTGCTCACAATCTTAATCCAACTC	656	
Db	189	AlaPheArgGlyLeuGlyGlyLeuArgGlnLeuValLeuAlaGlyAsnArgLeu---Ala	207	
QY	657	TTCAAAATTAAGTGAATTTTTCATATCTGACCAATCTAGACACTTGAGACCTTCCAGC	716	
Db	208	TyrLeuGlnProAlaLeuPheSerGlyLeuAlaGluLeuArgGluLeuAspLeuSerArg	227	
QY	717	AACAGAGTTTCAAGATTTATTATTCAGACAGCTTGGGGTTCTACATCAAAATCCCTCACTC	776	
Db	228	AsnAlaLeuAlaGlyAlaIle-----LysAlaAsnValPheAlaGlnLeuProArgLeu	244	
QY	777	AATCTCTCTTGAACCTGTCCCTGAACCTTAATGAATTTATCCAAACGAGTGCAATTAA	836	
Db	245	Gln---LysLeuTyrLeuAspArgAsnLeuIleAlaIleValAlaProGlyAlaPheLeu	263	
QY	837	GAATTTAGG---CTTCATAGCTGACTTTAAGAAATAATTTGATAGTTTAAATGATAG	893	
Db	264	GlyLeuLysAlaLeuArgTrpLeuAspLeuSerHisAsn---ArgValAlaGlyLeuLeu	282	
QY	894	AAAACCTGTATCAAGATCGTGGCTGGTTTGAAGCCATCGCTTGGTTCTGGAGAAATTTG	953	
Db	283	GlnAspThrPheProGlyLeuLeuGlyLeuArgValLeuAspGluLeu-----	297	
QY	954	AGAAATGAGAGAACTTGAAAGTTTGACAAATCTGTCTTAGAGGGCTTGCAATTTG	1013	
Db	298	-----SerHisAsnAlaIleAlaSerLeuArgProArg	308	
QY	1014	ACCATTTGAAGATTTCCGATTAGCATTACTTAGACTACTGCTGATGATTAATTAGACTTA	1073	
Db	309	ThrPheGluAspLeu-----HisPheLeuGlnGluLeu-----	319	
QY	1074	TTTAATTTGTTGACAAAATGTTTCTTCATTTCCCTGGAGATGTGACATTTGAAGGGTA	1133	
Db	320	-----GlnLeuGlyHisAsnAspArgIleArgGlnLeu	329	
QY	1134	AAAGACTTTTCTTAATTTTCCGATGCGACATTTAGATTTAGATTAATCTGAATTTTGA	1193	
Db	330	AlaGluArgSerPheGlu---GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsn	348	
QY	1194	CAGTTTCCGACTTGAATCTCAAAATCTCTCAAAAGCTTACTTCACTTCC-----AAC	1247	
Db	349	GlnLeuGlnGlnValLysValGlyAlaPheLeuGlyLeuThrAsnValAlaValaMetAsn	368	
QY	1248	AAAGGTGGGAATGCTTTTTCAGAAGTGGATTAACCAAGCTTGAGTTTCTAGATCTCAGT	1307	
Db	369	LeuSerGlyAsnCysLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGly	386	

D	283	-----ThralaleuHisLysLeuHisIsmecGlyTyrThrAsnLeuSerGly	297
Q	966	AACTGGAAAGTTGGACAAATCTGCTCTACAGGCGCTGTGCATTTGACG--ATTGAA	1022
D	298	ProIleProLys-----ProLeuTrpAsnLeuThrHisIleGlu	310
Q	1023	GAATTCCGATTGACACTTAGACTAC--TACCTCGATGATATTATGACTTATTAT	1075
D	311	SerLeu-----PheLeuAspTyrAsnHisIleuGluGlyProIleSerHisPheThr	327
Q	1080	TGTTTGGACAAATGTTCTTCATATTTTCCCGTGGAGTGTGCATATTGAA--AGGGTAA	1130
D	328	IlePheGluLysLeuLysSerLeuSerIleuGluYasnAsnAspPheAspLysArgLeuGlu	347
Q	1137	GACTTTCTTATATATTCGGATGGACAACTTTAGATTAGTT--AACTGT	1184
D	348	PheLeuSerPheAsnArgSerTrpMetLysIleuGluArgLeuAspPheSerSerAsnPhe	367
Q	1185	AAATTGGACAGTTTCCACA-----TTGAAATCTCAATCTCTCAAAAGCTTACTTTC	1233
D	368	LeuThrGlyProIleProSerAsnValSerGlyLeuGluAsnLeuGluIleuLysLeu	387
Q	1239	ACTTCCACAACAAA--GGTGGAGATCTTTTTCAGAAAGTT--GATCTCAACAGCTTGG	1299
D	388	SerSerAsnHisIleuAsnGlyThrIleProSerTrpIlePheSerLeuProSerLeuThr	407
Q	1293	TTTCTAGATCTTCAGTAGAAATGGCTGAGTTTCAAA-----	1328
D	408	ValLeuAsnLeuSerAspAsnThrLeuSerGlyLysIleGluGluPheLysSerLysThr	427
Q	1329	-----GGTGGCTGTCTCAAAAGTATTT	1355
D	428	LeuTyrPheValSerLeuGluGluAsnLysIleuGluGlyProIleProArgSerLeuLeu	447
Q	1353	GGGACAAACAGCGCTTAAGATTATGATCTGAGCTTCATGGGTGATT--ACCATGAGT	1409
D	448	AsnGluGlnPheLeuGlnAlaLeuLeuLeuSerHisAsnAsnIleSerGlyHisIleSer	467
Q	1410	TCAAATCTTGGGCTTAGAAACAACTAGAACATCTGAGATTTCAGACATTTCAATTGAA	1468
D	468	SerAlaIleCysAsnLeuLysThrPheIleLeuLeuAsnLeuLysSerAsnAsnLeuGlu	487
Q	1470	-----CAATGAGTGA GTTTCAATCTTCTTACTACGA	1505
D	488	GlyThrIleProGlnCysLeuGlyGluMetSerGluLeuGlnVal-----	502
Q	1506	AACGTCATTTACCTTGATCTTCATCTACACACAGAGTTGCTTCAATGGCATCTTC	1566
D	503	-----LeuAspLeuSerAsnSerLeuSerGlyThrMetAsnThrPhe	518
Q	1566	AATGGCTTGTCCAGCTCGAAGCTCTTGAATAATGGCTGCATATTTCTTCAGAGAAATTC	1628
D	519	SerIleGlyAsnProLeuHisIleIleLysLysAspTrpAsnLysLeuGlnGlyLysVal	538
Q	1626	CTTCCAGATATCTTCCACAGAGCTGAATACTTGACCTTCTGGACCTTCTTCAGTGTCAA	1685
D	539	ProProSerLeuIle--AsnCysLysLysLeuGluLeuLeuAspLeuSerAsnAsnGlu	557
Q	1686	CTGGAGAGAGTGTCTCCAAACAGCATTTATCATCTCTCAGTCTTCAGACTACTAATATG	1745
D	558	LeuAsnAspThrPheProLysTrpLeuGlyAspLeuProAsnLeuGlnValLeuAsnPhe	577
Q	1746	AGCCACAAC-----	1754
D	578	ArgSerAsnLysLeuTyrGlyProIleArgThrAsnAsnLeuPheAlaLysIleArgVal	597
Q	1755	-----AATTCTTTTCATGGATACGTTTCTTATTAAGTGTCTGAATCC	1799
D	598	ValAspLeuSerSerAsnGlyPheSerGlyAsp--LeuProValSerPhePheGluAsn	616
Q	1800	CTCCAGGCTCTT-----	1811
D	617	PheGluAlaMetLysIleAsnGlyGluAsnAsnGlyThrArgLysTyrValAlaAspLeu	636

QY 1812 -----GATTGACAGCTTCACATACATATGAGCTTCAAAA-----CAGAACTA 1856
Db 637 TyrsersaprrYTYLYAsenTYleuIeIaIthrThrlySGLYeuaSpIcinIueu 656
QY 1857 CAGCATTTTCCAGTAGCTCTAGCTTTCTTAAATCTTACTCAGAAAGTACTTGGTTGACT 1916
Db 657 SerarYValIeuthrThrGlnIleIleIleAspIeuserIySdenlyPheGlu----- 674
QY 1917 TGTGAACAC---CAGAGTTTCTCTGCAATGATGATCAAGACCGAGGCACTCTTGTTGGAA 1973
Db 675 ---glyhIleIProAsnIleIleIeGlyAspIeuleIleGlyeuaArgThrLeuAsnIeuser 693
QY 1974 GTTGAACAGATGATGCAACACCTTCACATTAAGCAGGGCAGCCCTGTGCTG----- 2027
Db 694 HisenValIeulGluGlyhIleIleIleProIAserPheGlnIasenIeSerValIeulIuser 713
QY 2028 -----AGTTGAATATGACCTGTGCATGATGAATGAACATCATTTGGTGTGCG 2075
Db 714 LeuAspIeuserSerAsnlyIleIleSerGlyalIaIleProGlnIleuAlaIserIeuthr 733
QY 2076 GTCTCTGATGTGCTGTGATGATCTCTGTGTAGCAAGTTCTGCTATTAAGTTCTATTTTAC 2135
Db 734 PheIeulGluValIeuaSnIeuser-----HisAsnHis 744
QY 2136 CTGATGCTTTTGTGCTGCTGATGAAGATGAGAGGTGAAGAAATCATATGATGACCTTT 2195
Db 745 LeuVal-----GlyCySIIeProIySGlyIySgIn-----PheAspSerIhe 758
QY 2196 GTTATCTACTCAAGCCAGATGAGACTGGGTGAAGAAATGAGCTAATGAATTTAGAA 2255
Db 759 GluAsenIeSerTYLeuGlyAsnAspOlyLeuArg----- 770
QY 2256 GAAGGAGTGCTCCATTTCAAGCTCTGC 2282
Db 771 ---GlyLeuProIeSerArgAspCys 778
RESULT 10
A41915
Insulin-like growth factor-binding complex acid-labile chain precursor - human
N1Alternate names: Acid-Labile Subunit (ALS)
C1Species: Homo sapiens (man)
C1Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C1Accession: A41915
R1Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A1Title: Structure and functional expression of the acid-labile subunit of the insulin-
A1Reference number: A41915; MUID:92357025; PMID:1379671
A1Accession: A41915
A1Status: preliminary
A1Molecule type: mRNA; protein
A1Residues: 1-605 <LRO>
A1Cross-references: UNIPROT:P35858; GB:M68826; NID:g184807; PIDN:AAA36047.1; PID:g184800
A1Experimental source: liver
A1Note: sequence extracted from NCBI backbone (NCBI:P.110171)
F.7-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F.123-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F.123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F.147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F.197-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F.219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F.243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F.267-280/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F.291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F.315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F.339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F.363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F.387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F.411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F.435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F.459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F.483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F.483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Alignment Scores:

Pred. No.:	6,82e-15	Length:	605
Score:	306.00	Matches:	160
Percent Similarity:	38.25%	Conservative:	94
Best Local Similarity:	24.10%	Mismatches:	258
Query Match:	4.55%	Indels:	152
DB:	2	Gaps:	24

US-09-396-985B-3 (1-3811) x AA1915 (1-605)

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QY 219 CCATGCTCTTCTTAATGCTGCGCTTTATACGAGGTGGTCTTCAATATTAATCTTAT 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 ProAlaCyseProAlaIaIaCyseValCyseSerTyAspAspAspAlaAspGlnLeuSerVal 58
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 279 CATGATGAGAGTGATTTCTACAAATCCCGACACCTCCCTTCATCAACCAAGAAC 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 59 PheCyseSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 339 CTGACCTGAGCTTTATATCCCGACATTTAGGACGATTAAGCTTTCAGTTTCCCA 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 LeuThrLeuAspGlyAsnAsnLeuSerSerValProProAlaIaIaPheGlnAsnLeuSer 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 399 GAACTGCAAGTGTGATTTATCCAGGTGTAATCCAGACAAATGGAATGGGCAATAT 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 459 CAGAGGCTTAAGCACCCTCTCTACCTTAATTTAGACAGAAACCCCATCCAGAGTTATGCC 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 119 LeuGlyLeuGlnAsnLeuCyHisIleuHisIleuGlnArgAsnGlnLeuArgSerIleuAla 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 519 CTGGAGACCTTTCT-----GACATTCAGATTTCAGAACCTGGTGGCTGTG 533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 LeuGlyThrPheAlaHisIsthrrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 534 -----GACATTCAGATTTCAGAACCTGGTGGCTGTG 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGly 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 GAGCAAAATCTACACTCTAGAGAACTTCCCATTTGACATCTCAAACTTGGAAAGAA 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuAspGln 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 627 CTTAATGTGGCTCACATCTTATCTCAATCTTCAATTAACCTGAGATTTTCTAATCTG 686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 LeuValLeuAlaGlyAsnArgLeu---AlaTyLeuGlnProAlaLeuPheSerGlyLeu 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 687 ACCAATCTAGAGCACTTGACCTTTTCCAGACACAGATTCAAAAGTATTTATTCACAGAC 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 218 AlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaIle-----Lys 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 747 TTGCGGGTTCTATATGAATGCCCTACTCAATCTCTTTAGACCTGTGCCCTGAACCT 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTyLeuAspArgAsnLeu 253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 807 ATGAACCTTATCCAACACAGGTGATTTAAAGAAATTAG--CTTGATTAAGCTGACTTTA 863
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 IleAlaIaValAlaIaProGlyAlaPheLeuGlyLeuIysAlaLeuArgTrpLeuAspLeu 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 864 AGAAATTAATTTTGATAGTTAAATGTAATGAAACCTTGATTCAGAGCTGTGGCTGTTTA 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 SerHisAsn--ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeu 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 924 GAAATCTCATGCTTTGGTCTGGGAGAAATTTAGAAATGAAAGAACTTGGAAAGTTTGAC 983
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 ArgValLeuArgLeu-----Ser 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 984 AAATGCTCTAGAGGCGCTGTGCAATTTGACCATTTGAGAATTCGATTAAGCATTA 1043
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 299 HisAsnAlaIleAlaSerLeuArgProAlaGlyThrPheIysAspLeu----- 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1044 GACTACTACCTCGATGATATTAATTAATTTAATTTGTTGCAAAATGTTTCTTCATTT 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 314 ---HisPheLeuGlnGlnLeu----- 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1104 TCCCGTGTAGGTGATCTATTGAAAGGGTAAGAACTTTCTTATATTTGGATGGCAA 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 320 GlnLeuGlyHisAsnArgGlyLeuArgGlnLeuAlaGlnArgSerPheGln--GlyLeuGly 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1164 CATTTAGAATTAGTTAATCTGTAATTTGGACAGTTTCCCACTTGAATCAATCTCTCTC 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 GlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValIleValIleAlaPhe 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1224 AAAAGCTTATCTTCACTTCC-----AACAAAGGTGGAAATGCTTTTCAAGATTGAT 1277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 359 LeuGlyLeuThrAsnValAlaValIleAsnLeuSerGlyAsnCyseLeuArg-----Asn 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1278 CTACAGACCTGAGCTTGTATCTATACCTGATAG---AATGGCTTGAAGTTCAAGGTTCC 1334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 377 LeuProGlnGlnValPheArgGlyLeuGlyIleValIleAsnLeuIleLeuGlnGlySer 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1335 TGT-----TCTCAAGTGAATTTTGGGACACACGACCTTAAGTATTAGAT 1379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 CyseLeuGlyArgGlyLeuArgProHisIsthrrPheThrGlyLeuSerGlyLeuAspArgLeuPhe 416
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QY 1380 CTGAGCTTCAATGTGTATTATTCATGAGTTCAAACTTCTTG--GGCTTGAACACTTA 1436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 417 LeuIysAspAsnGlyLeuValGlyIleGlnGlnGlnSerLeuThrProGlyLeuAlaGlnLeu 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1437 GAACATCTGGAATTTCCAGATCTCCAAATTTGAAACAAATGAGTGAATTTCAATATTCCTTA 1496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 437 LeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1497 TCACCTCAGAAACCTATTTACCTTGACATTTCTCACTACTCACACACAGATGCTTTCAT 1556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 -----ThrHisLeuPro-----His 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1557 GGCATCTTCAATGTGCTGTGCTGACGTTCCGAGTCTTGAAAGAGCTGGCAATTTCTTCCAG 1616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 452 ArgLeuPheGlnGlyLeuGlyIleValLeuGlyIleLeuLeuSerArgAsnArgLeuAla 471
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QY 1617 GAAAACTTCCTTCCA---GATATCTTCAACAGAGCTGAGAAATTTGACCTTCCGACATCC 1673
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DB 472 Gln-----LeuProAlaAspAlaLeuGlyIleProLeuGlnArgAlaPheThrLeuAspVal 489
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QY 1674 TCTCAAGTCACTGAGACAGTGTGTCTCCACAGACATTTAACTCACTCTCCAGTCTTCCAG 1733
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DB 490 SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaIaProLeuGlyArgLeuArg 509
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QY 1734 GTACTTAATATGAGCCACAACTTCTTTTATGATAGTTCCTTATATAGTGTCTG 1793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 510 TyLeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
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QY 1794 AACTCCCTCCAGGTTCTTGATTACAGTCTCATACATATATGACTTCCAAAAACAGAA 1853
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DB 524 ----- 524
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QY 1854 CTACAGCATTTTCCAAGTAGTCTAGCTTCTTAAATCTTACTCAGAAATGACTTGTCTGT 1913
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 -----ProProGlyLeuGlnArgLeuArgLeuTrpLeuGlnGlyAsnProTrpAspCyS 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1914 ACTGTGAACACCAAGATTTCTGCAATGATCAAGAC----- 1952
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 GlyCySPro-----LeuIysAlaIleuArgAspPheAlaLeuGlnAsnProSer 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1953 -----CAGAGCAGCTCTGTGTGGAAGTGAACGAATGGAATGTGCAACACTTCACAT 2006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 557 AlaValaProArgPheValGlnAlaIleCyseGlnGlyAspAspCySglnProProAlaTyR 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2007 AAGCAGGCGATCCTGTGCTGATTTGAATATCACTGTCCAGATGAATTAAGCACAAT 2066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 ThrTyTrpAsn-----AsnIleThrCyHisIaSerProProGlnValVal 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2067 GGTGTGTGGTGC 2078
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 591 G1yleuAspleu 594

RESULT 11

T17460

disease resistance protein - tomato

C/Species: Lycopersicon esculentum (tomato)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T17460

R/Parniske, M.; Jones, J.D.

Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999

A>Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist

A/Reference number: Z18801; M01D:99254130; PMID:10318973

A/Accession: T17460

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-855 <PAR>

A/Cross-references: UNIPROT:Q9ZS83; EMBL:AF119040; NID:g4235640; PID:g4235642; PIND:AD1

C/gene: NLOC

Alignment Scores:

Pred. No.:	2,26e-14	Length:	855
Score:	299.50	Matches:	213
Percent Similarity:	38.68%	Conservative:	115
Best Local Similarity:	25.12%	Mismatches:	307
Query Match:	4.45%	Indels:	213
DB:	2	Gaps:	43

US-09-396-985B-3 (1-3811) x T17460 (1-855)

```

QY 42 AGGATGATGTCCTCGCGCTGCTGGAGCTGTGATCCCA-----GCCATGGCC 92
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 17 GlnLeuValSerSerSerSerLeuArg--HisLeuCySerProGlnAspGlnAlaLeuAla 35
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 93 TTCCTCTCC-----TGCCTGAGACAGAAAGCTGGAGCCCTGC----- 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 36 LeuLeuGlnPheLysAsnMetPheThrValAsnProAsnAlaPheHisTyrCysProAsp 55
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 -----GTGAGACTGGCCCTTAACCAACAGAAAGCTGGAGCTGAAC 176
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 56 IleThrGlyArgGlnIleGlnSerTyrProArgThrLeu-----SerTyrAsnLysSer 73
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 CAGAGCTTTCAGATCCCGAGAGCTCAGCCCTTACACCCGATTCATGCTTCTGCTAA 236
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 74 ThrSer----- 75
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 TGTGCGCGTTTATTCAGAGAGGTGTTCTTAATATTAATTATGATGATGAGCTGAAT 296
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 76 CysCysSerTyrAspGlyValHisCysAspGlnThrThrGlnValIleAlaLeuAsp 95
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 297 TTCCTAC-----AAATCCCGACAACTCCCTTC-----TCAACCAAG 335
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 96 LeuGlnLeuGlnIlyLysPheHisSerAsnSerSerLeuPheGlnLeuSerAsnLeuLys 115
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 336 AACCTGAGCTGAGCTTAAAT-----CCCTGAGGACTTTAGGACCTAT 380
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 ArgLeuAspLeuSerPheAsnAspPheThrGlySerProIle-----SerPro 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 381 AGCTTCTTCAAGTTTCCAGAACTGACAGGTGCTGATTTATTCAGAGTGTGAATCCAGACA 440
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 LysPheGlyLysPheSerAspLeuThrHisLeuAspLeuSerHisSerSerPheThrGly 151
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 441 ATTGAAGATGGGCGCATATCAGAGCTGATGAGCACTCTTAATATTAATGACAGGAAC 500
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 152 LeuIleProPheGlnIleSerHisLeuSerLysLeuHisValLeuArgIleArgGlyGln 171
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 501 CCCATCCAGAGTTTAGCCCTGGAGAGCTTT-----TCTGAGACTTCAAGTTTA 548
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 TyrLysLeuSerLeuValProHisAsnPheGlnLeuLeuLysAsnLeuThrGlnLeu 191
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 549 CAGAGCTGTGCTGTGAGACAAATTAAGATCTTCA-----GAGAATTCCCAT 602
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 ArgAspLeuGlnLeuGlnSerIleAsnIleSerSerThrValProSerAsnPheSer--- 210

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QY 603 GGACATCTCAAAACTTTGAAA-----GAACTTAATGTGGCTGACAACTTATC 650
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 211 SerHisLeuThrAsnLeuArgLeuProPheThrGlnLeuArgGlyLe----- 226
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 651 CAATCTTTCAAAATTACCTGATATTTTCTAATCTGACCAATCTAGACACTTGAACCTT 710
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 227 -----LeuProGlnArgPhePheHisLeuSerAsnLeuGlnSerLeuAspLeu 242
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 711 TCCAGAACAAAGTTCAAAAGTATTTATTCGACAGACTTGGGGTCTTACATCAAAAGCCC 770
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 SerPheAsnProGlnLeuThrValArgPheProThrThrLysSerTyrAsnSerAlaSer 262
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 771 CTAAGTATCTCTCTTTAGACCTGTCCGGAACCTATGACATTTATCCAAAGGCTGCA 830
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 263 LeuValAsnLeuTyrLeu--AlaSerValAsnIleAlaAspArgIle--ProGlnSer 280
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 831 TTTAAAGAAATTAGCGCTTCAATAGCTGACTTTAAGAAATTAATTTGATGTTAAATGTA 890
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 281 PheSerHisLeu----- 284
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 891 ATGAAAACTTGATTTCAAGTCTGCTGCTTTAGAAAGTCATGCTTGTGCTGGAGAA 950
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 285 -----ThrAlaLeuHisGlnLeuTyrMetGlyArg 294
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 951 TTTAGAAATGAGAAACTTGGAAAGTTTGACAAATCTGCTCTAGAGGGCTGTGCAAT 1010
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 295 SerAsnLeuSerGlyHisIleProLys-----ProLeuTyrAsn 307
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1011 TTGACC---ATTGAAGAATTCGATTTAGCATATCTTAGACTAC---TACCTCGATGATAT 1064
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 308 LeuThrAsnIleGlnSerLeu-----PheLeuAspTyrAsnHisLeuGlnLysPro 324
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1065 ATGACTTATTTAATGTTTGAACAAAGTTTCTTCAATTTCCCTGGTGAAGTGAAT 1124
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 325 IleProGlnLeuProArgPheGlnLysLeuLysGlnLeuSerLeuGlnAsnAsnLeu 344
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1125 GAAAGGCTAAAGACTT---TCTTATATTTCCGATGCAACATTTAGATTA---GTT 1178
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 345 AspGlyGlyLeuGlnLeuLeuSerPheAsnThrGlnLeuGlnTyrIleAspLeuSerSer 364
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1179 AACTGTAAATTTGACAGATTTCCACA-----TTGAACCTCAAAATCTGCAAAAGCTT 1232
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 365 AsnSerLeuThrGlyProAsnProSerAsnValSerGlyLeuGlnAsnLeuGlnTyrPhe 384
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1233 ACTTCACTTCAACAAA---GATGGAAATGCTTTTCAAGATT---GATCTACCAAG 1286
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 385 TyrLeuSerSerAsnAsnLeuAsnGlySerIleProSerTyrIlePheSerLeuProSer 404
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1287 CTGAGTTTCTGATCTCAGTAGAATGAGCTTGAAGTTCAAGGTGCTGTTCTCAAGT 1346
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 405 LeuIleGlnLeuAspLeuSerAsnAsnThrPheSerGlyLys-----IleGln 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1347 GATTTTGGACA----- 1358
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 AspPheLysSerLysThrLeuSerValValSerLeuArgGlnAsnGlnLeuGlnLysPro 440
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1359 -----ACAGCTTAAGTATTTAGATGAGCTTCAATGGTGT 1397
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 441 IleProAsnSerLeuLeuAsnGlnSerLeuPheTyrLeuValLeuSerHisAsnLeuIle 460
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1398 ATT---ACCATGATTTCAAACTTCTGGCTTGAACAACTGAACATCTGATTTCCAG 1454
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 461 SerGlyHisIleSerSerSerIleCysAsnLeuLysLeuMetIleLeuLeuAspLeuGly 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1455 CATTCGAATTTGAACAAATGATGATGATTTTCAATGATTTCTTCACTGAAAGCCCAT 1514
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 SerAsnAsnLeuGlnGlyThrIleProGlnCysValGlyGlnMetLysLysLeuTyr 500
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1515 TACCTTGACATTTCTCATCTGACACACAGAGTGTCTTCAATGGCATCTTCAATGGCTTG 1574
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 501 SerLeuAspLeuSerAsnAsnArgLeuSerGlyThrIleAsnThrThrPheSerIleGly 520

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QY 1302 CTCAGTAGAAT-----GGCTGAGTTTCAAGGTTGCTTCTCAAGTAGATTTGGG 1355
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 LeuSerHisLeuLeuGlyIleSerIleAspSerProPheAsnGluAlaPheArg 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1356 ACAACACGCTTAAGATTATGATCTGAGCTTCAATGCTGTATTTACAGTGAATCAAC 1415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 ThrMetProLeuArgHisLeuAspLeuSerPheAsnHisMetAsnAspPheAspSerIle 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1416 TTCCTGGGC-----TTAGAACAACTAGAACATCTGATTTCCAGATTCCTCAATTGAA 1469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 326 TrpLeuGlyTrpAlaGlnGluLeuThrSerIleAlaLeuSerGlyAsnPheLeuVal 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1470 CAATGAGTGAAGTTTTCAGATTCTTATCTACCTAGAACACCTTATCTTGAATTTCT 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 AsnPheGlnGlu---SerTrpThrTrpThrLeuIleSerLeuIleHisLeuGluLeu--A 364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1530 CATACTCAACCCAGAGTTGCTTCAATGAGCATCTTCAATGAGCTTTCAGTCTCGAAGTC 1589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 LetyrAsnHis----- 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1590 TTGAATAGTGGTGGCAATTTCTTCCAGGAAACCTTCTCCAGATTCTTCCAGAGCTG 1649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 368 -----IleIlePheIleProValGlnLeuProSerArgIleTrpHisLeu--- 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1650 AGAACTTGACCTTCTCGAGCTCTCTCAGTGTCAACTGAGAGAGTTGTCTCCACAGCA 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 ----- 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1710 TTTACTACTCTCTCCAGTCTTCCAGTCTTAA-----TATGAGCCCAACAATCTTTT 1763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 383 -----IleSerLeuAsnIleSerGlyAsnGluLeuThrTrpLeuPro-AspAsnIleAsn 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1764 TCATGTGATACGTTCTCTTATAGTGTCTGAACCTCCCTCCAGGTTCTTGAATTCAGCTTC 1823
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 401 ThrLeu-----LeuProAsnValIleThrPheAspIleThrAla 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1824 AATCACAATATGACTTCCAAAAAAGAGAACTACAGCATTTTCCAAAGTACTGACTTTC 1883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 414 AsnArgPheHisThr-----PheSerHis-----ThrAspLeuAlaPhe 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1884 TTTAATCTTACTAG-----AATGACTTGTCTGACTTCTGAGACAC 1925
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 LeuAsnAsnValGlnGluValIleValAspGlyAsnProTrpAspCysSerCysAlaIle 446
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1926 CAAAGTTTCTGCAATGATCAAGAGACCAAGAGCAAGCTC-----TTGGTGAAGTTGAA 1979
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 447 GlnGlyLeuGlnValHisMetArgAspArgIleAlaMetArgHisIleLeuAsnTrpAsp 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1980 CGAATGGAATGTGCAACACCTTCAAGATAGCAGGAGCATGCTGCTGAGTTGAAATATC 2039
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 467 AsnValArgCysAlaThrProSerLeuValGlnGlyHisSerValLeuAlaIleThr-- 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2040 ACCTGTCAAGATTAAGACCATCAT-----GGTGTGCTGCTCTC 2081
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 -----AspValAsnAspCysAlaValLeuPheGlyAlaArgTrpGlyLeuThrGlnThr 503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2082 AGTGTGCTTGTAGTATGTGTGAGCAGTTCTGCTATTAAGTTCTATTTTCACTGATG 2141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 504 SerGlnMetLeuIleLeuLeuAlaGlyValLeuLeu-----PheAlaAlaLeuLeuLeu 521
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2142 CTTCCTGCTGGCTGCAATTAAGTATGTAGAGTGAATAACATCTATGATGCTTGTATTC 2201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 MetIleLeuGlyCysIleIleTrpPheLeuArg--GlnArgGlnTrpIleGlySerTrpVal 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2202 TACTCAAGCAGATGAGATGAGTGGTGAAGATGAGCTATTAAGATTTAAGAAAGAGG 2261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 -ThrArgGlnHisSerArgThrProLeuThrMetAla----- 552
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2262 GTGCTCATTTTGAAGCTCTGCTTCACTAAGAGACTTTATCCCGGTGGGCA----- 2316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 553 -AsnThrHisSerCysSerSerSerThrAsnAspThrHisGlyProLeuSerProProPh 572
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2317 -----TTGCTGCAACATCATCATCAAGAGTTTCC 2346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 572 eaSpProPheLeuValSerThrGluThrPheIleAlaThr 585
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 13
JC1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1282
R/Ref: J. Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fa
A/Reference number: JC1282; MUID:93038676; PMID:1384485
A/Accession: JC1282
A/Molecule type: mRNA
A/Residues: 1-603 <DAT>
A/Cross-references: UNIPROT:P93589; GB:S46785; NID:9258002; PIDN:AAB23770.2; PID:957059;
A/Experimental source: Liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-603/Product: Insulin-like growth factor binding protein, acid labile chain #status
F/267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Alignment Scores:
Pred. No.: 2,73e-14 Length: 603
Score: 298.00 Matches: 163
Percent Similarity: 37.11% Conservative: 89
Best Local Similarity: 24.01% Mismatches: 260
Query Match: 4.43% Indels: 167
DB: 2 Gaps: 26

US-09-396-985b-3 (1-3811) x JC1282 (1-603)
QY 185 TCAGACTCCGAGACCTCA-----GCCCTTACCCCGATTCATTCGTTCTTCTGAATG 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 ThrAspProGlyAlaSerAlaAspAlaGlnGlyProGlnCysProValAlaCys-ThrCys 47
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 239 CTGCCGTTTATCACCGAGTGGTCTCTAATATTACTTATCAATGATGAGTGAATTT 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47 SerHis-----AspAspTrpThrAspGluLeuSerValPheCysSerSerIleAsnLe 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 299 CTACAAATCCCGACACCTCCCTCTTCAACCAAGAACTGAGCTGAGCTTAAATCC 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 ValHisLeuProAspAspIleProValSerThrArgAlaLeuThrLeuAspIleAsnLe 85
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 359 CTGAGGCAATTTAGGAGCTATAGCTTCTTCACTTCCAGAACTGACAGTCTGATTT 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85 nLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSerSerLeuAspPheLeuAsnLe 105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 419 ATCCAGTGTGAATATCCACAATTAAGATGAGGAGCTATTCAGAGCTTAAGCACTCTC 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 105 ValGlnIleSerTrpLeuArgSerLeuValProGlnAlaLeuLeuGlyLeuGlnAsnLeuTr 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 479 TACCTTAATATTGACAGAGAAACCCCATCCAGAGTTTATGAGCTTGTCTGAGCT 538
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 TrpTrpLeuHisLeuGlnAlaArgAsnArgLeuArgLeuAlaValGlyLeuPheThrHis 145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 539 ATCAAGTTTACAGAACCTGAGCTGTGAGAGACAAATCTAGCATCTTCTAGAGAACTTCC 598
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 rProSerLeuAlaSerLeuSerLeuSerSerLeuLeuGlyArgLeuGlnGluGlyLe 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 599 CATTGACATCTTCAAAACTTTGAAAGAACTTAATGAGCT----- 638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 165 upheGlnIleLeuSerHisIleLeuTrpAspLeuAsnLeuGlyTrpAsnSerLeuValValle 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 639 -----CAAACTTATTC----- 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 uproAspThrValPheGlnGlyLeuGlyAsnLeuHisGlnLeuValLeuAlaGlyAsnLe 205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 651 -CATCTTTCAAAATTACCTGAGATTCTTAAATCTGACCAATCTTGAGACATTTGAGACT 709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 sLeuThrTrpLeuGlnProAlaLeuPheCysGlyLeuGlyGluLeuArgGluLeuAspLe 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


Score: 298.00 Matches: 186
 Percent Similarity: 38.87% Conservative: 95
 Best Local Similarity: 25.73% Mismatches: 258
 Query Match: 4.43% Indels: 184
 DB: 2 Gaps: 35

US-09-396-985B-3 (1-3811) x S42799 (1-662)

QY 240 TGGCGTTTATCAGGAGGAGGTTCCCTAATATTAATTATCAATGAGAGGAGTTC 299
 ||| : : : : : ||| : : : : :
 DB 26 CysIysMetValAAspIlyValVal-----SerCyGlnValLeuGlyLeu 40
 QY 300 TACAAATCCCGCAACCTCCCTTCAACCAAGAACTGAGCTTGAATATCC 359
 : : : : : ||| : : : : : ||| : : : : :
 DB 41 LeuGlnValProSerValLeuProProAspThrGluThrLeuAAspLeuSerGlyAsnGln 60
 QY 360 CTGAGGCAATTTAGGAGCTATAGCTTCTTCAAGTTTCCAGAACTGAGAGTCTGATTTA 419
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 61 LeuArgSerIleLeuAlaSerProLeuGlyPheTyThrAlaLeuArgHileuAAspLeu 80
 QY 420 TCCAGGCTGAATCCAGCAATGAGATGGGGATTCAGAGCTTACGCGCTTCTCT 479
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 81 SerThrAsnGluIleSerPheLeuGlnProGlyAlaPheGlnAlaLeuThrHileuGln 100
 QY 480 ACCTTAATATTCAGAGAAACCCCATCCAGATTAGCGCTTGTCTGAGCTA 539
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 DB 101 HisLeuSerLeuAlaHileuAsnArgLeuAlaMetAlaThrAlaLeuSerAlaGlyGlyLeu 120
 QY 540 TCAAGTTTACAGAACTGGCTGCTGTGAGACAAATCTAGCATTT----- 584
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 121 GlyProLeuProArgValThrSerLeuAAspLeuSerGlyAsnSerLeuTySerGlyLeu 140
 QY 585 CTAGAGAACTCCCATTTGCACTCTCAAACTTGAAGAATTAAATGTCCTACAAAT 644
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 141 LeuGlnIlyArgLeu---LeuGlyGlnAlaProSerLeuHileuThrLeuSerLeuAlaGlnAsn 159
 QY 645 CTATTCGAATCTTCAATTAATCTGAGAT---TTTCTAATCTGACCAATCTAGAGAC 701
 : : : : : ||| : : : : : ||| : : : : :
 DB 160 SerLeuThr-----ArgLeuThrArgHileuThrPheArgAspMetProAlaLeuGlnGln 177
 QY 702 TTGAGCTTTTCAGCAACAGATTCAAGATTATTAATGACAGACTGGCGGTTCTACAT 761
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 DB 178 LeuAspLeuHileuSerAsnValLeuMetAspIleGlnAspGlyAlaPheGlnGlyLeuPro 197
 QY 762 CAATGCCCTACTCAATCTCTCT----- 785
 : : : : : ||| : : : : : ||| : : : : :
 DB 198 ArgLeuThrHileuAsnLeuSerArgAsnSerLeuThrCysIleSerAspPheSerLeu 217
 QY 786 -----TTAGACCTGTCCCTGTAACCCCTATGAACTTTATC----- 818
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 DB 218 GlnGlnLeuArgValIleuAAspLeuSerCysAsnSerIleGlnAlaPheGlnThrAlaSer 237
 QY 819 CAACAGGTGATTTAAAGAAATTAGGCTTCATAGCTTATTAAGAAATATAT----- 872
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 DB 238 GlnProGlnAla-----GluPheGlnLeuThrTrpLeuAAspLeuArgGlnAsnIlyLeu 255
 QY 873 -----TTGATAGATTAAATGTAATGAAAACTGTATTCAGAGCTGGCTGGTTTGAA 926
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 DB 256 LeuHileuPheProAAspLeuAlaIleuProArgLeuIleTyIleuAsnLeuSerAsnAsn 275
 QY 927 GTCCATGTTTGGTTCTGGGAGATTTAGAAAT----- 959
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 DB 276 LeuIleArgLeuProThrGlyProProGlnAspSerIlyGlyIleHileuAlaProSerGln 295
 QY 960 -----GAGGAAACTTGGGAAAGTTTGACAAATCT 989
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 DB 296 GlyTrpSerAlaLeuProLeuSerAlaProSerGlyAsnAlaSerGlyArgProLeuSer 315
 QY 990 GCTTAAAGGCGCTGTGCAATTTGACATTTGAAAGAAATTCGATTTAGCATTTAGACTAC 1049
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 DB 316 GlnLeuLeuAsnLeu---AspLeuSerTyAsnGlnIleGlnLeu---IleProAspSer 333
 QY 1050 TACCTGATGATATTATTAATTT-----AATGTTTGACAAAT 1091

DB 334 PheLeuGlnHileuThrSerLeuCysPheLeuAsnLeuSerArgAsnCysLeuArgThr 353
 : : : : : ||| : : : : : ||| : : : : :
 QY 1092 GTTTCCTTCATTTTCCCTGGAGGTGATCATTTGAAAGGTTAAAGACTTTCTTATAT 1151
 : : : : : ||| : : : : : ||| : : : : :
 DB 354 PheGlnAlaArgArgLeuGlySerLeuProCysLeuMetLeuAAspLeuSerHileuAsn 373
 QY 1152 TTGGATGGCAACTTTAGAAATTAGTTAATGTAATTTGGACAGTTTCCACATTTGAA 1211
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 DB 374 ---AlaLeuGlnThrLeuGlnLeuGlyAlaArgAlaLeuGlySerLeuAAspThrLeuLeu 392
 QY 1212 CTCAATCTCTCAAAAGGCTTACTTTCATCTCCAAAGAGTGGGAATGCTTTTTCAGAA 1271
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 DB 393 LeuGln-----GlyAsnAlaLeuArgAsp 400
 QY 1272 GTT-----GATCTTCAAGCTTGTAGTTTCTAGATCTCAGATGAAAT 1313
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 DB 401 LeuProProTyThrPheAlaAsnLeuAlaSerLeuGlnArgLeuAsnLeuGlnIlyAsn 420
 QY 1314 GGGTGGAGT-----TTCAAAGGCTGCTGTCTCAAGT 1346
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 DB 421 ArgValSerProCysGlyIlyProAspGlnProGlyProSerGlyCysValAlaPheSer 440
 QY 1347 GATTTGGGCAACCAAGCTTAAAGTATTAGTCTGAGCTTCAATGGTTTATTCAGATG 1406
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 DB 441 ---GlyIleThrSerLeuArgSerLeuSerLeuValAspAsnGluIle----- 455
 QY 1407 AGTTCAAACTTTGGGCTTGAACAACATGAAATCTGAGATTTCAGCAATTCGAATTTG 1466
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 456 -----GluLeuLeuArgAlaGlyAlaPheLeuHileuThrProLeu 468
 QY 1467 AAACAATGATGATGTTTCAAGTATTCCTTCACTCAAGAAACCTATTACCTTGAAT 1526
 : : : : : ||| : : : : : ||| : : : : :
 DB 469 ThrGln-----LeuAAspLeu 473
 QY 1527 TCTCATCTACACACAGAGTTGCTTTCATAGCATCTTCAATGGCTTG---TCCAGTCTC 1583
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 DB 474 SerSerAsnProGlyLeuGlnValAlaThrGlyAlaLeuGlySerLeuGlnAlaSerLeu 493
 QY 1584 GAACTTGAATAATGGCTGCAATTTCTTTCAG-----GAAAATTCTTCCAGATATC 1637
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 DB 494 GluValLeuAlaLeuGlnGlnIlyAsnGlyLeuMetValLeuGlnValAAspLeuProCysPhe 513
 QY 1638 TTCACAGAGCTGAGAAACTTGACCTTCTGAGACTCTCTCAGTGTCAATGAGACAGTGTG 1697
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 514 IleCys-----LeuIlyArgLeuAsnLeuAlaGlnAsnArgLeuSerHileu 529
 QY 1698 TCTCAACAGCATTTAACTCACTCTCCAGCTTCAGGATCTAAATATGAGCCACAACAC 1757
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 530 -----ProAlaThrPheGlnAlaValSerLeuGlnValLeuAAspLeu---ArgAsnAsn 546
 QY 1758 TTCTTTTCATTTGATAGCTTTCCTTAAAGTGTCTGAACCTCCGAGGTTCTTGATATC 1817
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 547 SerPheSerLeu-----LeuProGlySerAlaMetCylGlyLeuGln----- 560
 QY 1818 AGTCTCAATCAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAAGTACTTA 1877
 : : : : : ||| : : : : : ||| : : : : :
 DB 561 -----ThrSerLeu 563
 QY 1878 GCTTCTTAATCTTACTCAGAAATGACTTGTGTGATCTTGAACACAGAGTTTCTGT 1937
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 564 ArgArgLeuTyIleuGlnGlyAsnProLeuSerCys---CysGlyAsn----- 578
 QY 1938 CAATGATCAAGAGCAG---AGGAGCTTGTGTGGAAGTTGAACGAATGAA----- 1988
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 579 GlyTrpLeuAlaIleGlnLeuHileuHileuGlnIlyArgValAspValaThrGlnAAspLeu 598
 QY 1989 ---TGTGCAACCTTCAATTAAGCAGGAGATCCTGTGCTGACTTTGAATATCACC--- 2042
 ||| : : : : : ||| : : : : : ||| : : : : :
 DB 599 IleCysArgPheSerSerGlnGlnIly-----ValSerLeuSerHileuValArg 614
 QY 2043 ---TGTCAAGTGAAT-----AAGACATCATTTGGTGTGCGCTCAGGCTG 2087
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```

Db      615  ProGUaaPcysGulLySGlyLeuLySasniLeaLeuLeileileuLeuThrhe 634
Qy      2088  CTTGAGATCTGTTGTAGACAGTTCTGCTCTAAGTCTATTCTACCTAGTGGTTCTT 2147
Db      635  lleuValSerAlaIleu-----LeuThrThrLeu 645
Qy      2148  GCTGCGTCG 2156
Db      646  AlaAlaCys 648
RESULT 15

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s1t-1 protein homolog - rat
 N:Alternate names: MEGF4 protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T142218
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: T14126, PMID:56360089, PMID:5639030

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 (NNK>
A:Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G
A:Experimental source: strain Sprague-Dawley; brain
A:Genetics:
A:Gene: MEQF4
A:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Alignment Scores:	
Pred. No.:	3,31e-14
Score:	298.00
Percent Similarity:	35.05%
Best Local Similarity:	22.28%
Query Match:	4.43%
DB:	2
Length:	1531
Matches:	164
Conservative:	94
Mismatch:	254
Indels:	225
Gaps:	26

US-09-396-985B-3 (1-3811) X T42218 (1-1531)

[illegible]

QY	753	GTTCATACATCAAAAGCCCCCTACTCAATCTCTTTAAAGCTGCTCCGACCCCATGAACTGAAC	812
Db	430	Ala1Leu-----ThrlenuhsleuAlaGlnAsnPro-----	440
QY	813	TTTATCCAAACAGAGTCATTTAAAGAAATTAAGGCTTCATTAAGCTGACTTAAAGAAATAT	872
Db	441	PhelIeCyAspCyAsnLeuLysTrpLeuAla-----Asp	452
QY	873	TTTGATGATGTTAAATGTATATGAAAACTTGATATTCAGAGTCTGGCTGTTTAAAGTCCAT	932
Db	453	PheluArTrgThrAsnProIleGluThr-----ThrlGlyAlaArgCysAlaSerProArg	470
QY	933	CGTTTGCTT-----CTGGAGGAAATTTAAGAAATAGAGAAACTTGAAAGCTTGGAC	983
Db	471	ArgLeuAlaAsnLysArgIleGlyGlnIleLysSer-----LysLysPheArg	486
QY	984	AAATCTGCTCTAGAGGCGCTGTGCAATTGACCATTTGAAGAAATTCGATTAGCATTA	1043
Db	487	CysSerAlaLysGlu-----GlnTrpPheIleProGlyThrGlu	499
QY	1044	GACTACTACCTCGAT-----GATATTAATGACTTATTTAAATGTTTGACA	1088
Db	500	AspTrpHisLeuAsnSerGluCysThrSerAspValAlaCysProHisLysCysArgCys	519
QY	1089	AATGTTCTTCATTTTCCCTGGTGAAGTGTCATCTATTAAGAAAGGCTTAAAGACTTTCTAT	1148
Db	520	GluAlaSerValValGluCysSerGlyLysLeuLysLeuSerLysIleProGlu--ArgIle	538
QY	1149	AATTCGAGATGGCAACATTTAGATTTAGTAACTGTAATTT-----	1190
Db	539	ProGlnSerThrTrpGluLeuArgLeuAsnAsnAsnGlnIleSerIleLeuGlnAlaThr	558
QY	1191	GGACAGTTTCCCACTTGAATGAATCTCTCAAAAGGCTTACTTTCACCTTCAACAAA	1250
Db	559	GlyLeuPheLys-----LysLeuSerHisLeuLysLysIleAsnLeuSerAsnAsnLys	576
QY	1251	GGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTTCTAGATCTCAGTAGA	1310
Db	577	-----ValSerGlnIleGluAspGlyThrPheGlu-----	586
QY	1311	AATGGCTTAGATTCAAAAGTGTGCTGTTCAAAGTATTTGGGCAACAGCAGCTTAAG	1370
Db	587	-----GlyAlaHisSerValSer	592
QY	1371	TATTTAGATCTGAGCTTCAATGATGTTATTACATGAGTTCAAC--TTCTTGAGGCTTA	1427
Db	593	GluLeuHisLeuThrAlaAsnGlnLeuGlnSerValArgSerGlyMetPheArgGlyLeu	612
QY	1428	GAACAACTAGAACACTCTGGATTTCCAGACATTTCCAAATTTGAACAAATAGAGAGTTTCA	1487
Db	613	AspGlyLeuArTrgThrMetLeuArgAsnAsnArgIleSerCysIleHisAsnAspSer	632
QY	1488	GTAATTCGATCACACAGAAACCTGATTAACCTTGACATTTCTCTACTACTCACACAGAGTT	1547
Db	633	---PheThrGlyLeuAsnArgAsnValArgLeuLeuSerLeuTrpAsnHisIleThrThr	651
QY	1548	GCTTTTCATGCGATCTTCATCAATGCGCTTCCAGCTCAGAGTCTTGAATAGCGTCGCAAT	1607
Db	652	IleSerProGlyAlaPheAspThrLeuGlnAlaLeuSerThrLeuAsnLeuLeuAlaAsn	671
QY	1608	TCCTTCCAGGAAACTTC-----	1625
Db	672	ProPheAsnCysAsnAsnCysGlnLeuAlaTrpLeuGlyAspTrpLeuArgLysArgLysIle	691
QY	1625	-----	1625
Db	692	ValThrGlyAsnProArgCysGlnAsnProAspPheLeuArgGlnIleProLeuGlnAsp	711
QY	1625	-----	1625
Db	712	ValAlaPheProAspPheAsnArgCysGlnGluGlnIleGlnGluValGlyCysLeuProArg	731
QY	1625	-----	1625

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Db      732 ProGlnGlySerProGlnGlnGlySerAlaCysLeuAspThrValValArgCysSerAsnLysHis 751
QY      1626 -----CTTCCAGATATCTCTCCACAGAGCTG----- 1649
Db      752 LeuGlnAlaLeuProLysGlyIleProLysAsnValThrGlnLeuTyrLeuAspGlyAsn 771
QY      1650 -----AGAACTTGACCTTCTGAGACCTG 1673
Db      772 GlnPheThrLeuValProGlnGlnLeuSerThrPheLysTyrLeuGlnLeuValAspLeu 791
QY      1674 TCTCAGTGCAGCTGAGAGAGTGTGTCACACAGCATTTAACTCACTCTCCAGTCTTACG 1733
Db      792 SerAsnAsnLysIleSerSerLeuSerAsnSerSerPheThrAsnMetSerGlnLeuThr 811
QY      1734 GTACTAAATATGACCCACACACAACTTTCTTTCATGTGATACGTTCTCTTAATAGTCTG 1793
Db      812 ThrLeuIleLeuSerTyrAsnAlaLeuGlnCysIleProProLeuAlaPheGlnGlyLeu 831
QY      1794 AACCTCCCTCCAGGTTCTTGATTAACGTCAATGCATTAATGACATTGCCAAAAACAGGAA 1853
Db      832 ArgSerLeuArgLeuLeuSerLeuHisGlyAsnAspValSerThrLeuGlnGlnGlyIle 851
QY      1854 CTACAGCATTTTCCAACTAGCTAGCTTTCTTAATCTTAATCTCAAGATGACATTGCTTGT 1913
Db      852 PheAlaAspVal---ThrSerLeuSerHisLeuAlaIleGlyAlaAsnProLeuTyrCys 870
QY      1914 ACTTGTAACACACAGAGTTCTCTGCAATGATCAAGACACAGAGCAGCTCTGGTGGA 1973
Db      871 AspCysHisLeuArgTrpLeuSerSerTrpValLysThrGlyTyrLys-----Gln 887
QY      1974 GTTGAACGATGGAAATGTGCACACACCTTCAGATTAAGAGGAGCATGCCGTGCTGAG---- 2029
Db      888 ProGlyIleAlaArgCysAlaGlyProProGlnMetGlnGlyLysLeuLeuLeuThrThr 907
QY      2030 -----TTTGAATATCACTGTCAATGATGAATAGACCATCATTTGCTGTCGCT 2077
Db      908 ProAlaLysLysPheGln-----CysGlnGly 916
QY      2078 CCT-----CAGTGTGCTTGATGATCTGTTGTAGCAGT 2110
Db      917 ProProSerLeuAlaValGlnAlaLysCysAspProCysLeuSerSer 932
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Search completed: March 29, 2005, 17:33:36
Job time : 100.695 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 205.959 Seconds
(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724
Sequence: 1 acaggagccactgctctcac.....ttcactgacaggaacta 3811

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p model -DEV=xjh
-O=/cgn2_1/USFTO_spool/US0939685B/runcat_28032005_155743_21146/app_query.fasta_1.85098
-DB=UniProt_03 -QFMT=faatan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US0939685B @CGN 1.1 5213 @runcat_28032005_155743_21146 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4325	64.3	839	1	TLR4_HUMAN
2	4311	64.1	839	1	TLR4_PANPA
3	4290	63.8	837	2	Q8SP88
4	4162	61.9	828	1	TLR4_PONPY
5	4013	59.7	826	1	TLR4_PAPAN
6	3312	49.3	843	1	TLR4_HORSE
7	3291.5	49.0	841	1	TLR4_BOVIN
8	3288.5	48.9	841	2	Q8SQD5
9	3286.5	48.9	841	2	Q8WCD5
10	3283.5	48.8	843	1	TLR4_FELCA
11	3277.5	48.7	841	2	Q6WCD4
12	3167.5	47.1	841	2	TLR4_PIG
13	3072.5	45.7	839	2	Q8MTD2
14	2987	44.4	838	1	TLR4_CRIGR
15	2850.5	42.1	835	1	TLR4_RAT
16	2822	42.0	835	2	Q8K2T5

17	2817	41.9	835	1	TLR4_MOUSE
18	2206	32.8	636	2	Q8SOH3
19	1828.5	27.2	843	2	Q7ZTG5
20	1276.5	19.0	819	2	Q6TS41
21	1265.5	18.8	817	2	Q6NV08
22	834.5	12.4	258	2	Q70DK4
23	693	10.3	961	2	Q76CT9
24	686	10.2	945	2	Q80IF9
25	685	10.2	940	2	Q8T753
26	685	10.2	961	2	Q76CT7
27	667.5	9.9	991	2	Q6R5N8
28	656.5	9.8	661	1	C180_MOUSE
29	641.5	9.5	784	2	Q6YGD2
30	638.5	9.5	661	2	Q8C251
31	633.5	9.4	973	2	Q6KCC7
32	619.5	9.2	661	1	C180_HUMAN
33	617.5	9.2	784	1	TLR2_MOUSE
34	616.5	9.2	784	2	Q8K3D9
35	613.5	9.1	784	2	Q811T5
36	602.5	9.0	784	1	TLR2_HUMAN
37	601.5	8.9	661	2	Q7YRL4
38	601.5	8.9	785	2	Q761Z4
39	600.5	8.9	785	2	Q6TN21
40	597	8.9	784	2	Q6T752
41	595.5	8.9	784	1	TLR2_MACFA
42	591.5	8.8	784	1	TLR2_CRIGR
43	580.5	8.6	1032	1	TLR2_MOUSE
44	577.5	8.6	785	2	Q689D1
45	576	8.6	781	1	TL22_CHICK

ALIGNMENTS

RESULT 1
TLR4_HUMAN
ID TLR4_HUMAN STANDARD; PRT; 839 AA.
AC 000206; Q9UK78; Q9UM57;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll-like receptor 4 precursor (Toll).
GN Name=TLR4;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlburt P., Janeway C.A. Jr.
RT "A human homologue of the Drosophila Toll protein signals activation
RT of adaptive immunity".
RL Nature 388:394-397(1997).
[2]
RP SEQUENCE OF 41-839 FROM N.A.
RC TISSUE=Petal liver, lung, and Placenta;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.586;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll".
RL Proc. Natl. Acad. Sci. U.S.A. 95:586-593(1998).
[3]
RP SEQUENCE FROM N.A., AND VARIANTS GUY-299 AND ILE-399.
RX MEDLINE=20558910; PubMed=11104518;
RA Shulimova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4)".
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
[4]
RP SEQUENCE FROM N.A., AND VARIANTS GUY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;
RA Atbour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,

FT VARIANT 299 299 /FtId=VAR_018730.
 D -> G (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986790).
 /FtId=VAR_012739.
 N -> S
 FT VARIANT 329 329 /FtId=VAR_018731.
 T -> I (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986791).
 /FtId=VAR_012740.
 F -> L
 FT VARIANT 443 443 /FtId=VAR_018732.
 E -> K
 FT VARIANT 474 474 /FtId=VAR_018733.
 O -> H
 FT VARIANT 510 510 /FtId=VAR_018734.
 K -> R
 FT VARIANT 694 694
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 95.45% Mismatches: 0
 Query Match: 64.32% Indels: 40
 DB: 1 Gaps: 1
 US-09-396-985B-3 (1-3811) x TLR4_HUMAN (1-839)
 QY 45 ATGATTCGCTCCCTGGGCGCTGGGAGCTGTGATCCGACCATGGGCTTCTCTCTGTC 104
 Db 1 MetMetSerLaserTrigLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 105 GTGAGACCAAGAACTGGGAGCCCTGTGGTGGAGACTTGGCCCTAAACACACAGAAAGAGC 164
 Db 21 ValArgProGluSerTrpGluProCysVal----- 30
 QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCTTCAGCCCTTCACCCGATTCATTG 224
 Db 30 ----- 30
 QY 225 CTTCTTGCTAAATGCTGCCCTTTATCAGGAGGTGGTCTTAATTAATTACTTATCAATGC 284
 Db 31 -----GluValValProAsnIleThrTyrglnCys 40
 QY 285 ATGAGCTGAATTTCTACAAATATCCCGACACCTCCCTTCTCAACCAAGAACTGGAGC 344
 Db 41 MetGluLeuAsnPheTyrlsIleProAsnLeuProPheSerThrTyrsAsnLeuAsp 60
 QY 345 CTGAGCTTAATCCCTGAGGACATTAGGAGCTATAGCTTCTTCAGTTTCCGAACTG 404
 Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheSerPheProGluLeu 80
 QY 405 CAGGTCTGATTTATCCAGGTGTGAATTCAGACATTTAGAGATGGGGCATATCGAGC 464
 Db 81 GluValLeuAsnPheSerArgCysGluIleGlnThrIleGluAsnGlyAlaTyrglnSer 100
 QY 465 CTAAAGCACCTCTCACTTAATATTTAGACAGAAACCCATCCAGAGTTTAAAGCCCTGGGA 524
 Db 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 525 GCGTTTTCGACTATCAAGTTTACAGAGCTGGTGGCTGTGGAGCAAAATCTAGCATCT 584
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCATTTGACACTTCGAAACCTTTGAAAGAACTTATGTGGCTCAAT 644
 Db 141 LeuGluAsnPheProIleGlyHisLeuTyrlsThrLeuGlyLeuLeuAsnValAlaHisAsn 160
 QY 645 CTTATCCAACTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTG 704
 Db 161 LeuIleGlnSerPheTyrsLeuProGluTyrlsPheSerAsnLeuThrAsnLeuGluHisLeu 180
 QY 705 GACCTTTCAGAACAAAGATTCAAGATTTATTTGACAGACTTGGGGTTCTACATCAA 764
 Db ----- 764

Db 181 AsnLeuSerSerAsnIlyHisIleGlnSerIleTyrlsCysThrAsnLeuArgValLeuHisGln 200
 QY 765 ATGCCCTCTCAATCTCTCTTATAGACCTGTCCCTGACCCCTTATGAACTTATCAACCA 824
 Db ----- 824
 Db 201 MetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GGTGCAATTAAGAAATTAAGCTTCAAGCTGACTTCAAGAAATTAATTAATTTGATAGTTTA 884
 Db 221 GlyAlaPheLeuSerIleIleArgLeuHisIlybLeuThrLeuArgAsnAsnPheAsnSerLeu 240
 QY 885 AATGTATGAAAATCTGTATTTCAAGCTGTGGCTGTTTGAAGATTCATGCTTGGTCTGC 944
 Db 241 AsnValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 945 GGAGAAATTAAGAAATTAAGAAATCTGAAAAGTTTGAACAAATCTGCTGAGAGGGCTGC 1004
 Db 261 GlyIlePheArgAsnGluGlyAsnLeuGluTyrlsPheAsnIlybSerAlaLeuGluGlyLeu 280
 QY 1005 TGCATTTTGAACCAATTAAGAAATTCGATTAAGCATTAAGTACCTGATGATATT 1064
 Db 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrlsLeuAspTyrlsLeuAsnAspIle 300
 QY 1065 ATGACTTAATTAATGTTTGAACAAATGTTTCTCAATTTCCCTGTGAGTGTGACTATT 1124
 Db 301 IleAsnLeuPheAsnCysLeuThrAsnValIleSerSerPheSerLeuValIleValThrIle 320
 QY 1125 GAAAGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTTAATTAAGTATCTG 1184
 Db 321 GluArgValIlybAsnPheSerTyrlsAsnGlyTyrlsGlnHisLeuGluLeuValAsnCys 340
 QY 1185 AAATTTGACAGCTTCCCATTTGAACCTCAATCTCTGAAAAGCTTACTTCACTTCC 1244
 Db 341 IlybPheGlyGlnPheProThrLeuTyrlsLeuTyrlsSerLeuIlybArgLeuThrPheThrSer 360
 QY 1245 AACAAAGTGGGAATGCTTTTTCAGAAAGTTATTCAGAAAGCTTGAAGTTTCAAGTCTC 1304
 Db 361 AsnIlybGlyGlyAsnAlaPheSerGluValAsnLeuProSerLeuGluIlePheLeuAsnLeu 380
 QY 1305 AGTAAAGATGCTTGAAGTTTCAAGGTTTCTGTTCAAAAGTATTTTGGGACAAACAGC 1364
 Db 381 SerArgAsnGlyLeuSerPheIlybGlyCysCysSerGlnSerAsnPheGlyThrThrSer 400
 QY 1365 CTAAAGATTTTGAATGCTTGAAGTTTCAAGGTTTATTAACCATGATGTTCAAACTTCTGGAGC 1424
 Db 401 LeuTyrlsTyrlsLeuAsnLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTAGAACCAATGAACATCTGAGATTTCCAGACTTCCAAATTTGAACAAATGAAGTGA 1484
 Db 421 LeuGluGlnLeuGluHisIleuAsnPheGlnHisSerAsnLeuIlybGlnMetSerGluPhe 440
 QY 1485 TCAATTTTCTTATCACTGAGAAACCTCATTTACCTTGAATTTCTGATATCTACACCA 1544
 Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyrlsLeuAspIleSerHisThrHisThrArg 460
 QY 1545 GTTGCTTCAATGGGATCTTCAATGCTTGTCCAGCTGAGAGTCTTGAAGATGCTGGC 1604
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuIlybSerAlaGly 480
 QY 1605 AATTTCTTCCAGAGAAACTTCTCCATATCTTCAACAGACTGAGAAATCTGACCTTC 1664
 Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1665 CTGACCTTCTCAAGTGTCAATCTGAGCAGTTGTCTCAACAGCAATTTAATCACTCTGC 1724
 Db 501 LeuAsnLeuSerGlnCysGlnIleuGluGlnIleuSerProThrAlaPheAsnSerLeuSer 520
 QY 1725 AGTCTTCAAGGTACTAAATATGAGCAACAACTTTTCAATTTGAGTACGTTTCTTAT 1784
 Db ----- 1784
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAsnSprThrPheProTyrls 540
 QY 1785 AAGTCTGAACTCTCCCTCAGGTTCTTGAATTAACGTTCAATCAATATGACTTCCAA 1844
 Db 541 IlybCysLeuAsnSerLeuGlnIleuAsnTyrlsSerLeuAsnHisIleMetThrSerIlyb 560

QY 1845 AAACAGAACTACAGATTTTCCAGATGCTGATCTTTCTTAATCTTACGAGATGAC 1904
 DB 561 LysGlnGlnLeuGlnIlnIspheProSerSerLeuAlaPheLeuGlnLeuIlnGlnIlnAsp 580
 QY 1905 TTTGCTTGACTTGTAAGACACAGATTTCTTGCAATGATGATGACAGACAGAGCTC 1964
 DB 581 PheAlaCysThrCysGlnIlnIspheGlnSerPheLeuGlnIlnIleGlnAspGlnIlnLeu 600
 QY 1965 TTGGTGAAGTTGAAGATGGAATGTGCAACCTTCAGATTAAGAGAGGAGCTGTG 2024
 DB 601 LeuValGlnValGlnIlnIspheGlnCysAlaIlnIspheSerAspGlnIlnIleTyr 620
 QY 2025 CTGAGTTTGAAATTCACCTGTGATGATGATTAAGACCATCATCTGGTGTGCTGCTCAG 2084
 DB 621 LeuSerLeuGlnIlnIlnIspheGlnIlnIspheGlnIlnIleGlnIlnIspheValLeuSer 640
 QY 2085 GTGCTTGATGATCTGTGTGATGAGATGCTGTGCTATGATGATGATGATGATGCTT 2144
 DB 641 ValLeuValValSerValValAlaValLeuValTyrIlnIspheThrPheIlnIspheLeu 660
 QY 2145 CTGCTGCTGCTGCTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2204
 DB 661 LeuAlaGlnCysIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIsphe 680
 QY 2205 TCAAGCAGAGATGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2264
 DB 681 SerSerGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 700
 QY 2265 CCTCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2324
 DB 701 ProProPheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIsphe 720
 QY 2325 AACATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2384
 DB 721 AsnIlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 740
 QY 2385 TTGATCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2444
 DB 741 PheIlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 760
 QY 2445 AGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2504
 DB 761 SerSerArgAlaGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 780
 QY 2505 CACGAGGTGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2564
 DB 781 GlnGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 800
 QY 2565 GTGCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2624
 DB 801 ValLeuGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 820
 QY 2625 TGGATTCAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2681
 DB 821 TrpAsnProGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGlnIlnIspheGln 839
 RESULT 2
 TLR4_PANPA
 ID TLR4_PANPA STANDARD; PRT; 839 AA.
 AC O9TND;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE TOLL-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 NCBI_TaxID=9597;
 RX MEDLINE=20558910; Pubmed=11104518;

RA Smitnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.,
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 RT locus (TLR4)";
 RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
 CC -1- FUNCTION: Cooperates with MyD88 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC the intracellular domain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF179220; AA05320.1; -.
 DR EMBL; AF179219; AA05320.1; JOINED.
 DR EMBL; AF179219; AA05320.1; JOINED.
 DR HSSP; Q15399; LFV.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macrophage activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:negative regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 DR GlycoProtein; Immune response; Inflammatory response;
 KW leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT CHAIN 1..23
 FT SIGNAL 1..23
 FT STAN 24..839
 FT DOMAIN 24..631
 FT TRANSMEM 632..652
 FT DOMAIN 653..839
 FT REPEAT 52..76
 FT REPEAT 77..100
 FT REPEAT 101..124
 FT REPEAT 125..149
 FT REPEAT 150..173
 FT REPEAT 174..197
 FT REPEAT 203..225
 FT REPEAT 226..252
 FT REPEAT 277..303
 FT REPEAT 307..330
 FT REPEAT 332..350
 FT LRR 11..

FT REPEAT 351 372 LRR 12.
 FT REPEAT 373 398 LRR 13.
 FT REPEAT 400 421 LRR 14.
 FT REPEAT 422 445 LRR 15.
 FT REPEAT 447 469 LRR 16.
 FT REPEAT 470 494 LRR 17.
 FT REPEAT 495 518 LRR 18.
 FT REPEAT 520 541 LRR 19.
 FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 839
 Score: 4311.00 Matches: 836
 Percent Similarity: 95.34% Conservative: 2
 Best Local Similarity: 95.11% Mismatches: 1
 Query Match: 64.11% Indels: 40
 DB: 1 Gaps: 1

US-09-396-985b-3 (1-381) x TLR4_PANPA (1-839)

QY 45 ATGATGCTGCTGCGCCCTGGCGCTGGAGACTGTGATCCAGCGCATGCGCTTCTCTCTGC 104
 |||||
 DB 1 MeMeSerIaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 105 GTGAGACGAGAAAGCTGGAGCCCTGGCTGGAGACTGGCCCTTAACACACAGAAAGC 164
 |||||
 DB 21 ValArgProGlnPheSerThrGlnProCysVal----- 30
 QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCCTTACCCGATTCATG 224
 |||||
 DB 30 ----- 30
 QY 225 CTTCTTCTAAAGCTGCGCTTTTATGACGAGGTGCTTCTTAATATTACTTATCAATGC 284
 |||||
 DB 31 -----GluValValProAsnIleThrTyGlnCys 40
 QY 285 ATGAGCTGAATTTCTCAAAATGCCGAGAACTCCCTTCTCAACAGAAAGCTGAGC 344
 |||||
 DB 41 MetGluLeuAsnPheTyLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 345 CTGAGCTTAAATCCCTGAGGACTTTAGGAGCTATAGCTTCTCACTTCCAGAACTG 404
 |||||
 DB 61 LeuSerPheAsnProLeuAlaGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 80
 QY 405 CAGGCTGTGATTTATTCAGAGTGTGAATCCAGAACTGAAGTGGAGCATATCAGAGC 464
 |||||
 DB 81 GluValLeuAsnLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyGlnSer 100
 QY 465 CTAGACCACTCTTACTTAATATTGACAGAAACCCATCCAGACTTTAGCCCTGGA 524
 |||||
 DB 101 LeuSerThrLeuSerThrIleLeuThrGlyAsnProIleGlnIleSerLeuAlaLeuGly 120
 QY 525 GCCTTTCTGAGTATCAAGTTTACAGAAAGCTGTGCTGTGAGAGAAATCTAGCATCT 584
 |||||
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAAATGTGGCTACAACT 644
 |||||
 DB 141 LeuGlnAsnPheProIleGlyIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIle 160

QY 645 CTTATCCAACTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 704
 |||||
 DB 161 LeuIleGlnSerPheIleuSerProGlnIlePheSerAsnLeuThrAsnLeuGlnIleLeu 180
 QY 705 GACCTTTCCAGAAACAAAGATTCAAGATTATTTATGACAGACTTGGCGGTTCTACATCA 764
 |||||
 DB 181 AspLeuSerSerAsnIleGlnIleSerIleTyCysThrAspLeuArgValIleHisGln 200
 QY 765 ATGCCCTACTCAATCTCTCTTGAACCTGCTCCCTGAGCCCTTGAACCTTATCCAGCA 824
 |||||
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GTGCAATTTAAAGAAATTAAGCTTCAATGCTGATTAAGAAATAATTTGATAGTTTA 884
 |||||
 DB 221 GlyAlaPheIleGlnIleArgLeuIleIleLeuIleLeuIleLeuIleLeuIleLeuIle 240
 QY 885 AATGTAATGAAAATTGTATTCAGAGTGTGGCTGTGTTTGAAGTCCATCGTTGGTTCTG 944
 |||||
 DB 241 AsnValMetIleThrCysIleGlnIleLeuAlaGlyLeuGlnValHisArgLeuValLeu 260
 QY 945 GAGAAATTTGAATGAGAAAGAACTTGAAGAACTTTGACAAATCTGCTTGAAGAGGCGCTG 1004
 |||||
 DB 261 GlyGlnPheArgAsnGlnIleGlnIleLeuGlnIleLeuPheAspIleSerAlaLeuGlnGlyLeu 280
 QY 1005 TGCATATTTGACCAATGAGAAATTCGATTAAGTACTTACTTACTGATGATATTT 1064
 |||||
 DB 281 CysAsnLeuThrIleGlnIleGlnIlePheArgLeuAlaIleTyLeuAspIleLeu 300
 QY 1065 ATTGACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTTCCCTGGTGAAGTGAATTT 1124
 |||||
 DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1125 GAAAGGCTAAAGACTTTCTTAATTTTGGAGTGGCAATTTGAATTAAGTTAATGTT 1184
 |||||
 DB 321 LysSerValIleAspPheSerIleTyAsnPheGlyTyProGlnIleIleuGlnLeuValAsnCys 340
 QY 1185 AAATTTGACAGTTTCCCATTTGAACCTGAATCTCTCAAAAGGCTTACTTCACTTCC 1244
 |||||
 DB 341 LysPheGlyGlnPheProThrLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 360
 QY 1245 AACAAAGTGGAAATGCTTTTTCAGAAAGTGAATCTTCAAGCTTGAATTTCTGATATCTC 1304
 |||||
 DB 361 AsnIleGlyIleAsnAlaPheSerGlnValAspLeuProSerIleuGlnPheLeuAspLeu 380
 QY 1305 AGTAGAAATGCTTGAATTTCAAAAGTGTGCTTCTCAAAAGTATTTGGAGCAACAGC 1364
 |||||
 DB 381 SerArgAsnGlyLeuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1365 CTAAAGTATTTAGATCGAGCTTCAATGAGTGTATTTACATGAGTTCAAACTTCTGGGC 1424
 |||||
 DB 401 LeuIleTyIleuAsnLeuSerPheAsnGlyValIleIleIleIleIleIleIleIleIleIle 420
 QY 1425 TTAGAACTAGAAACATCTGATTTTCAGCACTTCAATTTGAAACAAATGAGTGAATTT 1484
 |||||
 DB 421 LeuGlnIleuGlnIleuIleuAspPheGlnIleSerAsnLeuIleuIleuIleuIleuIleuIleu 440
 QY 1485 TCGATTTCTATACCTGACGAAACCTCATTTACTTCACTTCACTTCACTTCACTTCACTTCA 1544
 |||||
 DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAsnIleSerAsnIleSerAsnIleSerAsn 460
 QY 1545 GTTGCTTCAATGAGCACTTCAATGAGCTTCAATGAGCTTCAATGAGCTTCAATGAGCTTCA 1604
 |||||
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerIleuGlnValIleuIleuIleuIleuIleu 480
 QY 1605 AATTTCTTCCAGAGAAATCTTCCATGATATCTTCCAGAGCTTGAAGAACTTGAACCTTC 1664
 |||||
 DB 481 AsnSerPheGlnIleuAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 500
 QY 1665 CTGAGCTCTCTCAAGTCACTGAGAGCACTGTGTTCCAAACAGCACTTAACTCACTTCC 1724
 |||||
 DB 501 LeuAspLeuSerGlnCysGlnIleuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 520
 QY 1725 AGTCTTCAGGTATTAATATGAGCCCAACAACTTCTTTCAATGATGATGTTCTCTTAT 1784

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Db      521 SerLeuGlnValLeuSerMetSerHisAspAsnPhenSerLeuSerThrProTyr 540
QY      1785 AAGTGTCTGAATCCTCCAGGTTCTTGATTACAGTCAATCAATAGACTTCCAA 1844
Db      541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
QY      1845 AAACAGGAATACAGACTTTTCCAGAGTCTGAGCTTTCTTAATCTTACTACAGAAATGAC 1904
Db      561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuTrpGlnAsnAsp 580
QY      1905 TTTGCTGTGACTTGTGAAACACAGAGTTTCTGCAATGATGACAGACAGAGAGCTC 1964
Db      581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnAspGlnLeu 600
QY      1965 TTGGTGAAGTTGAACGAATGGAATGTGGCAACCTTCAGATAGACAGGGAGCTGTG 2024
Db      601 LeuValGlnValGlnAspMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 620
QY      2025 CTGAGTTGAATATCACTGTGCAAGTAATAGACCATCTAGTGTGTGCTGCTGACT 2084
Db      621 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLeuSer 640
QY      2085 GTGCTGTGATATCTGTGTGAGAGTTCTGAGTCTATAGTTCTATTTTCACTGATCTT 2144
Db      641 ValLeuValAlaSerValAlaAlaValLeuValTyrLysPheTyrPheHisIleMetLeu 660
QY      2145 CTTGCTGCTGTCATTAAGTATGTGTAAGGAGGAAAAACCTATGATGCTGTTTATCTAC 2204
Db      661 LeuAlaGlnCysIleLysTyrGlnTyrArgGlnGlnAsnIleTyrAspAlaPheValIleTyr 680
QY      2205 TCAAGCCAGATAGAGACTGGTGAAGGAATGAGTACTAATGAATTTAGAAAGAGGGGTG 2264
Db      681 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 700
QY      2265 CTTCCATTTAGAGCTGTGCTCTTCACTACAGAGACTTTATCCCGGTGTGGCATTGTGCTCC 2324
Db      701 ProProheGlnLeuGlnLysLeuHisIleTyrGlnAspPheIleProGlnValAlaIleAla 720
QY      2325 AACATCATCATGAAGGTTTCCATTAAGACCGAAAGGTGATGTTGTGTGTGCTCCAGAC 2384
Db      721 AsnIleIleHisGlnGlnPheHisIleLysSerArgLysValIleValIleValIleSerGlnHis 740
QY      2385 TTATCCAGAGCCGCTGTGATCTTGAATATGATGATGATGATGATGATGATGATGATGAT 2444
Db      741 PheIleIleSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnTrpGlnPheLeu 760
QY      2445 AGCAGTGTGCTGATCATCTTTCATTTCTGTCAGAGAGTGAAGAACCTGTCTCAG 2504
Db      761 SerSerArgAlaGlnIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 780
QY      2505 CAGAGAGTGAAGCTGTACCGCTTCTCAGCAGAGAACCTTACCTGAGTGGAGAGACAGT 2564
Db      781 ArgGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLysPse 800
QY      2565 GTCTGTGGGGGGACATCTTCTGAGAGACATCGAAGAACCTGCTGATGATGATGATGAT 2624
Db      801 ValLeuGlnTyrGlnHisIlePheTrpArgArgLeuArgLysAlaLeuAspGlnLysSer 820
QY      2625 TGGATCCAGAAAGAGAGTGGAGTCAAGAGATGCAATTTGCGAGAGAGACATCTATC 2681
Db      821 TrpAsnProGlnGlnTyrHisValGlnTyrGlnCysLeuSerTrpGlnGlnAlaThrSerIle 839

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RESULT 3

Q8SPB8 ID Q8SPB8 PRELIMINARY; PRT; 837 AA.

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AC      08SPB8;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Toll-like receptor 4.
GN      Name=TLR4;
OS      Gorilla gorilla (gorilla).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX      NCBI_TaxID=9593;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21405531; PubMed=11514453;
RA      Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT      "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RL      in humans".
RL      Genetics 158:1657-1664(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF497565; AAM18617.1; -
DR      EMBL; AF497563; AAM18617.1; JOINED.
DR      EMBL; AF497564; AAM18617.1; JOINED.
DR      HSSP; O60603; 1077.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; F:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macr cell activation; ISS.
DR      GO; GO:0045571; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR_Cterm.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF01463; LRRT; 1.
DR      Pfam; PF00560; LRR_1; 10.
DR      Pfam; PF01582; TIR_1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRRT; 1.
DR      SMART; SM00369; LRR_Typ; 2.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;

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Alignment Scores:

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Pred. No.: 0 Length: 837
Score: 4290.00 Matches: 832
Percent Similarity: 94.99% Conservative: 3
Best Local Similarity: 94.65% Mismatches: 2
Query Match: 63.80% Indels: 42
DB: Gaps: 1

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US-09-396-985b-3 (1-3811) x Q8SPB8 (1-837)

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QY      45 ATATGTCTGCTGCGGCTGTGGACTCTGATCCAGCAATGGCTTCTCTCTGCTC 104
Db      1 MetMetSerAlaSerArgLeuAlaGlnTyrLeuIlePheProAlaMetAlaPheLeuSerCys 20
QY      105 GTGAGCCGGAAGAGCTGGAGGCGCTGCGTGAAGACTTGCGCCCTAAACACAGAGAGAGC 164
Db      21 ValArgProGlnSerTrpGlnProCys----- 29
QY      165 TGGCATGAAGAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCTTCAACCCGATTCATTG 224
Db      29 ----- 29
QY      225 CTCTGTGCTAAATGCTGCGCTTTTATCAAGAGGTGGTTCCTTAATATTACTTATCAATGC 284
Db      30 -----ValValProAsnIleThrTyrGlnCys 38

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285 ATGAGCTGAATTTCTACAAAATCCCGACAACTCCCTTCACCAACAGAACTGGAC 344
Db MetGluLeuAsnProPheTyrLeuProAsnLeuProPheSerThrLeuAsnLeuAsp 58
345 CTGAGCTTTATCCCTGAGGACATTTGAGGAGCTATAGCTTCTTACGTTTCCCGAACTG 404
Db LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 78
405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATTCAGAGC 464
Db GluAlaLeuAspLeuSerArgCysGluLeuGlnThrIleGluAspGlyAlaTyrGlnSer 98
465 CTAAAGCACTCTCTCACTTAATATGACAGAAAACCCCATCCAGAGTTTAAAGCCCTGGA 524
Db LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 118
525 GCCCTTTCTGACATATCAAGTTTACAGAAAGCTGGTGGTGGAGACAAATCTAGCATCT 584
Db AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 138
585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAATGGCTCACACAT 644
Db LeuGluAsnProIleGlyHisLeuGlySerThrLeuGlySerGluLeuAsnValAlaHisAsn 158
645 CTATCCAACTTTCAATTAACCTGATATTTTCTAATCTGACCAATCTAGACACTGTG 704
Db LeuIleGlnSerPheLeuProGluTyrPheSerAsnLeuThrAsnLeuGluTyrLeu 178
705 GACCTTTCCAGCAACAAGATTCAAAAGTATTTATTTGACACAGACTTGGGGGTTTCAATCAA 764
Db AspLeuSerSerAsnLeuGlyLeuGlnSerIleTyrCysThrAspLeuAlaLeuHisGln 198
765 ATGGCCCTACATCTCTCTTTAGACCTGTCGCTGAAACCTTAGAACTTTATTCACACA 824
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825 GGTGCACTTTAAGAAATTAAGCTTCATAGCTGACTTAAGAAATTAATTTGATAGTTTA 884
Db GlyAlaPheLeuGlnIleArgLeuHisAlaLeuThrLeuArgAsnAsnProAspSerLeu 238
885 AATGTATGAAAACCTTGATTTCAAGGCTGCTGGCTGGTTTGAAGTCCATCGTTGGTCTG 944
Db AsnAlaMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValAlaGArgLeuValLeu 258
945 GGAGAATTTGAATGAAGAACTTGAAGAAAGTTTGAACAATGCTGCTTAGAGGGCTG 1004
Db GlyGluPheArgAsnGluGlyAsnLeuGlnLeuPheAspLeuSerAlaLeuGluGlyLeu 278
1005 TGCATTTGACATTTGAAGAATTCGATAGCATATTAAGACTACTGATGATATTT 1064
Db CysAsnLeuThrIleGluGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 298
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Db GluArgValAlaAspPheSerTyrAsnPheGlyTyrPheGlnHisLeuGluLeuValAsnCys 338
1185 AAATTTGACAGTTTCCCATTTGAACAATCTCAAAAGGCTTACTTCACTTCC 1244
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Db SerArgAsnGlyLeuSerPheLeuGlyCysCysSerIleAspPheGlyThrThrSer 398
1365 CTAAAGTATTTAGATCTGAGCTTCAATGCTGTTATTAACCATGAGTTCAAACTTCTTGGC 1424

399 LeuTyrTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 418
1425 TTAGAACAACATGAAACATCTGGAATTTCCACATTTCCAAATTTGAAACAAATGAGAGATT 1484
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1485 TCAGTATTTCTATCACTCAGCAAAACCTTATTAACCTTGAATTTCTATTACTCAACAGCA 1544
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1545 GTTGCTTTCAATGGCATCTTCAATGGCTGTCCAGTGTCCAGAGCTTGAATGAGTGGC 1604
Db ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuGlyMetAlaGly 478
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1665 CTGAGCTCTCTCAGTGTCAACTGAGACAGTGTCTCCAAAGCATTTAACTCACTCTCC 1724
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1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTTACAGTCTCAATCAATCAATGACTTCCAA 1844
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1845 AAACAGGAACATGACATTTTCCAGAGTCTGAGCTTTCTTAATCTTACTGCAAGAAC 1904
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1905 TTGCTTTGATCTTGTGAACACAGAGTTTCTGCAATGATGATCAAGACAGAGGACGCTC 1964
Db PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnAlaGlnLeu 598
1965 TTGCTGGAAGTTGAAGAAATGGAATGTGCAACCTTCAATTAAGACAGGAGGACGCTGTG 2024
Db LeuValGluValAlaGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 618
2025 CTGAGTTTGAATATCACTGTCAGATGAAATPAACACATCTTGGTGTGCGTCTGAGT 2084
Db LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLeuSer 638
2085 GTGCTGTAGTATCTGTTGAGAGTTCTGGTCTATTAAGTTCTAATTTTCACTGATGCTT 2144
Db ValLeuValValSerValValAlaValLeuValTyrLeuPheTyrPheHisLeuMetLeu 658
2145 CTGCTGGCTGATTAAGTATGAGTGAAGTGAAGAAACATCTATGATGCTTTGTATCTAC 2204
Db LeuAlaGlyCysIleLeuTyrGlyArgGlyGluAsnValTyrAspAlaPheValIleTyr 678
2205 TCAAGCGAGATGAGAGCTGGGTGAAGAAAGTGAAGTGAAGAAATTTAAGAAAGAGGCTG 2264
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2265 CTTCCATTTCAAGCTGCTGCTTCACTACAGAGCTTATTTCCCGGTGGGCACTTGGCTGC 2324
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Db 759 SerSerArgAlaGlyIleIleIleValLeuGlnValGlnValThrLeuLeuArg 778
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QY 2625 TGGATTCAGAGAAACAGTGGGATCAGATTCAGATTCGAGAGAGAAATCATTC 2681
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RESULT 4
TLR4_PONPY STANDARD; PRT; 828 AA.
AC QSPSP9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxId=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1405531; Pubmed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans.";
RL Genetica 158:1657-1664(2001).
CC -|- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -|- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TIRAP via
CC binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the Toll-like receptor family.
CC -|- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF497562; AAM18616.1; -
CC EMBL; AF497560; AAM18616.1; JOINED.
CC EMBL; AF497561; AAM18616.1; JOINED.
CC HSP; O66003; 1PTW.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004688; P:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:mac cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Tyr.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 12.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00369; LRR_Tyr; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 828
FT DOMAIN 24 629
FT TRANSMEM 630 650
FT DOMAIN 651 828
FT REPEAT 50 74
FT REPEAT 75 98
FT REPEAT 99 122
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FT REPEAT 148 171
FT REPEAT 172 195
FT REPEAT 201 223
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FT CARBOHYD 628 628
SQ SEQUENCE 828 AA; 94340 MW; 51AC0964E5970FDF CRC64;
Alignment Scores:
Pred. No.: 828
Score: 8.2e-306
Percent Similarity: 4162.00
Best Local Similarity: 93.79%
Query Match: 92.87%
DB: 61.90%
Length: 828
Matches: 808
Conservative: 8
Mismatch: 12
Indels: 42
Gaps: 1
US-09-396-985b-3 (1-3811) x TLR4_PONPY (1-828)
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Db 1 MetMetSerHisLeuValArgLeuValGlnValThrLeuIleProHisMetHisLeuSerCys 20
QY 105 GTGAGACAGAGAAAGCTGGAGAGCCCTGCGGAGAGCTTGCCCTTAAACACAGAGAGAGC 164
Db 21 ValArgProGlnSerThrPgluPProCys----- 29
QY 165 TGGCATGAAACCCAGAGCTTTTCAAGACTCCGAGAGCTCAGCCCTTCAACCCGATTCATTG 224
Db 29 ----- 29

QY 225 CTTCTGCTAAATGCTGCCGTTTATACGAGAGTGCTTCTAAATATTACTTATCAATGC 284
 Db 30 -----ValValProanilleThrTyGlnCys 38
 QY 285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 344
 Db 39 MetGluLeuAnPheTyLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 58
 QY 345 CTGAGCTTATCCCTGAGGACTTTAGGAGCTATACCTTCTCAGTTCCCGAACTG 404
 Db 59 LeuSerPheAnProLeuArgIleLeuGlySerTySerPhePheSerPheProGluLeu 78
 QY 405 CAGGTGCTGAATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATTCAGAGC 464
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 QY 465 CTAGGCCACTCTCTCACTTAAATTTGACAGAGAAACCCCATCCAGAGTTTACCCCTGGGA 524
 Db 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
 QY 525 GCCCTTTCTGACTATCAAGTTTACAGAGCTGGTGGTGGAGACAAATCTAGCACT 584
 Db 119 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 138
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAATTTATGTGGCTCACAAAT 644
 Db 139 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 158
 QY 645 CTTATCCAACTTTTCAAAATTACTGAGTATTTTCTAACTGACCAATCTAGACCACTTG 704
 Db 159 LeuIleGlnSerPheLysLeuProGluTyPheSerAsnLeuThrAsnLeuGluHisLeu 178
 QY 705 GACCTTTCCAGCAACAAGATTCAAGATTATTTGACAGACAGCTGGGGCTTCAATCA 764
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 QY 765 ATGCCCTACTCAATCTCTCTTTAGACCTGCTCCCTGAACCTTATGAACTTATCAACA 824
 Db 199 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnAlaMetAsnPheIleGlnPro 218
 QY 825 GGTGCACTTAAAGAAATTTAGGCTTCATAGCTGACTTTAAGAAATTTTGTATAGTTTA 884
 Db 219 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnSerPheAspSerLeu 238
 QY 885 AATGTATGAATACTGTATTCAGAGCTGCTGGCTGTTAAGAGCCATCGTTGGTCTG 944
 Db 239 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValAlaHisLysLeuValLeu 258
 QY 945 GGAGAAATTTGAATGAAGAACTTGAAGAAATTTGACAAATCTGCTAGAGAGGCTG 1004
 Db 259 GlyGluPheArgAsnGlnLysAsnLeuGluLysPheAspThrSerAlaLeuGlnGlyLeu 278
 QY 1005 TGCATTTGACCATTTGAAGAAATTCGATAGCATACTAGTACTACTCTGATGATATT 1064
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 QY 1065 ATGACCTTATTTAATTTTGAACAATGTTTCTCATTTTCCCTGGAGTGTGACTATT 1124
 Db 299 IleAspLeuPheAsnLysLeuAlaAsnValSerSerPheSerLeuValSerValThrIle 318
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 Db 379 SerArgAsnGlyLeuSerPheLysGlyCysGlySerGlnSerAspPheGlyThrThrSer 398
 QY 1365 CTTAAAGTATTTAGATCTGAGCTTCAATGTGTTTATACCATGAGTTCAAACTTCTGGGC 1424
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 Db 439 SerValPheLeuSerLeuAsnGlnLeuIleTyLeuAspIleSerHisThrHisThrArg 458
 QY 1545 GTTGCTTTCAATGGCATCTTCAATGCTTGTCCAGTCTCGAAGTCTTGAAGTGGTGGC 1604
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 QY 1605 AATTCCTTCAGAGAAACCTTCCCTCCAGATATCTTCAAGAGCTGAGAGAACTTCACTTC 1664
 Db 479 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 498
 QY 1665 CTGAGACCTCTCTCAAGTCAACTGAGACAGTGTGCTCAACAGCAATTTAACTCACTCTCC 1724
 Db 499 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 518
 QY 1725 AGTCTTCAAGTAAATATATGAGCCACACAACACTTCTTTTCAATTTGATGATGCTTAT 1784
 Db 519 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyx 538
 QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGAATTAAGTGTCAATCAACAATAAGACTTCCAA 1844
 Db 539 LysCysLeuAsnSerLeuGlnValLeuAspTyxSerLeuAsnHisIleMetThrSerLys 558
 QY 1845 AAACAGGAACTACAGCAATTTTCCAAAGTCTAGCTTTCTTAAATCTTACTCAGAAATGAC 1904
 Db 559 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 578
 QY 1905 TTTGCTTGATCTTGTGAACACAGAGTTTCTGCAATGATCAAGACAGAGGACCTC 1964
 Db 579 PheAlaCysThrCysGluHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 598
 QY 1965 TTGGTGAATTTGAACGAATGGAATGGAACACTTCAATTAAGACGAGGCACTGCTG 2024
 Db 599 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnLysMetProVal 618
 QY 2025 CTGAGTTTGAATATCACTCTGTCAGATGAATGAAGCACTCATTTGGTGTGGTCTCAGT 2084
 Db 619 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrValIleGlyValSerValPheSer 638
 QY 2085 GTGCTGTATGATCTGTGTGAGCACTTGTGCTATATAGTTTCACTGATGCTT 2144
 Db 639 ValLeuValValSerValValAlaValLeuValTyLysPheTyPheHisLeuMetLeu 658
 QY 2145 CTTGCTGGCTGCAATAAGTATGAGTGAAGGAAACATCTATGATGCTTGTATTTAC 2204
 Db 659 LeuAlaGlyCysIleLysTyxGlyArgGlyGluAsnThrTyxAspAlaPheValIleTyx 678
 QY 2205 TCAAGCCAGATGAGAGCTGGTGAAGAAATGAGCTGTAAAGAAATTTAGAAGAGGGGTG 2264
 Db 679 SerSerGlnAspGluAspIlePheValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 698
 QY 2265 CTTCAATTTGAGCTTGTGCTTCACTACAGAGACTTATTTCCCGTGTGGCATTTGCTGCC 2324
 Db 699 ProThrPheGlnLeuLysCysLeuHisTyxArgAspPheIleProGlyValAlaIleAlaAla 728
 QY 2325 AATCATCATCAATAAGTTCCTCAATAAAGCCGAAAGTGAATTTGTGTGTGCTCCAGCAC 2384
 Db 719 AsnIleIleHisGluGlyPheHisLysSerArgLysValIleValValValSerGlnHis 738
 QY 2385 TTCATCCAGAGCGGTGTGTATCTTTGAATATGAGATTTGCTCAGACCTGGCAGTTTCTG 2444


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Db      739 PheIIeGlnSerArgTrpCysIlePheGluTrpGluIleIleGlnThrTrpGlnPheLeu 758
Qy      2445 AGAGTCGTCGTCGTCATCTTCATCTTCGTCGAGAGGTGAGAGACCTGCTCAGG 2504
Db      759 SerSerArgIleGlyIleIlePheIleValLeuGlnIleValGluIleThrLeuLeuArg 778
Qy      2505 CACAGGTGAGCTGATCGCCTTCCTCAGCAGGAACTTACTGAGTGGAGAGACAGT 2564
Db      779 GlnGlnIleGlnLeuTrpIleArgLeuLeuSerArgPheThrIleGlnIleTrpGlnIlePheSer 798
Qy      2565 GTCCTGGGGGGCAGCATCTTCTGAGAGCAGCTCAGAAAGCCCTGCTGATGGTAATCA 2624
Db      799 ValIleGlyArgIleIlePheTrpArgArgLeuArgIleValLeuLeuIlePheGlyIleSer 818
Qy      2625 TGGAAATCCAGAGAAACAGTCGGTACAGCA 2654
Db      819 TrpAsnProGlnIleGlyThrValGlyThrGly 828

RESULT 5
TLR4_PAPAN STANDARD; PRT; 826 AA.
ID      TLR4_PAPAN
AC      Q9TSP2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Toll-like receptor 4 precursor.
GN      Name-TLR4;
OS      Papio anubis (Olive baboon).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Papio.
OX      NCBI_TaxId=9555;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=20558910; PubMed=11104518;
RA      Smitnova I., Poltorak A., Chan B.K.L., McBride C., Beutler B.;
RT      "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT      locus (TLR4)".
RL      Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
CC      -1- FUNCTION: Cooperates with MyD88 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, MyD88 and TIRAP via
CC      binds MyD88 via the extracellular domain. Binds MyD88 and TIRAP via
CC      their respective TIR domains (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC      -1- SIMILARITY: Contains 1 TIR domain.
CC      -----
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF180964; AAF07059.1; -.
DR      EMBL; AF180962; AAF07059.1; JOINED.
DR      EMBL; AF180963; AAF07059.1; JOINED.
DR      HSSP; Q15399; LFV.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungal; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:mast cell activation; ISS.

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DR      GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF00560; LRR; 13.
DR      Pfam; PF01463; LRRCT; 1.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PRO0019; LEURICRPT.
DR      SMART; SM00369; LRR_TYP; 2.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00255; TIR; 1.
DR      SMART; PS50104; TIR; 1.
DR      KMW Glycoprotein; Immune response; Inflammatory response;
DR      Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
DR      KMW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
DR      FT CHAIN 1 23
DR      FT DOMAIN 24 826
DR      FT TRANSMEM 24 631
DR      FT DOMAIN 632 826
DR      FT REPEAT 53 76
DR      FT REPEAT 77 100
DR      FT REPEAT 101 124
DR      FT REPEAT 128 149
DR      FT REPEAT 150 173
DR      FT REPEAT 174 197
DR      FT REPEAT 203 225
DR      FT REPEAT 228 252
DR      FT REPEAT 277 303
DR      FT REPEAT 327 350
DR      FT REPEAT 351 372
DR      FT REPEAT 373 398
DR      FT REPEAT 400 421
DR      FT REPEAT 422 445
DR      FT REPEAT 447 469
DR      FT REPEAT 470 494
DR      FT REPEAT 495 518
DR      FT REPEAT 520 541
DR      FT REPEAT 543 569
DR      FT REPEAT 571 592
DR      FT DOMAIN 672 818
DR      FT CARBOHYD 35 35
DR      FT CARBOHYD 173 173
DR      FT CARBOHYD 205 205
DR      FT CARBOHYD 282 282
DR      FT CARBOHYD 309 309
DR      FT CARBOHYD 497 497
DR      FT CARBOHYD 526 526
DR      FT CARBOHYD 575 575
DR      FT CARBOHYD 624 624
DR      FT CARBOHYD 630 630
DR      SQ SEQUENCE 826 AA; 94678 MW; 42277731855F1769 CRC64;

Alignment Scores:
Pred. No.: 1.52e-294
Score: 4013.00
Percent Similarity: 92.48%
Best Local Similarity: 89.81%
Query Match: 59.68%
DB: 1
Length: 826
Matches: 776
Conservative: 23
Mismatch: 25
Indels: 40
Gaps: 1

US-09-396-985b-3 (1-3811) x TLR4_PAPAN (1-826)
Qy      45 ATATATGTCTGCGCTCGGCTGCTGAGACTTCGACCAAGCCATGCGCTTCTCTCTG 104
Db      1 MetThrSerIleLeuIleuArgIleuValGlyThrIleIleProIleValIlePheLeuSerCys 20
Qy      105 GTGAGACCAAGAGCTGAGAGCCCTGCTGAGAGACTTGGCCCTTAACACACAGAGAGC 164

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Db      21 ValArgProGluSerThrGluProCysVal-----30
QY      165 TGGCATGAAGAACCGAGACTTCAGACTCCGAGAGCTCAGCCCTTCAACCCGATTCATTG 224
Db      30 -----30
QY      225 CTTCCTGTAAAGCTGCCGTTTATACAGAGAGGTGCTCTATATATTAATTATCAATGC 284
Db      31 -----GluValValProAsnIleThrTyrGlnCys 40
QY      285 ATGAGACTGAATTTCTACAAATATCCCGACACCTCCCTTCTCAACCAAGAACTTGAGC 344
Db      41 MetGluLeuAsnGlnPheTyrSileProAspAsnIleProPheSerThrTyrAsnLeuAsp 60
QY      345 CTGAGCTTAAATCCCTGAGGAGCTTATAGAGCTATAGCTTCTTCAGTTTCCAGAACTG 404
Db      61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheLeuArgPheProGluLeu 80
QY      405 CAGGTCTGGAATTTATCCAGGTGTGAATCCAGACAAATTGAAGTGGGAGCATTCAGAGC 464
Db      81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY      465 CTAAAGCACCTCTCTAATTAATTATGACAGAAACCCATCCAGAGTTTACGCTGGGA 524
Db      101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY      525 GCGTTTTCGAGCATTCAGATTACAGAGCTGTGGCTGTGAGACAAATCTAGCATCT 584
Db      121 AlaPheSerGlyLeuSerSerLeuGlnIleValLeuValAlaValGluThrAsnLeuAlaSer 140
QY      585 CTAGAGAACTTCCCACTTGAGCATCTCAAAACTTTGAAGAACTTATGTGGCTCAAT 644
Db      141 LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
QY      645 CTATATCAATCTTCAATTAATCTGAGTATTTTCTAATCTGACCAATCTGAGCACTTG 704
Db      161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180
QY      705 GACCTTTCAGACAAAGATTCAAAGTATTTATTTGACAGACCTTGGGGGTCTCAATCA 764
Db      181 AsnLeuSerSerAsnLysIleGlnAsnIleTyrCysLysAspLeuGlnValLeuHisGln 200
QY      765 ATGCCCTACTCAATCTCTTATAGACCTGCTGACCTGACCTTGAACCTTATTCACACCA 824
Db      201 MetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnProIleGlnPro 220
QY      825 GGTGATTAAAGAAATTAGGCTTCAATAGCTGATTTAAGAAATTAATTTGATAGTTA 884
Db      221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgSerAsnPheAspLeu 240
QY      885 AATGTATGAAAATTGTATTAAGGTCTGAGCTGTGTTAGAGTCCATCGTTGGTCTG 944
Db      241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
QY      945 GAGAAATTAAAGAAATGAAGAACTTGAGAAAGTTTGAACAATCTGCTAGAGGGCTG 1004
Db      261 GlyLysPheArgAsnGluArgAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 280
QY      1005 TGCATTTGACCACTTGAAGAAATCCGATTAGCATTAAGTACTGACTGATGATAT 1064
Db      281 CysAsnLeuThrIleGluGluPheArgLeuThrTyrLeuAspLysTyrTyrLeuAspAsnIle 300
QY      1065 ATTGACTTATTAATTTGACAAATGTTTCTTCATTTTCCCTGAGTGAAGTGAAT 1124
Db      301 IleAspLeuPheAsnGlySerLeuAlaAsnAlaSerSerPheSerLeuValSerValAsnIle 320
QY      1125 GAAGGGAATAAAGCTTTCTTATTAATTTCCGATGGCAATTTAGAAATTAAGTAACTGT 1184
Db      321 LysArgValAlaGluAspPheSerTyrAsnPheArgTyrGlnHisLeuGluLeuValAsnCys 340
QY      1185 AATTTGACAGTTTCCCATTTGAACCTCAATCTCTCAAAAGGCTTACTTCACTTCC 1244

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Db      341 LysPheGluGlnPheProThrLeuGluLeuGlnSerLeuLysArgLeuThrPheThrAla 360
QY      1245 AACAAAGTGGGAATCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCTAGATCTC 1304
Db      361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY      1305 AGTAGAAATGCTTGAGTTTCAAGGTTGCTGTCTCAAGTAGATTTTGGACACACAGC 1364
Db      381 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 400
QY      1365 CTAAAGTATTTAGATTGAGCTTCAATGGTGTATTAACATGAGTTCAAACTTCTGGGC 1424
Db      401 LeuLysTyrLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly 420
QY      1425 TTGAAACAACCTAGAACATCGATTCGAGATTCAGACATTCGAATTTGAACAAATGAGTGA 1484
Db      421 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 440
QY      1485 TCAGATTCCTATCACTCAGAAACCTCATTTTACCTTGAACATTTCTCATACTCAACACCA 1544
Db      441 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrThr 460
QY      1545 GTTGCTTTCAATGCACTTTCAATGGCTGTGCCAGTGTGCAAGCTTTGAAATGGCTGCC 1604
Db      461 ValAlaPheAsnGlyIlePheAspGlyLeuLeuSerLeuLysValLeuLysMetAlaGly 480
QY      1605 AATTTCTTCAGAGAAACCTTCTTCAGATATCTTCAAGAGCTGAGAACTGACCTTC 1664
Db      481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrAspLeuLysAsnLeuThrPhe 500
QY      1665 CTGACCTCTCTCAGTGTCAACTGAGACAGTGTCTCCAAACAGCATTTATCACTCTCC 1724
Db      501 LeuAspLeuSerGlnCysGlnLeuGlnLeuGlnLeuSerProThrAlaPheAspThrLeuAsn 520
QY      1725 AGTCTTCAGATTAATAATTAAGCCACAACAATCTTTTCAATGGAATAGTTTCTTAT 1784
Db      521 LysLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspValPheProTyr 540
QY      1785 AAGTGTCAACCTCCCTCAGGTTCTGATTTACGTTCAATCACTCAATTAATGACTTCCAA 1844
Db      541 LysCysLeuProSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
QY      1845 AAAAGGAACACTCAGCATTTTCCAGATGATCTAGCTTTCTTAATCTTACTCAGAAATGAC 1904
Db      561 AsnGlnGluProGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY      1905 TTGCTTGTACTTTGGAACAACAGATTTCTGCAATGGAATGAAGACCAAGCAGCTC 1964
Db      581 PheAlaCysThrCysGluHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 600
QY      1965 TTGCTGGAAGTTGAAGAAATGGAATGTGCAACCTTCAGATGAAGAGGCAATGCGCTG 2024
Db      601 LeuValAlaGluAlaGluArgMetGluCysAlaThrProSerAspLysGlnLysMetProVal 620
QY      2025 CTGAGTTGAATATCACTGTCAGATGAATGAAGAACATCATGATGCTGTGCTGCTCAGT 2084
Db      621 LeuSerValAsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValPheSer 640
QY      2085 GTGCTTGTAGTATCTGTTGTAGACGTTCTGCTATTAAGTTCTATTTTCACTGATGCT 2144
Db      641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 660
QY      2145 CTTGCTGCTGCATTAAGTAAGTGAAGGTGAAGAAACACTATGATGCTTTGTTATCTAC 2204
Db      661 LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 680
QY      2205 TCAAGCAGAGATGAAGAGCTGGGTGAAGATGAGCTGTAAAGAAATTGAAGAAAGGGGTG 2264
Db      681 SerSerGlnAspGluAspIlePyrValArgAsnGluLeuValLysAsnLeuGluGlyVal 700
QY      2265 CCTCATTTCAAGTCTGACCTTCACTACAGACATTTATTCGCGGTGAGCATTGCTGCC 2324
Db      701 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 720

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QY 2325 AACATCATCCAGTAAGTTTCCATATAAAGCCGAAAGTGATTTGTGTCGCCAGCAC 2384
Db 721 AahtlletlehlglngllyphehlstysSerArglyValIleValValaIserglNhls 740
QY 2385 TTCATCCAGAGCGCGGTGTATCTTTGAATATGAGATTGCTCAGACCTGAGATTTCG 2444
Db 741 PheileginSerArgTrpCysIlelePhegluYrGluIlealglNhtrpIglNhleu 760
QY 2445 AGCAGTCGTGCTGTATTCATTTTCATTTGCTTCGAGAGAGTGAGAAAGCCCTGCTCAG 2504
Db 761 SerSerArgAlaGlyIlelePheleValleuGlnlyValGluYsrThrleuAarg 780
QY 2505 CAGCAGGTGAGCTGTATCCGCTTCACAGAGAAACATTCCTGAGTGGAGAGCACT 2564
Db 781 GlnGlnValaGluLeuYrArgleuSerArgAsnThrlyleuGluTrpGluPser 800
QY 2565 GTCTCTGGGCGGACATCTTTCGAGAGCACTCAGAAAGCCCTGCTGAGTAAATCA 2624
Db 801 ValleuGlyGlnHlsIlePheTrpArgleuArglyAlaIleuAmpGlyArgSer 820
QY 2625 TGGATTCAGAA 2636
Db 821 TrpAenProGlu 824

RESULT 6
TIR4_HORSE STANDARD; PRT; 843 AA.
ID TIR4_HORSE STANDARD; PRT; 843 AA.
AC Q9MYW3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TIR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandenplas M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TIR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY005808; AAF91076.1; -.
CC HSSP; Q15399; LFYV.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016946; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.

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DR GO; GO:0045576; P:macr cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045672; P:negative regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR000157; TIR.
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF01582; TIR; 1.
DR PRINTS: PR00019; LEURICRPT.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS50104; TIR; 1.
DR Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 843
FT DOMAIN 24 633
FT TRANSMEM 634 654
FT DOMAIN 655 843
FT REPEAT 53 76
FT REPEAT 77 100
FT REPEAT 101 124
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FT REPEAT 174 197
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FT REPEAT 545 566
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FT CARBOHYD 527
FT CARBOHYD 576
FT CARBOHYD 626
SQ SEQUENCE 843 AA; 96495 MW; B5976898AD6F7A69 CRC64;

Alignment Scores:
Pred. No.: 1,61e-241
Score: 3312.00
Percent Similarity: 83.18%
Best Local Similarity: 74.65%
Query Match: 49.26%
DB: 1
Gaps: 3

US-09-396-985B-3 (1-3811) x TIR4_HORSE (1-843)
QY 45 ATGATGTGCTGCGCGGTGAGTATCCAGCCATGCGCTTCTCTCTG 104
Db 1 MetMeProProThrArgleuAaGlyThrleuIleProAlaMetAlaPheleuSerCys 20
QY 105 GTGAGACAGAAAGCTGGAGCCCTGCTGAGACTTGCCCTTAAACACACAGAAAGAC 164
Db 21 LeuArgProGluSerTrpPseProCysVal----- 30

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QY 165 TGGATGAACCCAGAGCTTTCAGACTCCGAGGCTCAGCCCTTACCCCGATTCATCG 224
 Db 30 ----- 30
 QY 225 CTTCTTGCTAAATGCTGCCGTTTATCAGGAGGTGCTCTTAATTACTTATCAATGC 284
 Db 31 ----- GlnValValProAsnThrThrTyrGlnCys 40
 QY 285 ATGAGCTGAATTTCTACAAATATCCCGACAACTCCCTTCTACACCAAGAACTTGAC 344
 Db 41 MetAspLeuAsnLeuTyrLysIleProGlnAsnIleProThrSerThrLysGlnLeuAsp 60
 QY 345 CTGAGCTTATCCCTCAGGAGCTTATGAGGAGCTTCTTCAAGTTTCCGAGACTG 404
 Db 61 LeuSerPheAsnProLeuLysGlnLeuGlySerHisSerPheSerAsnProGlnLeu 80
 QY 405 CAGGTGCTGATTTATTCAGGTGTGAATTCAGAACTGAGCAATGAGTGGGCAATTCAGAGC 464
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnMetIleGlnAspAlaTyrGlnGly 100
 QY 465 CTGAGCCACTCTCTACTTAAATTTTACAGAAACCCCATCCAGACTTACCCCTGGGA 524
 Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleArgSerLeuAlaLeuGly 120
 QY 525 GCCTTTCTGAGCTATCAAGTTTACAGAGTGTGCTGGAGCAAAATCTAGACTCT 584
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGlnThrLysLeuSer 140
 QY 585 CTGAGAACTTCCCATGAGCATCTCAAACTTTGAGAAACTTAAATGTGCTCACAAT 644
 Db 141 LeuGlnLysPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 160
 QY 645 CTTATCAATCTTCAAAATTAAGTATTTTCTAATCTGACCAATCTAGAGCACTTG 704
 Db 161 LeuIleHisSerPheLysLeuProGlnTyrPheSerLysMetProAsnLeuGlnLeu 180
 QY 705 GACCTTCCAGCAACAGATTCAAGATTATTTGACAGACTTGGGGTCTTACATCA 764
 Db 181 AspLeuSerAsnAsnLysIleGlnHisIleSerHisGlnLysLeuAlaValLeuHisGln 200
 QY 765 ATGCCCTTACTCATCTCTCTTATGAGCTGTCCCTGAAACCTTAACTTATTCACACA 824
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuGlnLysIleGlnPro 220
 QY 825 GGTGCATTAAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTTA 884
 Db 221 AspAlaPheLysGlnIleLysLeuHisLysLeuThrLeuArgSerAsnPheAspSerIle 240
 QY 885 AATGTAATGAACCTGTATTCAGAGTCTGGCTGTTTAAAGTCCATCGTTGGTTCTG 944
 Db 241 AspValMetLysSerCysIleGlnGlyLeuAlaGlyLeuLysValAlaAspGlyLeu 260
 QY 945 GGAGAAATTTGAATGAGAGAACTTGAAGAAAGTTTGAACAATCTGCTTGAAGAGGCTG 1004
 Db 261 GlyGlnPheLysAsnLysGlnLysGlnLysGlnLysPheSerAlaLeuAlaGlyLeu 280
 QY 1005 TGCATTTGACATGAGAAATTCGATTCAGTACTTACATCTGCTGAT--GAT 1061
 Db 281 HisAsnLeuThrIleGlnGlnPheArgLeuAlaTyrIleAspAsnTyrSerSerLysAsp 300
 QY 1062 AATATGACTTATTTATTTGACAAATGTTTCTTCATTTTCCCTGGAGTGGAGTACT 1121
 Db 301 SerIleAspLeuLeuAsnLysLeuAlaAspIleSerLysIleSerLeuValSerLeuAsp 320
 QY 1122 ATGGAAGGCTAAAGACTTCTTCTTAATTTGAGATGAGCAATTTAGATTAAGTTAGTAC 1181
 Db 321 LeuGlyAsnLeuLysAspPheProLysGlyPheGlyTyrGlnAspPheGlnLeuValAsn 340
 QY 1182 TGTAAATTTGAGACGTTTCCCACTTGAATGAATCAATCTGCAAAAGCTTACTTCACT 1241
 Db 341 CysArgGlnIleGlnLysPheProThrLeuGlnLeuThrSerLeuLysArgLeuValPheThr 360

QY 1242 TCCAAAGAAAGTGGGAATGCTTTTTCAGAGTTATCTACAAAGCTTGAATTTAGAT 1301
 Db 361 SerAsnLysAspMetLysSerPheAsnGlnValLysLeuProSerLeuGlnPheLeuAsp 380
 QY 1302 CTGAGTAGAAATGGCTTGAATTCGAAAGCTTGTCTTCAAAAGTGAATTTGGAGCAAC 1361
 Db 381 LeuSerArgAsnArgLeuSerPheLysSerCysCysSerGlnAlaAspLeuLysThr 400
 QY 1362 AGCTTAAGTATTTAGATCTGAGCTTCATGAGTGAATTAACATGATGATCAACTTGT 1421
 Db 401 ArgLeuLysHisLeuAspLeuSerPheAsnAspValIleSerMetSerAsnPheMet 420
 QY 1422 GGCCTAAGCAACTTAACATCTGATTTCCACATTTCCATTTGAAACAAATAGTAGAG 1481
 Db 421 GlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnAlaSerAsp 440
 QY 1482 TTTTCAGATTTCTTATCTACAGAAACCTTCATTTACCTTGACATTTCTACACTCAC 1541
 Db 441 PheProValPheLeuSerLeuLysAsnLeuArgTyrLeuAspIleSerTyrThrAsnThr 460
 QY 1542 AGAGTTGCTTTCAGATCTTCATGAGTGTGCTCCAGTCTCGAAGCTTGAATAGGCT 1601
 Db 461 ArgValValPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuLysMetAla 480
 QY 1602 GGCATTTCTTCCAGGAAACCTTCCATGATATCTTCCAGAGCTGAGAACTTGACC 1661
 Db 481 GlyAsnSerPheLysAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThr 500
 QY 1662 TTCCTGAGCTCTCTGAGTGTCACTGAGAGCACTTGTCCAAAGCAATTTAACTGACT 1721
 Db 501 ThrLeuAspLeuSerLysCysAsnLeuGlnGlnValSerGlnGlnAlaPheCysLeuLeu 520
 QY 1722 TCCAGTCTTCAAGTATTAATAGACCCACAAACTCTTTTCATTTGATAGTTTCTCT 1781
 Db 521 ProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspMetLeuPro 540
 QY 1782 TATAAGTGTGAACCTCCCTCCAGGTCTTGATTAAGCTTCATCAATCAATAGACTTCC 1841
 Db 541 TyrLysProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe 560
 QY 1842 AAAAAACAGAACTACAGCAATTTTCCAGTGTCTGAGCTTCTTAACTTACTTACAGAA 1901
 Db 561 LysTyrGlnGlnLeuGlnHisPheProSerSerLeuHisSerLeuAsnLeuThrGlnAsn 580
 QY 1902 GACTTGTCTTGAATCTTGTGAACCAAGATTTCTGCAATGATCAAGACCAAGAGCAG 1961
 Db 581 AspPheAlaCysValCysGlnTyrGlnSerPheLeuGlnTyrValLysAspGlnArgGln 600
 QY 1962 CTTCTGCTGGAAGTTGAACGAATGGAATGGAACCTTCAGATTAAGCAGGGCATGCT 2021
 Db 601 LeuLeuValGlnValGlnHisLeuValCysAlaAlaLeuProLeuGlnMetArgLysMetPro 620
 QY 2022 GTGCTGAGTTGTT--AATATCACTGTTCAGATGATGATTAAGCATCTGTGTGTGCTG 2078
 Db 621 ValLeuGlyPheAsnAsnAlaThrCysGlnIleSerLysThrIleValGlyLysVal 640
 QY 2079 CTGAGTGTCTTGAATCTGTGTGAACAGTTCGTCTTAATGTTTACTTACACTG 2138
 Db 641 PheSerIleLeuMetValSerValIleAlaValLeuValTyrLysPheTyrPheHisLeu 660
 QY 2139 ATGCTTCTGCTGGCGCATTAAGTATGAGTGAAGGGAACATCTATGATGCTTGTGT 2198
 Db 661 MetLeuLeuAlaLysLysLysLysTyrGlyArgGlyGlnSerIleTyrAspAlaPheVal 680
 QY 2199 ATCTACTCAAGCCAGATGAGAGCTGGTGAAGAAAGAGCTAGTAAAGATTTAGAGAA 2258
 Db 681 IleTyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGln 700
 QY 2259 GGGGTGCTTCATTTGAGCTCTGCTTTCATCAAGACATTTATTTCCGGGTGGCCAT 2318
 Db 701 GlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIle 720
 QY 2319 GCTGCAACATCATCATGAGGTTTCCATTAAGCGCAAGGATGTTGTTGTGTGTGCT 2378

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Db      721 AlaAlaAsnIleIleGlnGlnGlyPheHisIleValIleValIleValIleValSer 740
Qy      2379 CAGCACTTCAATCCAGAGCCGCTGGTGTATCTTGAATATGAGATTCCTAGACCTGGCAG 2438
Db      741 GlnHisPheIleIleInsErArgTrpCysIlePheGlnIleIleValIleGlnIleIleTrpGln 760
Qy      2439 TTTCTGAGAGTGTGCTGTATCATCTTCATGTCTCTGAGAGAGTGGAGAGACCCG 2498
Db      761 PheIleSerSerArgAlaGlyIleIlePheIleValIleHisIleValIleGlnIleValSerIleu 780
Qy      2499 CTCAGCAGCAGGTGAGCTGTATCCGCTTCTGAGAGAGAACCTTACCTGAGTGGAG 2558
Db      781 IeuArgGlnGlnIleValIleGlnIleuValArgIleuAsnArgSerHisTrpIleuGlnIleu 800
Qy      2559 GACAGTGTCTCTGGGGCGGCACATCTTCTGAGAGCACTGAGAAAGCCCTGCTGATGGT 2618
Db      801 AspSerValIleuIleArgHisIlePheIleTrpArgIleuArgIleuArgIleuAsnIleu 820
Qy      2619 AATCATGGAATCCAGAGAGACA 2642
Db      821 LysProIlePserProAlaGlyIleTr 828

RESULT 7
TLR4_BOVIN STANDARD; PRT; 841 AA.
AC      09GLF5;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
GN      Toll-like receptor 4 precursor.
OS      Bos taurus (Bovine).
OC      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Guionaud C.T., Dubey C., Jung T.W.;
RT      "Bovine Toll-like receptor 4 (TLR4).";
RL      Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MyD88, TRAP and TRAFs, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (by similarity).
CC      -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, LY96 and TLR4.
CC      Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC      their respective TIR domains (by similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC      -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
CC      -1- SIMILARITY: Contains 1 TIR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC      or send an email to license@ebi.ac.uk).
CC      -----
CC      EMBL; AF10952; MG32061.2; -.
CC      HSSP; 060603; LFYX.
DR      GO; GO:0046596; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macrophage cell activation; ISS.

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DR      GO; GO:0045671; P:negative regulation of osteoclast different. . . ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF00560; LRR_13.
DR      Pfam; PF01463; LRRCT; 1.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PR00019; LEURICRPT.
DR      SMART; SM00369; LRR_TYP; 1.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Glycoprotein; Immune response; Inflammatory response;
KW      Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT      SIGNAL 1 23
FT      CHAIN 24 841
FT      DOMAIN 24 632
FT      TRANSMEM 633 653
FT      DOMAIN 654 841
FT      REPEAT 53 76
FT      REPEAT 77 100
FT      REPEAT 102 124
FT      REPEAT 149 173
FT      REPEAT 174 197
FT      REPEAT 203 225
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FT      REPEAT 471 494
FT      REPEAT 495 518
FT      REPEAT 520 542
FT      REPEAT 544 566
FT      REPEAT 568 592
FT      DOMAIN 673 819
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FT      CARBOHYD 205 205
FT      CARBOHYD 238 238
FT      CARBOHYD 282 282
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FT      CARBOHYD 497 497
FT      CARBOHYD 526 526
FT      CARBOHYD 575 575
FT      CARBOHYD 625 625
SQ      SEQUENCE 841 AA; 96026 MW; CSEI7CB9C798CD16 CRC64;

Alignment Scores:
Pred. No.: 5,71e-240
Score: 3291.50
Percent Similarity: 82.48%
Best Local Similarity: 72.70%
Query Match: 48.95%
DB: 1 Gaps: 2

US-09-396-985B-3 (1-3811) x TLR4_BOVIN (1-841)
Qy      45 ATGATGTCTCCCTCGGCGCTGAGACTGTATCCAGCCATGGCCTTCTCTCTCG 104
Db      1 MetMetAlaArgAlaArgIleuAlaAlaIleuIleProAlaThrAlaIleuSerCys 20
Qy      105 GTGAGACCGAAGAGCTGGAGCCCTGCTGAGAGACTTGCCCTTAAACACAGAGAGC 164
Db      21 IeuArgThrGlnSerTrpAspProCysVal----- 30

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QY 165 TGGCATGAAAACCGAGCTTTCAGACTCCGAGCGCTCAGCCCTTACCCCGATTCCATG 224
 Db 30 ----- 30
 QY 225 CTCTTGTCTAAATGCTGCCGTTTATATACGAGGTGGTTCCCTAATATTACTTCAATGC 284
 Db 31 ----- GlnValValProAsnIleSerTyrGlnCys 40
 QY 285 ATGAGAGTGAATTTCTCAAAATCCCGACACCTCCCTTCAACCAAGAACCTGGAC 344
 Db 41 MetGlnLeuAsnLeuTyrLysIleProAspAsnIleProIleSerThrLysMetLeuAsp 60
 QY 345 CTGAGCTTAAATCCCTGAGGACATTTAGGACGATAGCTTCTTCACTTCCCGAAGCTG 404
 Db 61 LeuSerPheAsnTyrLeuArgHisLeuGlySerHisAsnPheSerSerPheProGlnLeu 80
 QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATTCAGACAAATTGAAGTGGGACATATCAGAGC 464
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleLysIleLeuIleGlnAspArgThrPheGlnGly 100
 QY 465 CTGAGCCACTCTCTACCTTAATTTATGACAGAAACCCCATCCAGAGTTTACCCCTGGG 524
 Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaTyrGly 120
 QY 525 GCCCTTTCTGACTATCAAGTTTACAGAGCTGGCTGGCTGAGACAAATCTAGCATCT 584
 Db 121 AlpheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuValSer 140
 QY 585 CTGAGAACTTCCCATTTGACATCTGAAAATTGAAAGACTTAAATGTGGCTCAGCAAT 644
 Db 141 LeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGlnLeuAsnValAlaHisAsn 160
 QY 645 CTATATCAATCTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGCACTTG 704
 Db 161 PheIleHisSerPheLysLeuProGlnLysPheSerAsnLeuProAsnLeuGlnHisLeu 180
 QY 705 GACCTTTCCAGCAACAAGATTCAAAAGTATTATTTGACAGACTTGCGGGTTTCAACATCA 764
 Db 181 AspLeuSerAsnAsnLysIleGlnAsnIleTyrTyrGlnAspValLysValLeuHisGln 200
 QY 765 ATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTTGAACCTTATTCACCA 824
 Db 201 MetProLeuAsnLeuAsnSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 825 GGTGCATTTAAAGAAATTAAGCTTCATTAAGCTGACTTAAAGAAATATTTTGATATGTTA 884
 Db 221 GlyThrPheLysGlnIleLysLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSerSer 240
 QY 885 AATGTATGAAAACTGTATTCAAGCTGGCTGGTTTGAAGTCCATCGTTGGTCTG 944
 Db 241 HisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThrAsnAlaGlyLeuValLeu 260
 QY 945 GGAGAAATTTGAATGAAGAAACTTGAAGAAAGTTTGAACAATCTGCTTGAAGAGGCGCTG 1004
 Db 261 GlyGlnPheLysAsnGlnLysGlyLeuGlnArgPheAspArgSerPheLeuGlnGlyLeu 280
 QY 1005 TGCATTTGACATTTGAAGAAATTCGATTAAGCATTAATTAAGCTTCACTCGATGATATT 1064
 Db 281 CysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspLysPheSerGlyAspAsp 300
 QY 1065 ATTAGCTATTATTAATGTTTGAACAATGTTTCTTCATTTCCCTGGAGTGGATGACATAT 1124
 Db 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerAlaIleSerLeuLeuSerIleSerLeu 320
 QY 1125 GAAAGGCTAAAGACTTTTCTTATTAATTTGAGATGACATTAAGTAAATGATTAATCTGT 1184
 Db 321 GlySerLeuGlnAlaLeuLeuLysAspPheArgTyrGlnHisLeuGlnIleIleAsnCys 340
 QY 1185 AAATTGAGACATTTCCCAATTTGAACCTCAATCTCTCAAAAGGCTTACTTCACTTCC 1244
 Db 341 AspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPheValPheThrAsp 360

QY 1245 AACAAAGTGGAAATGCTTTTTCAGAGTTGATCTACAAAGCTTGATGTTCTAGATCTC 1304
 Db 361 AsnLysAspIleSerThrPheThrGlnPheGlnLeuProSerLeuGlnTyrLeuAspLeu 380
 QY 1305 AGTAGAAATGCGCTTGAGTTTCAAAAGTGGTGTCTTCAAAAGTATTTTGGGACAAACGAC 1364
 Db 381 LysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAspPheGlyThrAsn 400
 QY 1365 CTAAAGATTTAGATCTGAGCTTCATGGGCTGATTAACATTAAGTTTCAAACTTCTGGGC 1424
 Db 401 LeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGlySerAsnPheMetGly 420
 QY 1425 TTGAAACAATGACATCTGATTTCCAGATTTCCAGATTTCAATTTGAAACAATGAGGATTT 1484
 Db 421 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnIleAsnAlaPhe 440
 QY 1485 TCGATATCTTATCACTCAGAAAACCTTCATTTACTGACATTTCTCATCTACACACAGA 1544
 Db 441 SerAlaPheLeuSerLeuArgAsnLeuArgLysLeuAspIleSerTyrThrAsnIleArg 460
 QY 1545 GTTGCTTTCATATGCAATCTTCAATGGCTTGTCAGCTGCTGCAAGTCTGAAATGGCTGGC 1604
 Db 461 IleValPheHisGlyLysIlePheThrGlyLeuValSerLeuGlnThrLeuLysMetAlaGly 480
 QY 1605 AATTCCTTCCAGGAAAACTTCTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1664
 Db 481 AsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGlnLeuThrAsnLeuThrVal 500
 QY 1665 CTGAGACTCTCTCAGTGTCACTGAGACAGCTGTCTCCAAACAGCATTTAACTCATCTCC 1724
 Db 501 LeuAspLeuSerLysCysGlnLeuGlnGlnValAlaGlnThrAlaPheHisSerLeuSer 520
 QY 1725 AGTCTTCAGGTAATTAATTAAGCAACAACACTTCTTTCAATGATAGTTTCCATAT 1784
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeuAspThrPheLysTyr 540
 QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTAACAGTCTCAATGACATTAATGACTTCCAA 1844
 Db 541 GlnProLeuHisSerLeuArgIleLeuAspCysSerPheAsnArgIleMetAlaSerLys 560
 QY 1845 AAACAGAACTACAGCATTTTCCAGATGCTTCAATGCTTCTTAAATCTTACTCAGAAATGAC 1904
 Db 561 GlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrTyrLeuAsnLeuThrGlnAsnAla 580
 QY 1905 TTGCTTTGACTGTGTAACACAGAGTTTCCGCAATGATGATCAAGACCGAGGACGCTC 1964
 Db 581 PheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgGlnLeu 600
 QY 1965 TTGCTGGAAGTTGAAGAAATGAATGTGCAACACTTCAAGATTAAGACAGGCGCATGCTGTG 2024
 Db 601 LeuValGlyAlaGlnGlnMetMetCysAlaGlnProLeuAspMetGlnAspMetProVal 620
 QY 2025 CTGAGTTTG---AATATCACTGTCAAGATGAATTAAGACATCAATGCTGTGTCGCTC 2081
 Db 621 LeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleLeuSerValSerValVal 640
 QY 2082 AGTGTGCTGTAGTACTGTGTGTAAGCAAGTTCTGTGTATTAAGTTTCACTTCACTGATG 2141
 Db 641 ThrValLeuLeuValSerValValGlyValLeuValTyrLysPheTyrPheHisLeuMet 660
 QY 2142 CTCTTGCTGGCTGCAATTAAGTATGTAAGAGGAAACATCATGATGCTTGTGTTATC 2201
 Db 661 LeuLeuAlaGlyLysLysLysTyrGlyLysGlyLysSerIleTyrAspAlaPheValIle 680
 QY 2202 TACTCAAGCCAGGATGAGACTGTGGTAAAGATGACATTAAGATTTAAGAAAGG 2261
 Db 681 TyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGly 700
 QY 2262 GTGCCCTCATTTAGCTGTGCTTCACTACAGACACTTTATTCGCGGTGGGCACTTGTCT 2321
 Db 701 ValProProPheGlnLeuCysLeuHisTyrTyrAspPheIleProGlyValAlaIleVal 720
 QY 2322 GCCAATCATCATCAAGGTTTCCATTAAGCGGAAAGGTGATGTTGTGCTGCCAG 2381

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Db      721 AlaenlllelenglnuglypnehlslvsserArglyvalleValValserGln 740
Qy      2382 CACTTATCCAGAGCCGCTGGTATCTTGAATATGAGATTCTCAGACCTGGCAGTT 2441
Db      741 HApheIllelserArgtrpCysllePneglurlygluileaglInhrtrpGlnpne 760
Qy      2442 CTGAGAGTGTCTGTATCATCTTCATGTCTCTCAGAGAGTGGAGAACCTGTCTC 2501
Db      761 LeuSerSerArgAlaqllyllellePheIlleValleuGlnlyseuGlysserleu 780
Qy      2502 AGGACAGAGTGTAGCTGTACCGCTTCAGAGAGAACCTTACCTGAGTGGAGAGC 2561
Db      781 ArgGlnGlnValGlnleuTyArgleuLeuSerArgAsnhrTytleuGlnurpGlnuap 800
Qy      2562 AGTGTCTGTGGGCGGACATCTTCTGAGAGCAGTCAAGAAAGCCCTGTGATGGTAA 2621
Db      801 SerValleuGlnlyArgHlsvalPneTrpArgArgleuArglysalaleuLeuAlaGlyls 820
Qy      2622 TCATGATCCAGAGGAACAGTGGGTACAGATGCATTCGAGAGAGCAACATCT 2678
Db      821 ProGlnSerProGlnGlnYlnrAlaaspAlaGlnThrAsnProGlnGlnAlaInrTr 839

RESULT 8
08S055 PRELIMINARY; PRT; 841 AA.
ID 08S055;
AC 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ito T., Morimatsu M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR HSP: AB056444; BAB8640.1; -.
DR HSP: O60603; 1077.
DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO: GO:0016046; P:detection of fungi; ISS.
DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO: GO:0042116; P:macrophage activation; ISS.
DR GO: GO:0045576; P:mast cell activation; ISS.
DR GO: GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO: GO:0045362; P:negative regulation of interleukin-1 biosyn. . .; ISS.
DR GO: GO:0045084; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO: GO:0045366; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR000157; TIR.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF00560; LRR_1; 11.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00369; LRR_Typ; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR RECEPTOR.
KM SEQUENCE 841 AA; 96054 MW; E08DCA840EA12DEF CRC64;

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Alignment Scores:
Pred. No.: 9,63e-240
Score: 3288.50
Percent Similarity: 82.48%
Best Local Similarity: 72.58%
Query Match: 48.91%
DB: 2 Gaps: 2

US-09-396-985B-3 (1-3811) x 08S055 (1-841)
Qy      45 ATGATGTCTGCTCGCGCTGGCTGGAGCTTGATCCAGCCATGGCCTTCTCTTCG 104
Db      1 MetMetAlaArgAlaArgleuAlaAlaAlauleProAlaThrAlaIleuSerCys 20
Qy      105 GTGAGACAGAAAGCTGGAGCCCTGCGTGGAGACTTGCCCTTAACACACAGAAAGAGC 164
Db      21 LeuArgThrGlnSerTrpAspProCysVal ----- 30
Qy      165 TGGCATGAAACCAGAGCTTTTCAGACTCCGAGCCTCAGCCCTTCACCCGATTCATTG 224
Db      30 ----- 30
Qy      225 CTTCCTGTAATGCTGCCGCTTTTATCAGCAGAGTGTCTTAATATTAATCAATGCG 284
Db      31 ----- 40
Qy      285 ATGAGAGCTGAATTTCTAAGAAATCCCGCAACCTCCCTTCACACAGAAACTGGAC 344
Db      41 MetGlnleuAsnleuTyArgylelleProAspAsnIleProIleSerThrlyseuLeuap 60
Qy      345 CTGAGCTTAAATCCCTGAGGCAATTTAGGACCTAATAGCTTTCAGTTTCCAGAACTG 404
Db      61 LeuSerPheAsnTytleuArgHlsleuGlySerHlsAsnPheserSerPheProGlnleu 80
Qy      405 CAGGTCTGTGATTTATCCAGGCTGTGAATTCAGACAAATGGAAGTGGGCATTCAGAGC 464
Db      81 GlnValleuAspLeuSerArgCysGlnIlelyllelleGlnAspAspThrPheGlnGly 100
Qy      465 CTAAAGCACCTCTCTAATATTAATGACAGAGAAACCCATCCAGAGTTAGCCCTGGGA 524
Db      101 LeuAsnHlsleuSerThrleuIleuThrGlyAsnProIleGlnSerleuAlaTrpGly 120
Qy      525 GCCTTTTCTGACTATCAAGTTTACAGAACTGTGGCTGTGGAGCAAAATCTAGACTCT 584
Db      121 AlaPheSerGlyleuSerSerleuGlnlyseuValAlaValGlnThrAsnleuValSer 140
Qy      585 CTAGAGAACTCCCAATGAGACTTCGAAACTTTGAAGAACTTAAATGTGGCTCAAT 644
Db      141 LeuAsnAspPheProIleGlyHlsleuTyAsnleuArgGlnleuAsnValAlaHlsAsn 160
Qy      645 CTATCCATCTTCAATTAATTAAGTATTTTCTATCTGACCAATGACATGAGCACTTG 704
Db      161 PheIleHlsSerPheHlsleuProGlnTyPheSerAsnleuProAsnleuGlnHlsleu 180
Qy      705 GACCTTTCAGCAACAAGATTCAAGATTATTTATGCAAGACTTGGCGGTTCTACATCA 764
Db      181 AspleuSerAsnAsnlylleGlnAsnIleTyTyGlnAspAlaIysValleuHlsGln 200
Qy      765 ATGCCCTTACTCAATCTCTTTTGAACCTGTCCCTGAACCTTGAACCTTATTCACCA 824
Db      201 MetProleuAsnleuAsnleuSerleuAspLeuSerleuAsnProleuAspPheIleGlnPro 220
Qy      825 GGTGCAATTTAAGAAATTAAGCTTCAAGCTGATGCTTAAAGAAATTAATTTGATAGTTA 884
Db      221 GlyThrPheHlsGlnleuHlsleuAsnGlyleuThrleuArgSerAsnPheAsnSer 240
Qy      885 AATGTAATGAAGAACTGTATTCAGGCTGTGCTGTTTGAAGATTCATCGTTTGTCTG 944
Db      241 HlsValMetUySerThrCysIleGlnGlyleuAlaGlyleuUySerHlsAsnArgleuValleu 260
Qy      945 GGAAGATTTAGAAATGAGAGAACTTGAGAAAGTTTGACAAATCTGCTTAGAGGGCTTG 1004
Db      261 GlyGlnPheHlsAsnGlnurGlyleuGlnArgPheAspArgSerPheleuGlnGlyleu 280

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QY	1005	TGCATTTTGCACTTGAAGAAATCCGATTACATTAAGTCACTTGAAGTTCATGCAATGCTT	1064
Db	281	Cysasnleuethrilleuglnpneargllaleatryleuabprrlyspheasercllyaspar	300
QY	1065	ATTGACTTATTTAAATTGTTTGACAAATGTTTCTTCATTTTCCGTGAGTGATTAATT	1124
Db	301	ThraspneuPhenancysleualasbnvaliseralliserleuLeuSeriliserleu	320
QY	1125	GAAAGGGTAAAGACTTTTCTTAATAATTCCGATGGGCAACATTTAAGATTAGTAACTGT	1184
Db	321	GlyserleuGlnalaleuLeuLysasrpheargrrgrrglnhlsleuglnlleilelsnys	340
QY	1185	AAATTTGGACAGTTTCCACATTTGMAATCCAAATCTCTCAAAAGGCTTACTTCACTTCC	1244
Db	341	AspheaaprrlyspheproalaleuLysleuSerleuLyslysphevalPheThrasp	360
QY	1245	AACAAAGGTGGAAATGCTTTTTCAGAGTTGATTTACCAAGCTTGAATTTCTAGATTC	1304
Db	361	AsnlyasaprrliserThrPheThrclupheglnleuProserleuGlntryleuabprr	380
QY	1305	AGTGAATAGGCTTGAGTTTCAAAAGGTGCTGTTCTCAAAAGTGAATTTGGACAAACGC	1364
Db	381	LysargasnhsleuSerPheLyscllyscysethrstrhrasrphelgrrlyThrTrasn	400
QY	1365	CTAAAGTATTTAGATCTGAGCTTCAATGTTTATTTACCAAGTCTCAAACTTCTTGAGC	1424
Db	401	LeuylshlsleuabprrleuSerPheasnarpvalllethrleugliserAsnphemetlly	420
QY	1425	TTTAACAACATCGAATCCTGATTTCCAGACATTTCCATTTGAAACAATGAGTGAAGTT	1484
Db	421	LeuGlnGlnleuGlnhsleuabprrheglnhserrhrleuLysglnlleasnlaPhe	440
QY	1485	TCAGTATTCCTATACCTACAGAAACCTCATTTACCTTGACATTTCTACACTACACSCGA	1544
Db	441	SerlarpheleuSerleuabprrasnleuabprrlyrleuabprrliserTyThrAsnlearg	460
QY	1545	GTTGCTTTCAAATGGCATTTTCAAATGGCTTTGTCCAGTCTGCAGTCTGAAATGGCTGGC	1604
Db	461	llevalPhehlisgrrlylePheThrcllyleuvaliserleuGlnthrleuLysmetlalely	480
QY	1605	AAATCTTTCCAGGAAAACTTCCCTTCCAAATATCTTCAAGAGCTGAGAACTTGACCTTC	1664
Db	481	AsnserPheglnaasnleuabprrleuProasprrllephehrglnleuThrAsnleuthrval	500
QY	1665	CTGACACTCTCTCAGGTGCAACTGAGGAGGTGTCTCCAAAGCATTTTAAGTCACTTCC	1724
Db	501	LeuabprrleuSerlyscysGlnleuGlnvalalaglnthrAlaPhehliserleuSer	520
QY	1725	AGTCTTACGGTACTTAATAATGAGCCAAACAACATTTCTTATTTGATTAAGTTCCTTAT	1784
Db	521	SerleuGlnvalleuAsnmetSerhsasnlylsleuSerleuAsprrPheleuLysr	540
QY	1785	AAAGTGTGGAATCCCTCCAGGTTCTTGATTTACAGTCTCAATTCACATATGACTTCCAA	1844
Db	541	GlnproleuHlssetleuabprrlleuabprrcysSerPheabnargllemetlaserlys	560
QY	1845	AAACAGCAACTACAGACTTTTCCAAATGCTGTAAGTCTTCTTAATCTTACTCAGATGAC	1904
Db	561	GlnGlnGlnleuGlnaasnleuProargSerleuThrtryleuAsnleuThrGlnasnla	580
QY	1905	TTTGCTGTACTTGGAACACAGAGTTTCCGCAATGAGATCAAGACACAGAGGAGCTC	1964
Db	581	PhealacysvalcysGlnHlsGlnserPheleuGlntrpvallyasrGlnhrGlnleu	600
QY	1965	TTGTGTGAAGTGAACGAATGGAATGTGCAACACTTCAATGAATGAGGAGGAGCTGTG	2024
Db	601	LeuvalGlyalaglnGlnmetmetCysalaglnProleuabprrmetGlnasrmetProval	620
QY	2025	CTGAGTTG---AATATACCTGTTCAGATGAATTAAGACATCATTTGGTGTGGTCTCTC	2081
Db	621	LeuSerPheargasnlaAlaThrCysGlnleuSerlystrlleliserValserVal	640

Oy		2082	AGTGGTGTTGAGATCTGTGTGTAAGACAGTTCTGGTCTCATTAAGTTCTTAATTTTCACCTGATG	2144
Db		641	ThrValLeuLeuValSerValValGlyValLeuValTyxysPheTyxysPheHisLeuMet	660
Oy		2142	CTTCTTGCTGGCTGCATAAAGTAAAGTAAAGTAGAGAGTGAACAACATCTATGATGACTTGTATTC	2201
Db		661	LeuLeuAlaGlyCysIysIysTyrtgIYArgGlyGlusertleTyraPalalpheValile	680
Oy		2202	TACTCAAGCCAGAGATGAGACCTGGGTAAAGGAATGACCTAGTAAAGAATTGAAAGAAAGG	2261
Db		681	TyrserserGlnserpGluasprTrpaValArgAsnGluLeuValIysaaLeuGluGluGly	700
Oy		2262	GTCGCTTCATTTTGAAGCTCTGGCTTCACTACTAAGAGACCTTTATTCGCCGGTGGSCATTTGCT	2321
Db		701	ValProProPheGlnLeuCySleuHisTyrARXasPheIleProGlyValAlaIleAla	720
Oy		2322	GCCAACATCATCCATGAAAGTTTCCATTAAGAAGCCGAAGGTGATTTGTTGTGTGTCCAG	2381
Db		721	AlaasnIlelleGlnGluGlyPheHieIysSerHrgylstallleValValaserGln	740
Oy		2382	CATTTCATCCAGAGCCGCTGGTGTATCTTGTGAATATGATGATGCTCGACCTGGACGTTT	2441
Db		741	HlspherleGlnserargrTrpcysIlePheGluTyrtglurlelaGlnInThrTrpglnPhe	760
Oy		2442	CTGAGCAGCTGTGTGTGTATCATCTTCATTTGCTCTCGAAGAAGGTGAAGAGAACCCGCTC	2501
Db		761	LeuserSerarPaagIylelleIlePheIleValleuLndImlysSerLeuLeu	780
Oy		2502	AGGACAGAGGTGAGCTGTATCCGCTTCTCAGCAGGAACCTTAACCTGAGTGGAGAGAC	2561
Db		781	ArgGlnGlnValGluLeuTyrrAgIeuleuserHrgshnthryrLeuGluITrpGluasp	800
Oy		2562	AGTGTCTCTGGGGCGGACATCTTCTGTGAGACGACTCGAAGAAAGCCCTGTGGATGTAA	2621
Db		801	SerValleuGlyargHtsValPheTrpArgArgLeuHrgysAlaLeuAlaGlyLys	820
Oy		2622	TCATGAATCCAGAGGAACAGTGGGGTACAGAGATGCATTTGGCAGAGAAAGAACATCT	2678
Db		821	ProGlnInsPrroGluGlyThrAlaAspAlaGluThrAsnProGlnGlnValatThr	839
RESULT 9				
Q6WCDS		PRELIMINARY;	PRT; 841 AA.	
Q6WCDS		Q6WCDS;		
AC	05-JUL-2004	(TREMBLrel, 27, Created)		
DT	05-JUL-2004	(TREMBLrel, 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel, 27, Last annotation update)		
DE	Toll-like receptor 4.			
GN	Name=TLR4;			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovinae; Bos;			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2283971; PubMed=12915733; DOI=10.1073/pnas.1339571100;			
RA	White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;			
RT	"Haplotype variation in bovine Toll-like receptor 4 and computational			
RT	prediction of a positively selected ligand-binding domain."			
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).			
DR	EMBL; AY297040; AAO62700.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000483; LRR_cterm.			
DR	InterPro; IPR003885; LRR_cyst.			
DR	InterPro; IPR003591; LRR_typ.			
DR	InterPro; IPR000157; TIR.			
DR	Pfam; PF01463; LRRC7; 1.			
DR	Pfam; PF00560; LRR_1; 12.			
DR	Pfam; PF01582; TIR; 1.			
DR	PRINTS; PR00019; LEURICHRPT.			

QY	1965	TTGGTGGGAAGTTGAACTGGAAATGGATGCAACCTTCAGATTAAGCAGGAGCTGCTG	2024
Db	601	LeuValIGLYalagluGlnImeMcCysAlaGluProLeuAapMeGluAapMeProVal	620
QY	2025	CTGAGCTTGG---AATATCACTGTGCAGATGATAAAGACCATATGCTGTGTGGCTCTC	2081
Db	621	LeuSerPheArgAsnAlaThrCysGlnLeuSerLysTrnIleIleSerValSerValVal	640
QY	2082	AGTGTGCTTGAAGTATCTGTGTGTAGCAAGTTCTGTGCTTAAAGTTCTATTTTCACTGATG	2141
Db	641	ThrValLeuLeuValSerValValGlyValLeuValTYrLysPheTYrPheHisLeuMet	660
QY	2142	CTTCTGTGCTGGCTGATAAAGATGATGGTGAAGGATAAACATCTAATGAGCCTTTGTTATC	2201
Db	661	LeuLeuAlaGlyCysLysLysTYrCylTYrGlyGluSerTrnTYrAspAlaPheValIle	680
QY	2202	TACTCAAGCCAGATGAGAGACTGGGTAAAGATGAGCTACTGAAGAATTATTAAGAAAGG	2261
Db	681	TYrSerSerGlnAapGluAapTrpValArgAsnGluLeuValLysAsnLeuGluGlu	700
QY	2262	GTGCTTCATTTCACTCTGCTGCTTCATCAAGAGCTTTATTCCTGGGTGGCCATTGCT	2321
Db	701	ValProPheGlnLeuCysLeuHisTYrArgAspPheIleProGlyValAlaIleAla	720
QY	2322	GCCAAATCATTCATGAAAGGTTTCCATAAAGCCGAAAGGATGTTGTGTGCTCCAG	2381
Db	721	AlaAsnIleIleGlnGluGlyPheHisLysSerArgLysValIleValValValSerGln	740
QY	2382	CACCTTCATCCAGAGCCGCTGGGTATCTTGAATATGATGATGGTCACAGCTGGCAGTTT	2441
Db	741	HisPheIleGlnSerArgTrpCysIlePheGlnTYrGluIleAlaGlnTrnTrpGlnPhe	760
QY	2442	CTGAGCAGCTGTGCTGTATCATCTTCATTGTCTCGCAAGAGTGAGAGAACCCGTGCTC	2501
Db	761	LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGluLysSerLeuLeu	780
QY	2502	AGGACAGCAGGTGAGAGCTTACCGCTTTCAGACAGAACCATTTACCTGAGATGGAGAC	2561
Db	781	ArgGlnGlnValAlaGluLeuTYrArgLeuLeuSerArgAsnTrnTYrLeuGluTrpGluAap	800
QY	2562	AGTGTCCCTGGGGCGGCACATCTTCCTGAGAGAGACTCAGAAAGCCCTGTGATGTAA	2621
Db	801	SerValLeuGlyArgHisValAlaPheTrpArgLeuArgLysAlaLeuLeuAlaGlyLys	820
QY	2622	TCATGGAATCCAGAAAGAACGTGGGTACAGAGATGATCATTTGCGAGAGCAACATCT	2678
Db	821	ProGlnSerProGlnGlyThrAlaAspAlaGluTrnAsnProGlnGlnAlaIleThrThr	839
RESULT 10			
TLR4_FELCA	STANDARD;	PRT;	833 AA.
ID	TLR4_FELCA		
AC	P58727;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUN-2004 (Rel. 44, Last annotation update)		
DE	Toll-like receptor 4 precursor.		
GN	Name=TLR4;		
OS	Felis silvestris catus (Cat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
OX	NCBI_TaxID=9685;		
RN	SEQUENCE FROM N.A.		
RP	Yoshioka N., Kano R.;		
RL	"Felis catus Toll like receptor 4.",		
RL	Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.		
CC	-i- FUNCTION: Cooperates with ly6e and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (By similarity).		
CC	-i- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a		
CC	multi-protein complex containing at least CD14, ly6e and TLR4.		
CC	Binds ly6e via the extracellular domain. Binds MYD88 and TIRAP via		

CC		-1	the respective TIR domains (By similarity).	(By similarity)
CC		-1	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).	
CC		-1	SIMILARITY: Belongs to the Toll-like receptor family.	
CC		-1	SIMILARITY: Contains 1 leucine-rich (LRR) repeats.	
CC		-1	SIMILARITY: Contains 1 TIR domain.	
CC				
CC			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC				
DR	EMBL	AB060687	BAB3947.1; .	
DR	HSSP	O60603	1EYX.	
DR	GO	GO:0046696	C:lipopolysaccharide receptor complex; ISS.	
DR	GO	GO:0001550	F:lipopolysaccharide binding; ISS.	
DR	GO	GO:0004888	F:transmembrane receptor activity; ISS.	
DR	GO	GO:0007250	P:activation of NF-kappaB-inducing kinase; ISS.	
DR	GO	GO:0016046	P:detection of fungi; ISS.	
DR	GO	GO:0009598	P:detection of pathogenic bacteria; ISS.	
DR	GO	GO:0042116	P:macrophage activation; ISS.	
DR	GO	GO:0045671	P:negative regulation of osteoclast different. . . ; ISS.	
DR	GO	GO:0045362	P:positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO	GO:0045084	P:positive regulation of interleukin-12 biosyn. . . ; ISS.	
DR	GO	GO:0045368	P:positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO	GO:0045410	P:positive regulation of interleukin-6 biosyn. . . ; ISS.	
DR	GO	GO:0042088	P:T-helper 1 type immune response; ISS.	
DR	InterPro	IPR001611	LRR.	
DR	InterPro	IPR004483	LRR_Cterm.	
DR	InterPro	IPR003591	LRR_Typ.	
DR	InterPro	IPR00157	TIR.	
DR	Pfam	PF00560	LRR: 12.	
DR	Pfam	PF01463	LRRCT: 1.	
DR	Pfam	PF01582	TIR: 1.	
DR	PRINTS	SMO0019	LEURICHRPT.	
DR	SMART	SMO0369	LRR_TYP; 1.	
DR	SMART	SMO0082	LRRCT; 1.	
DR	SMART	SMO0255	TIR; 1.	
DR	PROSITE	PS50104	TIR; 1.	
KW	GlycoProtein		Immune response; Inflammatory response;	
KW	Leucine-rich repeat		Receptor; Signal; Transmembrane.	
FT	SIGNAL	1	23	Potential.
FT	CHAIN	24	833	Toll-like receptor 4.
FT	DOMAIN	24	632	Extracellular (Potential).
FT	TRANSMEM	633	653	Potential.
FT	DOMAIN	654	833	Cytoplasmic (Potential).
FT	REPEAT	53	76	LRR 1.
FT	REPEAT	77	100	LRR 2.
FT	REPEAT	101	124	LRR 3.
FT	REPEAT	128	149	LRR 4.
FT	REPEAT	150	173	LRR 5.
FT	REPEAT	174	197	LRR 6.
FT	REPEAT	203	225	LRR 7.
FT	REPEAT	228	252	LRR 8.
FT	REPEAT	310	334	LRR 9.
FT	REPEAT	350	372	LRR 10.
FT	REPEAT	373	398	LRR 11.
FT	REPEAT	399	421	LRR 12.
FT	REPEAT	422	445	LRR 13.
FT	REPEAT	447	469	LRR 14.
FT	REPEAT	470	494	LRR 15.
FT	REPEAT	495	518	LRR 16.
FT	REPEAT	520	542	LRR 17.
FT	REPEAT	544	566	LRR 18.
FT	REPEAT	568	592	LRR 19.
FT	DOMAIN	673	819	TIR.
FT	CARBOHYD	35	35	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	173	173	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	205	205	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	238	238	N-linked (GLNAC. . .) (Potential).

FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 570 570 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 625 625 N-linked (GlcNAc . . .) (Potential) .
 SQ SEQUENCE 833 AA; 95592 MW; 3E3A84F2BB8A55EA CRC64;

Alignment Scores:
 Pred. No.: 2,29e-239 Length: 833
 Score: 3283.50 Matches: 637
 Percent Similarity: 83.49% Conservative: 86
 Best Local Similarity: 73.56% Mismatches: 102
 Query Match: 48.83% Indels: 41
 DB: 1 Gaps: 2

US-09-396-985B-3 (1-3811) x TLR4_FELCA (1-833)

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OY 45 ATGATGTCGCGCGCGGCTGGAGCTGTGATCCAGACCATGGCTTCTCTGTCG 104
   ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MetMetProProThrArgLeuAlaGlyThrLeuIleProHlaMetAlaPheLeuSerCys 20

OY 105 GTGAGACCAAGAACTGGAGAGCCCTGCGTGAGACTTGGCCCTTAAACAACAGAAAGAC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 21 LeuArgProGluSerTrpAspProCysVal----- 30

OY 165 TGGCATGAACCCAGAGCTTTCAGACTCGGAGACCTCAGCCCTTACCCCGATTCCATTG 224
   30 ----- 30

OY 225 CTTCCTGTAATAGTCGCGGTTTATCACGAGAGTGATTCCTAATATTACTTCAATGC 284
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 -----GluValAlaProAsnIleThrTyrGlnCys 40

OY 285 ATGAGACTGAATTTCTACAAATCCCGACACCTCCCTTCTCAACCAAGAACTGGAC 344
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 41 MetAspLeuAsnLeuHisTyrSileProAspAsnIleProSerSerThrTyrSAspLeuAsp 60

OY 345 CTGAGCTTAAATCCCTGAGGACTTAAAGCACTAATAGCTTCTTCAAGTTTCCAGAAATG 404
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 MetSerPheAsnProLeuArgAsnLeuGlySerHisSerPheSerAsnPheProGluLeu 80

OY 405 CAGGCTGCTGATTTATCCAGAGTGTGAATCCAGACATTTGAAGATGGGCAATTCAGAGC 464
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 GluValLeuAspLeuSerAspGlyGlnIleGlnIleIleGlnAspAspAlaTyrGlnGly 100

OY 465 CTAAAGCACCTCTCTACTTAATATTGACAGAAACCCCATCCAGAGTTTGAAGCTGGGA 524
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 101 LeuAsnHisLeuSerIleLeuIleLeuThrGlyAsnProIleGlnArgLeuPheProGly 120

OY 525 GCGTTTTCGACTTATCAAGTTTACAGAGCTGTGCTGTGGAGCAAACTTACGATCT 584
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AlaPheSerGlyLeuSerSerIleuGlnThrLeuValAlaValIuThrAsnIleAlaSer 140

OY 585 CTAGAGAACTTCCCAATGGACATCTCAAAACTTTGAAAGACTTAATGGCTCAAT 644
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 141 LeuGlnAspPheProIleGlyHisLeuGlyThrLeuGlyGluLeuAsnValAlaHisAsn 160

OY 645 CTATTCCAATCTTTCAATTAACCTAGATATTTTCTAATCTGACCAATCTAGAGACTTG 704
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 161 LeuIleHisSerPheLeuSerProGluTyrPheSerAsnMetSerAsnLeuGluTyrLeu 180

OY 705 GACCTTTCAGACCAAGATTGAAAGTATTATTATTCACACACTGGGGTTTCAATCA 764
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 181 AspLeuSerAsnAsnTyrSileGlnAsnIleTyrHisTyrAspLeuGlnValLeuHisGln 200

OY 765 ATCCCTTACTATCTCTCTTAGACCTGTCCCTGAACCTTGAACCTTATTCACACCA 824
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 201 LysProLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220

OY 825 GGTGCAATTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATAATTTGATAGTTTA 884
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 221 GlyAlaPheGlyGluValTyrLeuArgGluLeuThrLeuArgSerAsnPheAsnSerThr 240
  
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OY 885 AATGTAAAGAAAATTGTATTCAAGATCGCTGGGTTTGAAGTCCATGTTGGTTCTG 944
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 AspValMetLeuValSerIleGlnGlyLeuAlaGlyLeuGlnIleHisGlnLeuValLeu 260

OY 945 GGAGAATTTAGAAATGAAGAAACTTGGAAAGTTTGACAAATTCGCTCTAGAGGCGCTG 1004
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 261 GlyGluPheLeuAsnGluArgAsnLeuGlyArgPheAspLysSerIleLeuGluGlyLeu 280

OY 1005 TGCATTTGACCATTTGAAGAAATTCGAGTATAGATCTTAGACTACTCGATGATATT 1064
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 281 CysAsnLeuIleIleGlnLysPheArgIleAlaTyrPheAspLysPheSerGluAspAla 300

OY 1065 ATTTGACTTAATTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGGTGAGTGACTATT 1124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IleAspSerPheAsnCysLeuAlaAsnValSerThrIleSerLeuValHisLeuTyrPhe 320

OY 1125 GAAAGGGTAAAGACTTTTCTTAATAATTTGGAGTGAACATTTAGATTTAGTTAACTGT 1184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 LysGlyLeuGlyGlnLeuProLysAsnLeuGlyTyrGlnArgGlnGlyLeuValAsnCys 340

OY 1185 AAATTTGACAGATTTCCCATTTGAATCTCAAAATCTTCAAAAGCTTACTTCACTTCC 1244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 GluPheGluGlnPheProThrTrpLysLeuAspProLeuLysGluLeuValPheSerAla 360

OY 1245 AACAAAGGTGGGAATGCTTTTCAAGAGTTGATCTTCAAGAGCTTGAAGTTTCTAGATCTC 1304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 AsnGluValArgAsnHisPheThrGlnValTyrGlnGluSerLeuGluLeuAspLeu 380

OY 1305 AGTAGAATGCGTTGAGTTCAAGGTTGCTGTTTCAAGAGATTTGGACACACACAC 1364
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 381 SerArgAsnAspPheSerLeuLysSerCysSerGluArgAspLeuIleThrTrpArg 400

OY 1365 CTAAAGTATTAGATTTGAGCTTCAATGCTGTTATACATAGATGTTCAAACTTCTGGGG 1424
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 401 LeuTyrHisLeuAspLeuSerPheAsnAsnIleIleThrIleSerSerAsnPheLeuGly 420

OY 1425 TTAGAACACTGAACATCTGATTTCCAGACTTCCAACTTTGAAACAAATGAAGTGAATT 1484
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 LeuGluGlnLeuGluTyrLeuAspPheGlnHisSerSerLeuLysGlnValSerAspPhe 440

OY 1485 TCAGATTCCTTACTCTACAGAAACCTCATTTACTTGAATTTCTCATCTCACACACGA 1544
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 441 SerValPheLeuProLeuLysAsnLeuArgTyrLeuAspIleSerTyrThrHisIleGln 460

OY 1545 GTTGCTTTCAATGGCACTTTCGAATGGCTGTGCAAGTCTGGAAGCTCTTGAAGAGCTGCG 1604
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 461 ValAlaPheHisGlyLeuPheAsnGlyLeuIleSerLeuGlnIleLeuLysMetAlaGly 480

OY 1605 AATTTTCCAGGAAAACTTCTTCCAGATATCTTCAAGAGCTGAGAAACTTGAACCTTC 1664
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 AsnSerPheGlnAspAsnPheLeuProAsnIlePheMetGlnLeuThrAsnLeuThrIle 500

OY 1665 CTGAGACCTCTCTCAGTGTCAACTGAGACAGTGTCTTCAACAGACTTTAACTCACTCTCC 1724
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 501 LeuAspLeuSerAspCysGlnLeuGlnGlnValIleSerGlnValAlaPheAsnSerLeuPro 520

OY 1725 AGCTTTCAGGTACTAAATATGAGCCCAACAACCTTCTTTCAATGGATACGTTCCATT 1784
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 521 LysLeuGlnLeuLeuAsnMetSerHisAsnHisLeuLeuSerLeuAspThrLeuProTyr 540

OY 1785 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTACAGCTCACTCAATATGACTTCAAA 1844
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 541 GluProLeuHisSerLeuGlnThrLeuAspCysSerPheAsnArgIleValAlaSerTyr 560

OY 1845 AAACAGAACTACAGCAATTTTCCAGATGCTTAGCTTTCTTAATCTTACTCAAGATGAC 1904
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 561 GluGlnGluLeuAsnArgHisPheProSerAsnLeuSerSerLeuAsnLeuThrArgAsnAsp 580

OY 1905 TTTCCTTGTACTTGTGAAACCAAGATTTCTTGCATATGATCAAGACCAAGGACGCTC 1964
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 581 PheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgGlnLeu 600
  
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QY 1965 TTGGTGAAGTGAACGAATGGAATGTGCAACCTTCAGATAAGAGGGCATGCTGTG 2024
 Db LeuValGluValGluGlnMetValCysAlaIleProLeuAspMetGlnGlnMetProMet 620
 QY 2025 CTGAGTTG--AATATCACTGTGCAGATGAATAAGCCATCTTGGTGTGGTCTC 2081
 Db LeuAspMetArgAsnAlaThrCysGlnValAlaArgLysThrIleThrGlySerValPhe 640
 QY 2082 AGTGTCTGTGATATCTGTGTAGAGTCTGTGCTGATATGAATGTTCTATTTTCACCTGATG 2141
 Db ThrValLeuLeuValPheLeuValValValLeuValTyrLysPheTyrPheHisLeuMet 660
 QY 2142 CTTCCTGTGGCTGCATTAAGTATGTAGAGGTGAAGAAACCTATGATGCTTGTATTC 2201
 Db LeuLeuAlaGlyCysLysLysTyrSerArgGlyGluSerThrTyrAspAlaPheValIle 680
 QY 2202 TACTCAAGCCAGATGAGACTGGGTGAAGAAATGAGCTAGTAAAGAAATTTGAAGAGG 2261
 Db TyrSerSerGlnAspGlnAspTyrValAlaArgAsnGlnLeuValLysAsnLeuGlnGlnGly 700
 QY 2262 GTGCTTCATTTAGCTGTGCTCTTCACTACAGAGACTTATTCCTGGGTGGCATTTGCT 2321
 Db ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
 QY 2322 GCCACATCATCCATGAAGTTTCCATAAAGCCGAAAGGTGATGTTGTGTGTCCAG 2381
 Db AlaAsnIleIleGlnGlnGlnGlnPheHisLysSerArgLysValIleValValValSerGln 740
 QY 2382 CATTTATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGCGAGTTT 2441
 Db HisPheIleGlnSerArgTyrCysIlePheGlnTyrGlyIleAlaGlnThrTyrGlnPhe 760
 QY 2442 CTGAGAGTGTGCTGTATCATCTTCACTGTGCTGAGAGAGGTGAAGAGACCTGCTC 2501
 Db LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu 780
 QY 2502 AGGACAGAGGTGAGCTGTACCGCTTCTCAGCAGAGAAACCTTACCTGAGTGGAGAGC 2561
 Db ArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgAsnThrTyrLeuGlnTyrPheGlnAsp 800
 QY 2562 AGTGTCTGTGGGGCGGACATCTTCTGAGAGCACTCAGAAAGCCCTGCTGATGTAA 2621
 Db SerValLeuGlnTyrArgHisIlePheTyrArgArgLeuArgLysAlaLeuLeuAspGlyLys 820
 QY 2622 TCATGGAATCCAGAGGA 2639
 Db ProArgCysProGlnGlnGly 826
 RESULT 11
 O6MCD4 PRELIMINARY; PRT; 841 AA.
 AC O6MCD4; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.13339571100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL; AY297043; AA062701.1; -
 DR EMBL; AY297041; AA062701.1; JOINED.
 DR EMBL; AY297042; AA062701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_cyst.
 DR InterPro; IPR003591; LRR_tyrp.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01562; LRR_1; 12.
 DR Pfam; PF01582; TIR_1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRCT_1.
 DR SMART; SM00365; LRR_S022; 6.
 DR SMART; SM00369; LRR_TYP; 13.
 DR SMART; SM00255; TIR_1.
 DR PROSITE; PS50104; TIR_1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 95954 MW; AD6D06ACEF4CC91 CR64;
 Alignment Scores:
 Pred. No.: 6,54e-239 Length: 841
 Score: 3277.50 Matches: 637
 Percent Similarity: 82.25% Conservative: 86
 Best Local Similarity: 72.47% Mismatches: 115
 Query Match: 48.74% Indels: 41
 DB: Gaps: 2
 US-09-396-985b-3 (1-3811) x O6MCD4 (1-841)
 QY 45 ATGATGTGTGCTCGCGCTGTGGCTGTGATCTGATCCAGACCTTCTCTCTGCTGC 104
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
 QY 105 GTGAGCCAGAAAGCTGGAGCCCTGCTGAGAGACTTGGCCCTAAACACAGAAAGAGC 164
 Db 21 LeuArgThrGlnSerTyrAspProCysVal ----- 30
 QY 165 TGCGATGAAAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCTTCAACCCGATTCATTG 224
 Db 30 ----- 30
 QY 225 CTTCCTGTAATGCTGCGGCTTTTATCAGGAGGTGGTCTTAATATTACTATCAATGC 284
 Db 31 -----GlnValValProAsnIleSerTyrGlnCys 40
 QY 285 ATGAGAGTAATTTTCACAAAATCCCGCAACCTCCCTTCCACCAAGAACCTGAGAC 344
 Db 41 MetGlnLeuAsnLeuTyrLysIleProAspAsnIleProIleSerThrLysMetLeuAsp 60
 QY 345 CTGAGCTTAATCCCTGAGAGCATTTAGGAGAGCTATGACTTCTTCAGTTTCCAGAACTG 404
 Db 61 LeuSerPheAsnTyrLeuArgHisIleGlnLysSerHisAsnPheSerSerPheProGlnLeu 80
 QY 405 CAGGTCTGATTTATTCAGGTGTGAATTCAGACAAATTGAAGATGGGCATATCAGAGC 464
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleLysIleIleGlnLysAspThrPheGlnGly 100
 QY 465 CTGAGCACTCTCTACCTTAATATGACAGAGAAACCCATCCAGAGTTTAAAGCCCTGGGA 524
 Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleAsn 120
 QY 525 GCCTTTCTGAGACTATCAAGTTTACAGAGCTGTGGTGTGGAGCAAAATCTAGACATCT 584
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuValSer 140
 QY 585 CTGAGAGACTTCCCATTTGAGCATCTCAAAATTTGAAGAACTTAATGTGGCTCACAAT 644
 Db 141 LeuAsnAspPheProIleGlnHisLeuLysAsnLeuLysGlnLeuAsnValAlaHisAsn 160
 QY 645 CTATTCATCATCTTGAATTAATCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTTG 704
 Db 161 PheIleHisSerPheLysLeuPro*****PheSerAsnLeuProAsnLeuGlnHisLeu 180
 QY 705 GACCTTTCAGAGAAACAGATTCAAAGTATTATGACAGAGACTTGGGGTTCATCAATCA 764

RC TISSUE=Alveolus;
 RA Shinkai H., Uenishi H.;
 RT "The function of porcine TLR4 gene."
 RL Submitted (Aug-2004) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB188301; BAD36843.1; -.
 DR PROSITE; PS50104; TLR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 841
 FT DOMAIN 24 632
 FT TRANSMEM 633 653
 FT DOMAIN 654 841
 FT REPEAT 53 76
 FT REPEAT 77 100
 FT REPEAT 102 124
 FT REPEAT 149 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 277 300
 FT REPEAT 310 334
 FT REPEAT 350 372
 FT REPEAT 373 398
 FT REPEAT 400 421
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 FT REPEAT 446 469
 FT REPEAT 471 494
 FT REPEAT 495 518
 FT REPEAT 520 542
 FT REPEAT 544 566
 FT REPEAT 568 592
 FT DOMAIN 673 819
 FT CARBOHYD 35 35
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 FT CARBOHYD 282 282
 FT CARBOHYD 309 309
 FT CARBOHYD 526 526
 FT CARBOHYD 575 575
 FT CARBOHYD 625 625
 SQ SEQUENCE 841 AA; 96308 MW; C52B2622D1C0E253 CRC64;

Alignment Scores:

Pred. No.: 1,37e-230
 Score: 3167.50
 Percent Similarity: 80.20%
 Best Local Similarity: 69.74%
 Query Match: 47.11%
 DB: 1
 Gaps: 2

US-09-396-985B-3 (1-3811) x TLR4_PIG (1-841)

Qy	45	ATGATGCTGCCTGCGCGCTGGTGGAGCTGTGATCCAGCAAGTGGCTTCCTCTG	104
Db	1	MetilethronylleuAlaValAlaThrilethronylleuAlaPheLeuSerCys	20
Qy	105	GTGAGACCAAGAAAGCTGGAGCCCTGGCTGGAGACTTGGCCCTTAACACAGAGAAGC	164
Db	21	LeuArgSerGluSerThrPheProCysVal	30
Qy	165	TGGATGAACCCAGACCTTTCAGACTCCGAGGCTCAGCCCTTACCCGATTCATTG	224
Db	30		30
Qy	225	CTTCTGCTAAATGCTGCCGTTTATGACGAGGTGCTCTATATTACTTAACTGAC	284
Db	31	-----GlnValAlaProleuIleSerTyrGlnCys	40
Qy	285	ATGAGCTGAATTTCTACAAATCCCGACAACTCCCTTTCACCAAGAACTGGAC	344
Db	41	MetGluLeuAsnPhenTyrIlePheProAsnIleProThrSerValIleLeuAsp	60
Qy	345	CTGAGCTTATATCCCGAGGACATTTAGAGGCTATGCTTTCAGTTCCCGAGACTG	404
Db	61	LeuSerPheAsnTyrLeuSerThrLeuAspSerAsnSerPheSerPheProGluLeu	80
Qy	405	CAGGTGCTGATTTATCCAGGTGTGAATCCAGACATTTAGATGGGATATCAGAGC	464
Db	81	GlnValLeuAsnLeuSerThrArgCysGlnIleGlnThrIleAspPhePheAlaTyrGlnGly	100
Qy	465	CTAAGCCACTCTCTAATTAATTGACAGAAACCCATCCAGACTTTAGCCCTGGGA	524
Db	101	LeuAsnTyrLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly	120
Qy	525	GCTTTTCTGAGCTATCAATTTACAGAACTGGCTGGCTGGAGACAAATTCAGACTC	584
Db	121	AlaPheSerGlyLeuProSerLeuGlnValAlaValGlnThrAsnLeuAlaSer	140
Qy	585	CTAGAGACTTCCCAATGAGACATCTCAAACTTTGAAAGACTTAATGTGGCTCACAAT	644
Db	141	LeuGluAspPheProIleGlyHisLeuValThrLeuAsnGluLeuAsnValAlaHisAsn	160
Qy	645	CTTATCCATCTTTCAATTAATCTGAGATTTTCTGATTTGACCAATTCAGACACTTG	704
Db	161	HisIleHisSerPheLeuProGluTyrPheSerAsnLeuProAsnLeuGluHisLeu	180
Qy	705	GACCTTTCAGCAAGATTCAAAGTATTATTTGACACAGACTTCGGGGTTTCATCAAA	764
Db	181	AspLeuSerSerLeuAsnValIleGluAsnIleTyrHisGlnHisLeuHisGln	200
Qy	765	ATGCCCCCTACTCAATCTCTTATAGACCTGCTGACCTTGAACCTTATTCACACA	824
Db	201	ValProLeuHisAsnLeuSerLeuAspLeuSerLeuAsnProLeuAsnPheIleGluPro	220
Qy	825	GCTGCAATTAAGAAATTAAGCTTCAAGCTTCAAGCTTCAAGAAATTAATTTGATAGTTA	884
Db	221	GlyAlaPheAsnValIleArgLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSerSer	240
Qy	885	AATGTAATGAAGAACTGTATTAAGCTGTGGCTGGTTTGAAGTCCATCGTTGGTCTG	944
Db	241	AspValMetCysThrCysIleGlnGlyLeuAlaGlySerValAsnGlnLeuValLeu	260
Qy	945	GGAAGATTTTGAAGTAAGAGAACTTGAAGAACTTGAAGAACTGCTGAGAGGGCTG	1004
Db	261	GlyGluPheLeuAsnGluArgAsnLeuGlySerPheSerPheValLeuGluGluLeu	280
Qy	1005	TGCAATTTGACATTTGAGAAATTCGATTTAGACATTTAGACATTTAGACATTTAT	1064
Db	281	CysAsnLeuThrLeuGluGlnPheArgIleAlaHisPheGlyGluPheProAspArgVal	300
Qy	1065	ATTGACTTATTTATTTGTTTGAAGAAATGTTTCTTCAATTTTCCCTGGTGAAGTAT	1124
Db	301	SerAspLeuPheAsnValCysLeuAlaAsnAlaSerValIleSerLeuLeuSerLeuAsnLeu	320
Qy	1125	GAAAGGTAAGAAAGCTTTCTTATTAATTTGAGTGGCAATTTAGAAATTTAGTAACTGT	1184


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Db      321  HisGlyLeuGlu1aLeuProAsnAspPheArgTrpGlnHisLeuGluValaValaAsnCyS 340
      1185  AAATTTGGACAGTTTCCACATTTGAAACSTCAATCTCTCAAAAGGCTTACTTCACTTCC 1244
      341  LysLeuGlnGlnPheProAlaLeuLysPheAsnSerLeuLysPheValPheLysAsp 360
      1245  AACAAAGTGGAGATGCTTTTTCAGAAAGTGAATCTACCAAGCCCTGAGTTTCTAGATCTC 1304
      361  AsnLysHisMetHisThrPheThrGlnHisLeuAsnLeuProAsnLeuGlnPheLeuAspLeu 380
      1305  AGTGAAGATGGCTTGAAGTTTCAAAAGTTGCTGTCTCAAGATGATTTTGGACACACAGC 1364
      381  SerGlyAsnHisLeuSerPheLysGlyCysCysSerHisAsnGluPheGlyThrHisLys 400
      1365  CTAAAGATTTTGAATCGAGCTTCAATGGTTCAGTGTATTTATTCAGATGTTGAAACCTTGGGC 1424
      401  LeuLysHisLeuAspLeuSerPheAsnGlnHisLeuThrMetLysSerAsnPheMetGly 420
      1425  TTGAACAACATGACATGATCTGATTTTCACAGATTTCTCAATTTGAAACAAATGAGTGAATT 1484
      421  LeuGlnGlnLeuGluTrpLeuAspPheGlnHisSerSerLeuLysGlnHisAsnAspPhe 440
      1485  TCAATATTTCTATCACTCAAGAAACCTGATTTTACCTTGAATTTCTCACTTCAACACAGA 1544
      441  SerLeuPheLeuSerLeuArgAsnLeuHisLeuTrpLeuAspHisLeuSerTrpThrAsnHis 460
      1545  GTTGGCTTCAATGGACATTTCAATGGTTCAGTGTTCAGCTGTGCAAGTCTGAAATGGAGCTGC 1604
      461  ValValaPheArgGlyLeuPheAlaGlyLeuValaSerLeuGlnHisLeuLysMetAlaGly 480
      1605  AATTTCTTCCAGGAAACCTTCTCCAGATATCTTCCAGAGCTGAGAGCTGAGAACTTGCCTTC 1664
      481  AsnSerPheGlnAsnAsnLeuLeuProAspValPheThrAspLeuThrAsnLeuHisLeu 500
      1665  CTGAGACTCTCTCACTCACTCACTGAGACAGTGTCTCCAAACAGATTTAACTCACTCTCC 1724
      501  LeuAspSerLeuLysCysGlnLeuGlnValaSerGlnArgAlaPheHisSerLeuPro 520
      1725  AGCTTTCAGGTACCAATATATGAGCAACAGACTTCTTTCATCTGATTAAGTTTCCCTAT 1784
      521  ArgLeuGlnValaLeuAsnMetSerHisAsnArgLeuLeuPheLeuAspTrpLeuProTrp 540
      1785  AAGTGTGTGAACCTCCACAGTCTTCTGATTTACAGTCAATCAATATGATCAATGCTTCCAA 1844
      541  LysPheLeuHisSerLeuAlaGlyLeuAspCysSerTrpAsnLeuHisLeuAlaSerLys 560
      1845  AAACAGGAACTACAGCAATTTTCCAGATGATCTTCTTAAATCTTACTCAGAAATGAC 1904
      561  GlnGlnGlnLeuGlnHisLeuProArgSerLeuAlaPheLeuAsnLeuThrLysAsnAsp 580
      1905  TTTGCTTGTACTGTGTAACACAGAGTTCCTGCAATGATCAAGCAACAGAGCACTC 1964
      581  PheSerCysAlaCysGlnHisGlnHisPheLeuGlnHisValLysAspGlnLysGlnLeu 600
      1965  TTGGTGAAGTGAATGCAATGATGTAACACACTTCAATGATTAAGAGGAGCTGTG 2024
      601  LeuValGlyAlaGlnMetValCysThrGlnPheLeuGlnMetGlnAspLeuProVal 620
      2025  CTGAGATTG--AATATCACCTGTGAGATGAATAGACATCATTTGTTGTGTGCTGCTC 2081
      621  LeuSerPheArgAsnAlaThrCysGlnHisSerGlnHisValHisSerAlaSerValLeu 640
      2082  AGTGTGTTGATGATATCTGTTGAGACAGTCTGTCTATAGTTCTATTTTACCTGATG 2141
      641  ThrPheLeuLeuValSerValAlaGlyLeuValaLysPheTrpPheHisLeuLeu 660
      2142  CTCTTCTGCTGCTCATAAAGTATGATGAGAGTGAACATCTTATGAGCTTGTATGCT 2201
      661  LeuPheValGlyCysLysLysTrpGlyArgGlyLysSerThrTrpAspAlaPheValHis 680
      2202  TACTCAAGCAGAGATGAGACTGGGTAAAGAAATGAGCTAAGAAATTTAGAAAGAGG 2261

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Db      681  TyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValaLysAsnLeuGlnGly 700
      2262  GTGCCCTCATTTCAAGCTGTGCTTCACTCACTACAGAGATTTATTTCCCGTGTGGCATTTGCT 2321
      701  ValProProPheHisLeuLysCysLeuHisTrpArgAspPheHisLeuProGlyValaHisLeu 720
      2322  GCCAATCATTCATGAAAGTTCATTAAGCCGAAAGGTGATTTGTGTGCTCCAG 2381
      721  AlaAsnHisLeuGlnGlnGlnPheHisLysSerArgLysValaHisValaValaSerGln 740
      2382  CACTTATTCACAGACCGCTGTGTATCTTGAATATGAAATTTCTCAAGCTGAGCTT 2441
      741  HisPheHisLeuSerTrpTrpCysHisLeuPheGlyTrpGlnHisLeuHisThrTrpGlnPhe 760
      2442  CTGAGACGTGCTGTGATTCATCTTCAATGCTTCAAGAGTGTGAGAGAGACCTGTCTC 2501
      761  LeuArgSerHisAlaGlyLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeu 780
      2502  AGGACGACGTGAGCTGTACCGCTTCTCAAGAGAGACATTTACCTGAGTGGAGAGAC 2561
      781  ArgGlnGlnValaGlnLeuTrpArgLeuLeuSerArgAsnThrTrpLeuGlnTrpGluAsp 800
      2562  AGTGTCTGTGGCGGACATCTTCTGAGACACATCAAGAAACCTGCTGATGTTAA 2621
      801  SerValLeuGlyArgHisLeuPheTrpArgLeuLysAlaLeuLeuAspGlyLys 820
      2622  TCATGATTCAGAGAAACAGTGGGTACAGATGCAATTTGGACGAGAAACAATCT 2678
      821  ProTrpSerProGlnGlyThrGluAspSerGlnSerGlnHisAspThrThrAla 839

RESULT 13
ID      08MIQ2      PRELIMINARY;      PRT;      839 AA.
AC      08MIQ2;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      T011-like receptor 4.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kajihawa O., Frevort C.W., Goodman R.B., Wong V.A., Martin T.R.,
RA      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AI101394; AA050060.1; -.
DR      HSSP; 060603; 1077.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Cyp.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF00560; LRR_1; 11.
DR      Pfam; PF01582; TIR_1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00369; LRR_TYP; 1.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SHQUNCE 839 AA; 96338 MW; 09F7D401EC14B6A CRG64;

Alignment Scores:
Pred. No.:      2,09e-223      Length:      839
Score:          3072.50      Matches:      611
Percent Similarity: 78.89%      Conservative: 84
Best Local Similarity: 69.35%      Mismatches: 141
Query Match:     45.69%      Indels:      45
DB:              2      Gaps:      4

US-09-396-985b-3 (1-3811) x 08MIQ2 (1-839)

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Qy	45	ATATGTCCTGCTCGGCGCTGGGAGACTGTCATGCTCCAGGACCTTCTCTCCGAC	104
Db	1	MetMetProArgLeuArgLeuAlaGlyThrIleValProAlaMetAlaPheLeuSerTyr	20
Qy	105	GTGAGACCAAGAAAGCTGGAGCCCTGCTGAGAGACTTGCGCTTAAACCAACAGAAAGC	164
Db	21	LeuArgProGluIleTyrGluProCysVal	30
Qy	165	TGGCATGAAACCCAGAGCTTTCAGACTCCGGAGCCTCAGCCCTTACCCCGCATTCATG	222
Db	30	-----	30
Qy	225	CTTCTTGCTAAATGCTGCGCTTTTATCAGAGAGTGCTTCTAATATCTTATCAATGC	284
Db	31	-----GluValValProMetIleThrTyrGlnCys	40
Qy	285	ATGAGACTGAATTTCTACAAATCCCGCAACACTCCCTCTTCAACCAAGAACTGGAC	344
Db	41	MetGluIlyAsnLeuTyrLysIleProAspAsnIleProPheSerThrLysAsnLeuAsp	60
Qy	345	CTGAGCTTAAATCCCTGAGGCACTTAAAGGACCTTAGCTTTCATGTTCCCGAACTG	404
Db	61	LeuSerPheAsnLeuLeuGluHisLeuGlySerHisSerPheLeuHisValSerGluLeu	80
Qy	405	CAGGTGCTGGATTTATCCAGTGCTGTGAATCCAGACAATTGAAGATGGGGCATATCAAGC	464
Db	81	HisPheLeuArgPheLeuSerArgCysLysIleHisThrIleGluAspArgAlaTyrGlnGly	104
Qy	465	CTAAGCCACCTCTCTACCTTAATATTATGACAGAAACCCATCTCAAGATTAGCCCTGGGA	524
Db	101	LeuLysAsnLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuSerProGln	120
Qy	525	GCGTTTCTGAGATCATCAAGTTTACAGAGCTGGTGCGTGGAGACAATCTGACATCT	584
Db	121	AlaPheSerGlyLeuSerAsnLeuGlnLysLeuValAlaValGluThrHisIleuThrSer	144
Qy	585	CTAAGAACTTCCCAATGGACATCTCAAACTTGAAGAATTAATGTGGCTCACAAT	644
Db	141	LeuGluYAspPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn	160
Qy	645	CTTATCCAACTTTCAAAATTAACCTGAGTATTTTCTAATCTGACAACTTGAAGACATG	704
Db	161	LeuIleHisSerPheSerIleProAspArgTyrPheSerAsnLeuSerLeuGlnHisLeu	180
Qy	705	GACCTTCCAGACAAGATTCAAAGATATTATTCAGACAGACTTGCGGGTCTACATCA	764
Db	181	AspLeuSerAsnAsnLysIleGlnSerIleTyrHisValAspLeuArgValLeuHisGln	200
Qy	765	ATGCGCCTACTCAATCTCTCTTTTAAACCTGTCCCTGAACCCCTATGACTTTATCCAA	824
Db	201	MetProLeuGlyThrLeuSerLeuAspLeuAlaLeuAsnProIleAspPheIleProPro	220
Qy	825	GGTGCAATTAAAGAAATTTAGGCTTCAAGCTGATTCATTAAGAAATTTTGTATGATTTA	884
Db	221	GlyAlaPheGluAlaIleArgLeuHisGluIleuIleLeuLysSerAsnPheLysSerThr	244
Qy	885	AATGTAAAGAAACTTGATTCAGAGCTGTGCGTGGTGTGAAGTCCATCGTTGGTCTG	944
Db	241	AsnIleMetLysIleCysIleGlnGlyLeuSerGlyLeuGluValHisArgLeuValLeu	260
Qy	945	GGAGAAATTGAATGAAGAACTGAGAAAGTTTGAACAATCGCTCTAGAGGGCTG	1004
Db	261	GlyGluPheLysAsnGluLysArgMetCysLysAsnPheAspLysSerAlaLeuGlnGlyLeu	280
Qy	1005	TGCAATTGACCAATTGAAGAAATTCGATTTAGCATTTAGACTACTACCTCGATGATATT	1064
Db	281	CysAsnLeuAlaIleGlnGluPheArgLeuAlaTyrIleAspArgLeuGluGlyYAsnIle	300
Qy	1065	ATTGACCTATTAAATGTTTGAACAATGTTTCTCATTTCCCTGGTGAAGTGATCATATT	1124
Db	301	ThrAspLeuPheAspCysLeuGluAsnValSerValMetAlaLeuValHisMetCysTyrIle	320

QY	1125	GAAGGGTAAAGACCTTTCTCTAAATTTGGAGATGGCAACATTAGATTAAGTAACTGT	118
Dp	321	AspansnglmgulIephroPolysAspPheSerTripySerLeuGluPheIleAsnCys	340
QY	1185	AAATTTGGACGG--TTTCCACATTGMAACTCAAACTCTCCAAAAGGCTTACTTTCACT	1241
Dp	341	GluPheSerGluAsnIlePhePheLeuLysLeuSerSerLeuArgLeuIlePheThr	360
QY	1242	TCCACAAAGGTGGAAATGCTTTTTCAGAGTTGATCTACAGGCTTGAAGTTTCTGAT	1301
Dp	361	AlaAsnLysGlyValArgThrPheProGluLeuAsnThrProSerLeuGluPheLeuAsp	380
QY	1302	CTCAGTGAATATGGCTTGAGTTTCAAAGCTTGCCTTCCAAAGTAGATTTTGGACACAC	1361
Dp	381	IleSerAsnAsnGlyLeuSerLeuGlnSerCysCysSerValAsnSerLeuArgLeuThr	400
QY	1362	AGCCTAAAGATTTAGATCTGAGCTTCAAAGTGTTTTCACATGAGTCCAAACTTCTTG	1421
Dp	401	GlnLeuLysPheIleuAsnLeuSerPheAsnGlyValIleThrThrSerAsnPheVal	420
QY	1422	GGCTTGAACACACTAGAACACTTGGAATTTCCAGCATTCCAATTTGAAAACAATGAGTAG	1481
Dp	421	GlyLeuGlnGlnLeuGlnIleuThrPheGlnIleSerAsnLeuArgAsnIleAsnGln	440
QY	1482	TTTTCAATATTCCTATACCTCAGAAACCTCATATTACTTCACATTTCTCATACACACC	1541
Dp	441	PheSerIlePheLeuSerLeuAsnAsnLeuLysLeuLysAspIleSerTyrThrHisIle	460
QY	1542	AGACTTGCCTTTCAAATGCGATCTTCAAATGGCTTGCCTCCAGTCTCGAAAGCTTGAATGGCT	1601
Dp	461	ArgValAlaPheArgGlyIlePheAspGlyLeuTyrSerLeuArgValLeuLysMetAla	480
QY	1602	GGCAATTCCTTCCAGAAAACTTCTCTCAGATATCTTCACAGAGCTGAGAACTTGACC	1661
Dp	481	GlyLysnAlaPheGlnAspAsnArgLeuLeuAsnIlePheThrGluMetThrSerLeuThr	500
QY	1662	TTCTGTGACCTCTCTCAGTGTCACTGGAGCAGTGTGTCTCCAAACGATTTAACTACTC	1721
Dp	501	ThrLeuAspLeuSerSerCysGlnLeuGlnGlnValTyrGlnGlyAlaPheGlnSerLeu	520
QY	1722	TCCAGTCTCAGGATCTAAATATATAGGCCAACAACTCTTTTCATGTAGATAGTTCCT	1781
Dp	521	ProArgLeuGlnSerLeuAsnMetSerHisAsnAsnLeuValLeuAspThrLeuThr	540
QY	1782	TATAAGTGTCTGAACCTCCCTCCAGGTTCTTGATTACAGTCCATCATCATATGACTCC	1841
Dp	541	TyrIleCysLeuTyrSerLeuGlnValLeuAspLeuSerPheAsnHisIleGlyAsnIle	560
QY	1842	AAAAACAAGAACTACAGCACTTTTCCAGTAGTCTAGCTTTCTTAATCTTTACTCAGAA	1901
Dp	561	ThrGluProGlyGlnGlnHisPheProSerAsnLeuThrLeuLeuHisIleuThrLysAsn	580
QY	1902	GACTTTCCTTGACTTGTTGTAACACCAAGTTTCTCTGAAAGATTCAGAACCCAGAGCAG	1961
Dp	581	AlaPheValCysAspCysGlnHisGlnIlePhePheCdnTrpIleLysAspGlnAspArg	600
QY	1962	CTCTTGTGTGAAGTTGACAGCAATGAGATGTGCACACTTCAGATTAAGCAGGCGATGCT	2021
Dp	601	LeuLeuValGlnValGlnGlnMetValCysIleThrProProAsn-----MetPro	617
QY	2022	GTGCTGAGTTGG--AATATCACCTGTCCAGATGAAATAAGCACTATGTGTGTGCGCT	2078
Dp	618	ValLeuSerPheThrAsnAlaIleThrCysGlnIleSerThrIleIleSerValSerVal	637
QY	2079	CTCAGTGTGCTGAGTATCTGTTGTGTAGCAGTTCTGTCTATATAGTCTATATTTTCACTG	2138
Dp	638	PheSerValLeuValValSerPheAlaValValLeuValTyrLysPheTyrPheProLeu	657
QY	2139	ATGCTTTCGTGCTGCATAAAGATATGATAGAGTGTAAGAAACATCTATGATGCTTTGT	2198
Dp	658	MetLeuLeuValGlyAspArgLysTyrGlyArgGlyLysLeuSerValTyrAspAlaPheVal	677
QY	2199	ATCTACTCAAGCCAGATGAGACTGGGTAAAGGATAGCTAGTAAAGAAATTTAGAAAGA	2258

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Db 678 IletySerSerGlnAspArgIuAspTrpValArgAsnGluLeuValLysAsnLeuGluGlu 697
QY 2259 GGGGTGCTTCATTTACGCTCTGCTTCACTACAGAGACTTTATCCCGGTGGCCATT 2318
Db 698 GLYVALProProPheArgLeuCySLeuH1stYArgAspPheIleProGlyValAlaIle 717
QY 2319 GCGCCAAACATCATCCATGAAGGTTTCCATAAAGCGGAAGGATGTGTTGGGTCC 2378
Db 718 AlaAlaAsnIleIleGlnGluGlyPheH1sbSerArgLysValIleValValSer 737
QY 2379 CAGCACTTCATCCAGAGCCGCTGGTGTATTTGAATATAGATTGCTCAGACCTGAG 2438
Db 738 GlnH1sPheIleGlnSerArgTrpCySLeuPheGluTrpGluIleGlnTrpGln 757
QY 2439 TTTCTGAGCAGTGTGTGTATCATTTATGTTCTCTGAGAAAGGTGGAAAGACCTG 2498
Db 758 PheLeuSerSerH1sbArgIleIlePheIleValLeuGlnLysValGlnLysSerLeu 777
QY 2499 CTCAGGAGAGAGGTGAGCTGTACCGCTTCTCAGAGAAACCTTACCTGAGTGGAG 2558
Db 778 LeuArgGlnArgValGluLeuTrpYArgLeuSerArgAsnTrpYLeuGluTrpGlu 797
QY 2559 GAGAGTGTCTGGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCCTGTGATGT 2618
Db 798 AspThrValLeuGlyArgH1sIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGly 817
QY 2619 AAATCATGATCATCAGAAAGAAACAGTGGTACAGGATGATGATGGCAGAGCAATCT 2678
Db 818 LysThrLeuSerProGluGluMetValArgAlaArgAlaAsnGlnGlnAlaMetThr 837
QY 2679 ATC 2681
Db 838 Leu 838

RESULT 14
TLR4_CRIGR ID TLR4_CRIGR STANDARD; PRT; 838 AA.
AC 09WV82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_Taxid=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=20148868; PubMed=10683379;
RA Lien B., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,
RA Penton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,
RA Ingalls R.R., Golenbock D.T.;
RT "Toll-like receptor 4 imparts ligand-specific recognition of bacterial
lipopolysaccharide."
RL J. Clin. Invest. 105:497-504(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
CC their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
CC hamster ovary fibroblast cell line.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF153676; ABD41891.1; -.
DR HSSP; Q15399; IPTV.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01562; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 838
FT DOMAIN 26 629
FT TRANSMEM 630 650
FT DOMAIN 651 838
FT REPEAT 31 52
FT REPEAT 53 75
FT REPEAT 76 99
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FT REPEAT 351 370
FT REPEAT 371 393
FT REPEAT 396 419
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FT REPEAT 494 516
FT REPEAT 517 538
FT REPEAT 541 563
FT REPEAT 565 589
FT REPEAT 670 816
FT DOMAIN 34 34
FT CARBOHYD 115 115
FT CARBOHYD 172 172
FT CARBOHYD 204 204
FT CARBOHYD 237 237
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FT CARBOHYD 572 572
FT CARBOHYD 622 622
SQ SEQUENCE 838 AA; 96277 MW; 129B33596B908B48 CRC64;

Alignment Scores:
Pred. No.: 6.13e-217
Score: 2987.00
Percent Similarity: 78.84%
Best Local Similarity: 66.10%
Query Match: 44.42%
DB: 1 Gaps: 5

US-09-396-985b-3 (1-3811) x TLR4_CRIGR (1-838)
QY 45 ATATGTCTGCTGCGGCTGAGTGTGATCCAGCATGAGCTTCTCTCTGCTG 104

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[illegible][illegible]

QY 225 CTTCTGCTAATGCTGCCGTTTATGACGGAGTGGTTCCTAATATTATTAATTATCAATGC 284
 DB 30 -----GluValLeuProAsnIleThrTyrGlnCys 39
 QY 285 ATGAGAGCTGAATTTCTACAAATATCCCGACAACTCCCTTCTGACCAAGAACCTTGAC 344
 DB 40 MetAspGlnAsnLeuSerTyrIleProIleAspIleProTyrSerThrIleValAsnLeuAsp 59
 QY 345 CTGAGCTTTAATCCCGTGGAGCAATTTAGGACCTTATGCTTTCAGTTTCCCGAACTG 404
 DB 60 LeuSerPheAsnProLeuTyrIleLeuArgSerTyrSerPheThrAsnPheSerGlnLeu 79
 QY 405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGACAAATTGAAGATGGGACATATCAGAGC 464
 DB 80 GlnThrLeuAspLeuSerTyrGlyIleGlnThrIleGlnAspTyrValIleThrPheGly 99
 QY 465 CTAGGCAACCTCTCTACCTTAATATATGACAGAAACCCCATCCAGAGTTTATGACCTGGGA 524
 DB 100 LeuAsnGlnLeuSerThrIleValIleThrGlyAsnProIleTyrSerPheSerProGly 119
 QY 525 GCCCTTTCTGACATATCAAGTTTACAGAGCTGGTGGCTGGAGCAAACTTACATCT 584
 DB 120 SerPheSerGlyLeuThrAsnLeuGlnAsnLeuValAlaValGlnThrTyrSerMetThrSer 139
 QY 585 CTAGAAACCTTCCCATTTGACATCTGCAAACTTTGAAAGAACTTAATGGCTGACAAAT 644
 DB 140 LeuGlnGlyPheAsnIleGlyGlnLeuIleSerLeuTyrValAsnValAlaIleAsn 159
 QY 645 CTATTCGAATCTTTCAATATTAACCTGATATTTTCTAATCTGACCAATCTTACGACCTTG 704
 DB 160 LeuIleIleSerPheTyrLeuProGlyTyrPheSerAsnLeuThrAsnLeuGlnIleVal 179
 QY 705 GACCTTTCCAGCAACAAAGATTCAAGTATTATTCACACAGCTTGGGGTTCTACATCA 764
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 DB 200 AsnProGlnValAsnLeuSerLeuAspLeuSerLeuAsnProIleAspSerIleGlnAla 219
 QY 825 GGTGCAATTTAAGAAATTAAGCTTCATACCTGACCTTAAAGAAATTTTGTATAGTTTA 884
 DB 220 GlnIlePheGlnGlyIleArgLeuIleGlnLeuThrIleuArgSerAsnPheAsnSerSer 239
 QY 885 AATGTAATGAAAATTTGTATTAAGAGTCTGGCTGGTTTAAAGATCCATCGTTGGTTCTG 944
 DB 240 AsnValLeuTyrMetCysLeuGlnAsnMetThrGlyLeuIleValIleAspLeuIleLeu 259
 QY 945 GGAGAAATTTGAATGAAGAACTTGAAGAAAGTTTGAACAAATTCGCTTACAGAGGCTG 1004
 DB 260 GlnGlnPheTyrAsnGlnIleArgAsnLeuGlnSerPheAspArgSerValMetGlnGlyLeu 279
 QY 1005 TGCATTTGACATTTGAGAAATTCGATTTAGCATATTAAGACTTACCTGATGATAT 1064
 DB 280 CysAsnValSerIleAspGlnPheArgLeuThrTyrIleAsnIlePheSerAspAspIle 299
 QY 1065 ATTGACTTATTTAATTTGTTGACAAATGTTTCTTATTTCCCTGGAGTGTACATAT 1124
 DB 300 TyrAsnLeu--AsnCysLeuAlaAsnIleSerIleAsnSerPheThrGlyValIleIle 318
 QY 1125 GAAAGGTAAAGACTTTTCTTAATTTGGAGAGCAACTTGAAGATTGAATTAAGTACGT 1184
 DB 319 LysIleIleAlaAspValProArgIlePheTyrTrpGlnSerLeuSerIleIleArgCys 338
 QY 1185 AATTTGACAGTTTCCACATTTGAATCTCAAAATCTCAAAAGCTTACTTTCATCTCC 1244
 DB 339 HisLeuTyrProPheProTyrLeuSerLeuProPheLeuTyrSerTrpIleThrThr 358
 QY 1245 AACAAAGGTGGAGATCTTTTTCAGAAAGTTGATTTACCAAGCTTTGAGTTTCTAGATCTC 1304
 DB 359 AsnArgGlnAspIleSerPheGlyGlnLeuAlaLeuProSerIleuArgTyrLeuAspLeu 378

QY 1305 AGTAAATATGCTGAGTTTCAAAAGTTCGTCTTCAAGATATTTGGAGAACACG 1364
 DB 379 SerArgAsnIleMetSerPheArgGlyCysCysSerTyrSerAspPheGlyThrAsnAsn 398
 QY 1365 CTAAAGTATTTAATGCTGAGCTTCAATGGTGTATTATCACTAGATTAACCTTTGGGC 1424
 DB 399 LeuTyrTyrLeuAspLeuSerPheAsnGlyValIleLeuMetSerAlaAsnPheMetGly 418
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 QY 1485 TCAGTATTTCTTACCTACAGAAACCTCATTTTACCTTGACATTTCTCTACTACACACAGA 1544
 DB 439 SerValPheLeuSerLeuGlnTyrValSerLeuTyrLeuAspIleSerTyrThrAsnThrLys 458
 QY 1545 GTTGCTTTCAATGGCATCTTCAATGGCTTTCGAGTCTGCAAGTCTTGAATATGGCTGGC 1604
 DB 459 IleAspPheAspGlyIlePheLeuGlyLeuIleSerLeuAsnThrLeuTyrMetAlaGly 478
 QY 1605 AATTTCTTCCAGGAAACTTCCCTTCCAGATATCTTCCAGAGCTGAGGAAACCTTGACCTTC 1664
 DB 479 AsnSerPheTyrAspAsnThrIleLeuSerAsnValPheThrAsnThrIleAsnLeuThrPhe 498
 QY 1665 CTGAGACCTCTCTGAGTGTCAACTGAGACAGTGTCTTCCACAGCATTTAATCTACCTGCC 1724
 DB 499 LeuAspLeuSerTyrCysGlnLeuGlnGlnIleSerArgGlyValPheAspThrLeuTyr 518
 QY 1725 AGTCTTCAAGTAAATATATGAGCCACACAACTCTTTTCAATGATGATACGTTTCTTAT 1784
 DB 519 ArgLeuGlnIleLeuAsnMetSerThrIleAsnAsnLeuLeuPheLeuAspProSerHisTyr 538
 QY 1785 AAGTGTCTGAACCTCCCGACGTTTCTGATTAAGTCTGATCAAGATCAAGATGATGCAAA 1844
 DB 539 LysGlnLeuTyrSerLeuArgGlnThrLeuAspCysSerPheAsnArgIleGlnThrSer-- 557
 QY 1845 AAACAGGAACATACAGATTTTCCAAAGTGTCTGATTTCTTAATCTTACTACAGATGAC 1904
 DB 558 LysGlyTyrIleLeuGlnIlePheProTyrSerLeuAlaValPheAsnLeuThrAsnAsnSer 577
 QY 1905 TTGCTTGTACTGTGTGAACACCAAGATTTCTGCAATGATCAAGACCAAGGACACTC 1964
 DB 578 ValAlaCysIleCysGlnTyrGlnAsnPheLeuGlnThrValTyrAspArgGlnTyrMetPhe 597
 QY 1965 TTGCTGAAAGTGAACAAATGGAATGGAACAACCTTCAATTAAGCAAGGGACATCCCTGTG 2024
 DB 598 LeuValAsnValGlnGlnMetLysCysAlaSerProIleAspMetCysAlaSerLeuVal 617
 QY 2025 CTGAGTTTG--AATATCACTGTGACAGATGAATGAAGCAATCATTTGGTGTGCGTCTC 2081
 DB 618 LeuAspPheThrAsnSerThrCysTyrIleTyrLysThrIleIleSerValSerValVal 637
 QY 2082 AGTGTGCTTGTAGTACTGTGTGAGCAAGTTCTGCTGTATTAAGTTCTTATTTTCACTGATG 2141
 DB 638 SerValLeuValValAlaThrValAlaPheLeuIleTyrHisPheTyrPheHisLeuIle 657
 QY 2142 CTTCTGCTGGCTGCATTAAGTATGTAAGAGGTGAAGAAACATCATGATGATGCTTGTATC 2201
 DB 658 LeuIleAlaGlyCysLysTyrSerArgGlyGlnSerIleTyrAspAlaPheValIle 677
 QY 2202 TACTCAAGCAGAGATGAGACTGGGTGAAGAAAGAGCTAATGAAGATTTGAAGAAAGG 2261
 DB 678 TyrSerSerGlnAsnGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGly 697
 QY 2262 GTGCTTCATTTCACTGTGCTGCTTCACTACAGAACTTTATTTCCGGTGTGGCCATTTGCT 2321
 DB 698 ValProArgPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 717
 QY 2322 GCCAATCATTCATGAAGTTTCCATTAAGCCGAAAGGTGATGTTGTGGTGTGCCAG 2381
 DB 718 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgGlyValIleValValIleSerArg 737
 QY 2382 CACTTATCCAGAGCCGCTGTGTATCTTTGAATATGATGATGCTCAGACCTGCGACGTTT 2441

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Db      ||| 738 HisPheIleGlnSerArgTrpCysIlePheGluTrpGluIleAlaGlnThrTrpGlnPhe 757
QY      ||| 2442 CTGAGCAGTGTGTGCTGATCATCTTCTGAGAGCTGCGAAGGTGAGAGACCTGCTC 2501
Db      ||| 758 LeuSerSerArgSerGlyIleIlePheIleValLeuGluIlyValGluIlySerLeu 777
QY      ||| 2502 AGGACAGAGGTGAGCTGACCGCTTCTCAGCAGAACTTACCTGAGTGGAGAGAC 2561
Db      ||| 778 ArgGlnGlnValGluLeuTrpArgLeuLeuSerArgPheThrTrpLeuGluTrpGluAsp 797
QY      ||| 2562 AGTGTCTGTGGGCGGACATCTTCTGAGAGCGACTCAGAAAGCCCTGCTGATGGTAA 2621
Db      ||| 798 AsnAlaLeuGlyArgHisIlePheTrpArgArgLeuIlySalLeuLeuAspGlyIly 817
QY      ||| 2622 TCATGGAATCCAGAGAGACAGTGGGTACAGGATGCATTGGCAGAGACACATCTATC 2681
Db      ||| 818 AlaLeuAsnProAsp-----GluThrSerGlnGluGlnGlnIleAlaThrThrLeu 834
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Search completed: March 29, 2005, 17:28:15
Job time : 280.959 secs

XX

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

XX WPI, 2003-040607/03.
XX
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX
XX Example 2; SEQ ID NO 1439; 1349p; English.
XX
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Alignment Scores:

Pred. No.:	2,7e-303	Length:	839
Score:	2792.00	Matches:	557
Percent Similarity:	79.35%	Conservative:	100
Best Local Similarity:	67.27%	Mismatches:	166
Query Match:	53.93%	Indels:	6
DB:	6	Gaps:	4

US-09-396-985B-46 (1-2951) X ABU04773 (1-839)

QY	208	ATGATGACCTCCCTGGCTCTCGGTAGAGACTCTGATCATGGCACTG--TTCTTCTCTGC	264
Db	1	MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys	20
QY	265	CTGACACCAAGAAAGCTTGAATCCCTGCATAGAGTATGTTCTATATTACTTACCAATGC	324
Db	21	ValArgProGluSerThrGluProCysValGluValAlaProAsnIleThrTyrGlnCys	40
QY	325	ATGGATCAGAAACTCAGCAAAAGTCCCTGATGATTCCTTCTTCAACCAAGAACATGAT	384
Db	41	MetGluLeuAsnBheTyrLysIleProAspAsnLeuProBheSerThrLysAsnLeuAsp	60
QY	385	CTGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTATGCTTCTCCAAATTTTTCAGAACTT	444
Db	61	LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheSerPheProGluLeu	80
QY	445	CAGTGCCTGATTTATTCAGGTGTGAATTGAAACAAATGGAAGCAAGCATGGCATGGC	504
Db	81	GlnValLeuAspLeuSerSerArgCysGlnIleGlnThrIleGluAspGlyAlaTyrGlnSer	100
QY	505	TTACACCACTCTCAAACTGTATGTACAGACAGAAACCTTTCACAGATTTTCCCCCAGA	564
Db	101	LeuSerHisLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly	120
QY	565	AGTTTCTTGAGCTTAACAAGTTTAAACAATCTGGTGGCTGTGGAGACAAATTGGCTCT	624
Db	121	AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValAlaGlnThrAsnLeuAlaSer	140
QY	625	CTAAGAAAGCTCTCTTGTGAGTACAGCTATTAACCTTAAAGAAACCAATGGGCTCAAAAT	684
Db	141	LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn	160
QY	685	TTTATATATCTCCGTAGATTAAGTACTGTCAATATTTTCCATCTGACGAACCTAGTACATGTG	744

Dd	161	Leu1IegInserPheIysLeuProGluTyrPheSerSerLeuThrAsnLeuGluHisIleu	180
Qy	745	GATCTTTCTTAATTAATAATTCAAACTATTACTGTCAACGACTTACAGTTTCTTACGTGA	804
Dd	181	AspLeuSerSerAsnIysIleGlnSerIleTyrCyThrAspLeuArgValIleuHisIleGln	200
Qy	805	AATCCACAGTCATATCTCTCTTGGACATGCTTTGAACCCATTAATGACTTCATTCAAGAC	864
Dd	201	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro	220
Qy	865	CAACGCTTTTCAGGAAATTAAGTCTCAAGACTGTCACTGAAGGTAATTTTAATAGTCA	924
Dd	221	GlyAlaPheIysGluIleArgLeuHisIbysLeuThrLeuArgAsnAsnPheAspSerLeu	240
Qy	925	AATTAATTAAGAAATCTGCTTCAAAACCTGGCTGGTTTACACGTCCATCGGTTGATCTTG	984
Dd	241	AsnValMetCysIleArgLeuHisIbysLeuIleGluValHisArgLeuValIleu	260
Qy	985	GGAGAAATTTAAAGATGAAGAAAGATCTGGAAATTTTGAACCCCTTATCATGGAAAGACTA	1044
Dd	261	GlyIleuPheArgAsnGluGlyAsnLeuGluIlePheAspPheSerIleAlaLeuGluGlyLeu	280
Qy	1045	TGTGATGTGACCATTTGATGAGTTGAGGTTAAACAATGATGATTTTTCAGATGATATT	1104
Dd	281	CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspIleTyrIleAspAspIle	300
Qy	1105	GTTAAG--TTCATCTGCTTGGCCGCAATGTTTCTTGCAACATGCTCTGGCAGGTGATCTATA	1161
Dd	301	IleAspLeuPheAsnCybLeuThrAsnValSerSerPheSerLeuValSerValThrIle	320
Qy	1162	AAATATCTAGAAAGATGTTCTTAACATTTCAATGGCAATCTTTATCATCATTAAGATGT	1221
Dd	321	GluArgValIysAspPheSerTyrAsnPheGlyTyrGlnHisIleuGluLeuValAsnCys	340
Qy	1222	CAACTAAG-CAGTTTCCAACTCTGGATCTAACCTCTTCTTAATAAGTTGACCTTAACTAG	1280
Dd	341	LysPheGlyGlnPheProThrLeuIbysLeuIbysSerLeuIbysArgLeuThrPheThrSer	360
Qy	1281	AACAAAGGGTATCATGTTTAAAAAAGTGCGCCCTCAACCAAGTCTCAGCATCTAGATCTT	1340
Dd	361	AsnIysGlyGlyAsnAlaIaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu	380
Qy	1341	AGTAGAAATGCACTGACGCTTTATGTTGGTGGCTGTTCTTATTTGTGATTTGGGAACAAACAGC	1400
Dd	381	SerArgAsnGlyLeuSerPheIysGlyCySerCysSerGlnSerAspPheGlyThrThrSer	400
Qy	1401	CTGAGACACTTAAGACCTTCAAGTTTCAATGGTCCATCATTAAGATGGCCATTTATGAGGT	1466
Dd	401	LeuIbysTyrLeuAspLeuSerPheAsnGlyAlaIleThrMetSerSerAsnPheLeuGly	420
Qy	1461	CTAGAAGCGTCGACAGCACTGATTTTTCAGACACTTCACTTAAAAAAGGCGACAGAATT	1520
Dd	421	LeuGluGlnLeuGluHisIleLeuAsp-PheGlnHisSerAsnLeuIbysGlnMetSerGluPhe	440
Qy	1521	CTCAGCGTCTTATTCCTTGAAGAAAGCTATTACCTTGACATCTCTTATTAACCAACCA	1580
Dd	440	AsnValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisIleThrHisIleThr	460
Qy	1581	AATTGACTTCATGGTATATTTCTTGGCTTGAACAGTCTCAACACTTAAAAAAGGCTGG	1640
Dd	460	GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuIbysMetAlaGly	480
Qy	1641	CAATCTCTTGAAGAGCAACGCTTTCAAAGTCTTTGCAAAACACAACAAACTTGACATTT	1700
Dd	480	YAsnSerPheGlnGluHisnPheLeuProAspIlePheThrGluIleuArgAsnLeuThrPhe	500
Qy	1701	CTCGATCTCTTAATAGTCAATTTGGAACAATATCTTGAGGAGGATATTGACACCTTCA	1760
Dd	500	eleuAspLeuSerGlnCybGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeu	520
Qy	1761	TAGACTTAATTTAAATATGAGTCACACAAATCTATGTTTGGATTCATCCCATTA	1820

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Dh 520 rSerLeuGlnValLeuAsnMetSerHisAsnAsnPhenSerLeuAspThrPheProty 540
Qy 1821 TAACCAGCTGATTCCTCAGACACTCTTGATGTGAGTTCAATGGCATAGAGATCT-- 1878
Dh 540 rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy 1879 -AAGGAATAGTACGACATTTTCCAAAGAGCTTCGCTCTTCAATCTTCAATATTC 1937
Dh 560 sLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 580
Qy 1938 TGTTCCTGTATATGTGAAACATCAGAAATTCCTCAGTGGGTCAAGAAACAGAGAGTT 1997
Dh 580 pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleIleLysPheGlnArgIle 600
Qy 1998 CTTGTGTAATGTGAACAATGACATGTGCACACCTGTAGAGATGAAATCCTCTTAGT 2057
Dh 600 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVa 620
Qy 2058 GTTGAATTTTAATATCTACCTGTATATGTGAAACATCAGTACAGTGTGAGTGT 2117
Dh 620 lLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValle 639
Qy 2118 CAGTGTATGTGTGATTCACCTGATGCAATTTCTGATATACACTTCAATTTTCACTGAT 2177
Dh 639 uSerValLeuValValSerValValAlaValLeuValTyrLysPheThrPheHisLeuMe 659
Qy 2178 ACTTATTTGCTGGCTGTAAAAAGTACAGACAGAGAAAGCATCTATGATGATTTGGAT 2237
Dh 659 tLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIle 679
Qy 2238 CTACTCGAGTACAGATGAGACCTGGTGGAGAAATGAGCTGGTAAAGATTTAGAAAGAG 2297
Dh 679 eLysSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 699
Qy 2298 AGTCCCGCTTTTCACTCTGCTTCACTACAGACATTTATCTGCTGAGTGGCATTC 2357
Dh 699 yValProProheGlnLeuGlnCysLeuHisTyrArgAspPheIleProGlyValAlaIleAl 719
Qy 2358 TGGCAACATCTCCAGAGAGGCTTCACAGAGCCGGAAGGTTATGTGTAGTGTCTAG 2417
Dh 719 aAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGI 739
Qy 2418 ACACCTTATTCAGAGCGGTGGTGTATCTTGAATATGAGATGCTGCTCAACATGAGCAGT 2477
Dh 739 nHisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPh 759
Qy 2478 TCTGAGACGCGCTCTGGCATCATCTTCAATGCTCTTGAAGAGGTGAGAGTCCCTGCT 2537
Dh 759 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLe 779
Qy 2538 GAGCGACAGGATGGAATTTATCGCTTCTTAGAGAAACCTTACCTGGAATGGAGAGA 2597
Dh 779 uArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLys 799
Qy 2598 CAATCTCTGGGGAGGACATCTCTGAGAGAACTTAATAATGCCATTTGAGATGGAAA 2657
Dh 799 pSerValLeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLys 819
Qy 2658 AGCCTCGAATCTGAGCAACA 2679
Dh 819 sSerTrpAsnProGlnGlyThr 826

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KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS Homo sapiens.
PN WO200278524-A2.
PD 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
PF 28-MAR-2001; 2001US-0279495P.
XX 28-MAR-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
PA Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1440; 134p; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 839 AA;
SQ

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Alignment Scores:

Pred. No.:	2,7e-303	Length:	839
Score:	2792.00	Matches:	557
Percent Similarity:	79.35%	Conservative:	100
Best Local Similarity:	67.27%	Mismatches:	166
Query Match:	53.93%	Indels:	6
DB:	6	Gaps:	4

US-09-396-985b-46 (1-2951) x ABU04774 (1-839)

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Qy 208 ATGATGCTCTCCCTGCTCTGCTGAGTCTGTATGACATGCACTG---TTCTTCTCTGC 264
Dh 1 MetMetSerAlaSerArgLysAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
Qy 265 CTGACACAGAGAGCTTGAATCCCTGATGAGTGTCTCTATATATTACCTACCAATGC 324
Dh 21 ValArgProGlnubertTrpGluProCysValGlnValValProAsnIleThrTyrGlnCys 40
Qy 325 ATGATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTCAACCAAGAAATATGAT 384

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RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA.
AC ABU04774;
XX 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #1440.
DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW

Db	41	MetGluLeuAenPheTyLysIleProkaspAsnLeuProPheSerThrIlyAsnLeuAsp	60
Qy	385	CTGAGCTTCAACCCCTTGAAGAATCTTAAAAAGTATAGCTTCTCCAAATTTTTCAGAACTT	444
Db	61	LeuSerPheAenProLeuAArgHileuGlySerTyIserPhePheSerPheProGlyLeu	80
Qy	445	CAGTGGCGTGAATTTATCCAGATGAGAAATTTGAAACAATTGAAGCAAGACGATGGCAATGCG	504
Db	81	GlnValLeuAspLeuSerArgCysGlyIleGlnThrIleGluAspGlyAlaTyIcGlnSer	100
Qy	505	TTACACACACCTCTCAAACTTATATATGACAGAAAACCCATATCCAGAGTTTTCACAGCA	564
Db	101	LeuSerHileuSerThrLeuIleLeuThrGlyAenProIleGlnSerLeuAlaLeuGly	120
Qy	565	AGTTTCTGTGACATCAACAGATTGACAACTGTGGTGGCTGTGGAGACAAAATTGGCTCT	624
Db	121	AlaPheSerGlyLeuSerSerLeuGlnIlySerLeuValAlaValGlyThrAsnLeuAlaSer	140
Qy	625	CTAGAACCTTCCCATTTGACAGCTTATTAACCTTAAGAAATCAATGGTGCACAAAT	684
Db	141	LeuGluAenPheProIleGlyHileuTySerThrLeuTySGluLeuAsnValAlaHileAsn	160
Qy	685	TTTATACACTCTGTGAAGTTTACCTGCATATTTTTCATCTGCAGCAACCTAGTACATG	744
Db	161	LeuIleGlnSerPheTyLeuProGlyTyIserAsnLeuThrAsnLeuGlyHileu	180
Qy	745	GATCTTCTTATTAACATATATTCAACTATTACTGTACGACGACTTACAGTTTCTTACGTGA	804
Db	181	AspLeuSerSerAsnTyIleGlnSerIleTyIcTyIserAenLeuArgValIleuHileGln	200
Qy	805	AATCCACACATCAATCTCTCTTTAGACATGCTTTTGAACCCCAATGATTCATTCACAGC	864
Db	201	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAenProMetAsnPheIleGlnPro	220
Qy	865	CAAGCGCTTTCAGGGAAATTAAAGCTCCATGACATCTCAAGAGGATTTTATTAAGTCSCA	924
Db	221	GlyAlaPheTyLysGlyIleArgLeuHileuTySerThrLeuAlaGlnAsnPheAspSerLeu	240
Qy	925	AATATATGAAGAACTTGGCTTCAAAACCTGGCTGGTTTCAACGTCATCGAGTTGACTTG	984
Db	241	AsnValMetTyIserTyIleGlnIlyLeuAlaGlyLeuGlyValHileArgLeuValLeu	260
Qy	985	GGAGCAATTTAAAGATGAAAGGAATTTGGAAATTTTGAACCTCTATCATGGAAGAGATA	1044
Db	261	GlyGluPheArgAsnGlyIlyAsnLeuGlyIlySerPheAspTyIserAlaLeuGlnIlyLeu	280
Qy	1045	TGTGATGACCATATGAGTGAAGTGTGTTAAACATATTAACAAATGATTTTTCAGATGAT	1104
Db	281	CysAsnLeuThrIleGlnIlyPheArgLeuAlaTyIleuAspTyItyIleuAspAspIle	300
Qy	1105	GTTAAG--TTCCATGTGCTGGCGCAATGTTTCTGCAGATGCTTGGCGAGTGATCTATA	1161
Db	301	IleAspLeuPheAsnCysLeuThrAsnValIserSerPheSerLeuValSerValThrIle	320
Qy	1162	AAATATCTAGAAGATGTTCTTAACAATTTCAATGGCAATCTTATCAATCATAGATGT	1221
Db	321	GluArgValTyIAspPheSerTyIAsnPheGlyTyIArgGlnHileuGlyLeuValAsnTyS	340
Qy	1222	CAACTAAG-CAGTTTCCAACTGTGATCTACCCCTTCTTAAAGTTTCACTTATGATG	1280
Db	341	LysPheGlyGlnPheProThrIleuTyLeuTySerLeuTyIAspGlyThrPheThrSer	360
Qy	1281	AACAAAGGCTATATAGTTTAAAAAAGTGCGCCCTACCAAGTCTGAGCTATCTAGATCT	1340
Db	361	AsnTyIserGlyGlyAsnAlaPheSerGlyValaIAspLeuProSerLeuGlyIlyPheLeuAspLeu	380
Db	381	SerArgAsnGlyLeuSerPheTyIleGlyTyIcTyIserGlnSerAspPheGlyTyIThrThrSer	400
Qy	1401	CTGACACACTTAGACTCAGCTTATGAGTGAGCTGATCTTATTTGATTTGGAAACAAACAGC	1460
Db	401	LeuTyItyIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuIly	420

QY	1461	UTAGAAGAGCTGACAGACCTCGAATTTTTCAGCACTCTACTTTAAAGGGTCACAGATT	1520
Db	421	LeuGlnGlnLeuGlnHisLeuAsp-PheGlnHisSerAsnLeuGlySerGlnSerGlnPh	440
QY	1521	CTCAGCGCTTCTATCCCTTGAGAAAGCTACTTTCACCTTGACATCTCTATATCAACCAA	1580
Db	440	eserValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrAr	460
QY	1581	AATTGACTTCGATGGTATATTTCTTGGCTTCGACCAAGCTTCACACATTTAAAAATGGCTGG	1640
Db	460	GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIleuSerMetAlaG	480
QY	1641	CAATTTCTTCAAAACACAAACCCCTTCAATGTCTTTGGCAACACACAAACCTTGACATT	1700
Db	480	YAsnSerPheGlnIleuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPh	500
QY	1701	CGTGGATCCCTTCAAAAGTCAATTTGGAACAAATCTCTGGGGGGATTTTGACACCCCTCCA	1760
Db	500	eLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSe	520
QY	1761	TAGACTTCAAATTTAAATATGACTGCACAAACATCTATGTGTTTGGATTCTCCCATTA	1820
Db	520	rSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr	540
QY	1821	TAAACAGCTGATTTCCCTGACGACTCTTGATTCGAGTTCAATGGCATAGAGACTCT--	1878
Db	540	rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys	560
QY	1879	-AAAGGAATATGGACACTTTTCCAAAGAGCTGACCTTCTCAATCTTTCATCAATTC	1937
Db	560	SlyGlnGlnLeuLeuIleHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs	580
QY	1938	TGTTGCTTTGTATATGTGAACATCAGAAATTCCTGCACTGGCTCAAGAACACAGACATT	1997
Db	580	pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrIleLysAspGlnArgGlnLe	600
QY	1998	CTTGGTGAAATGTGAACAAATGACATGTGCACACCTGTGAGATGAATACCTCTTAACT	2057
Db	600	uLeuValGluValGlnArgMetGlnCysValaThrProSerAspLysGlnGlyMetProVa	620
QY	2058	GTTGGATTTTAATTAATCTCAACCTGTTATATGTAACAGACATCATCAGTGGTACAGGGT	2117
Db	620	lleuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLe	639
QY	2118	CAGTGTGATTTGGTATCCACTGTAGACATTTCTGATATACCACTTCTATTTTTCACCTGAT	2177
Db	639	uSerValLeuValValSerValValAlaValLeuValTyrLysPheThrPheHisLeuMe	659
QY	2178	ACTTATTTGCTGGCTGTAAAAAGTACAGCAGAGAGAAAGCATCTATGATGCATTTTGAT	2237
Db	659	tLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValI	679
QY	2238	CTACTCAGTTCAGAAATGAGACTGGGGTGAAGAAAGACTGGTAAAGAAATTTAGAAAGAG	2297
Db	679	eTyrSerSerGlnAspGlnAspTrpValArgAsnGluLeuValLysAsnLeuGlnGluG	699
QY	2298	AGTGGCCCGCTTTTCAACTCTGCTCTTCACTACAGAGACTTTATTTCTGCTGTAGACATTCG	2357
Db	699	yValProPheGlnLeuCysLeuHisTyrArgAspPheLeuProGlyAlaAlaIleAl	719
QY	2358	TGCCAACATCATCCAGAGAGGCTTCCACAAAGCCGGAAGGTTATGTGTAGTGTCTAG	2417
Db	719	aAlaAsnIleIleHisGlnGlyPheHisbLysSerArgLysValIleValValValSerG	739
QY	2418	ACACTTTATTCAGAGCCGTGTGTATCTTTGAATATGAAATGTCTCAAACTATGGCATT	2477
Db	739	nHisPheIleGlnSerArgTrpCysIlePheGluTyrGluIleAlaGlnThrTrpGlnPh	759
QY	2478	TCTAGAGCCGCGCTGGCATCACTTTCATTTGTCTTGGAGAAAGGTGAGAACTCCGCT	2537
Db	759	eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysTrpIleMet	779

QY 2538 GAGGACAGAGTGAATTTGATGCTTTTATGACAGAAACCTTACCTGGAAATGGAGGA 2597
 |||||
 Db 779 uArgGInGInValGInLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGInuTrpGluAs 799
 QY 2598 CAATCTCTGGGAGGACATCTTTGGAGAAAGCTTAAATGCCCTTATGGATGAAA 2657
 |||||
 Db 799 pSerValLeuGInYArgHisIlePheTrpArgLeuArgLysLeuLeuAspGlyLy 819
 QY 2658 AGCCTGCAATCTGACGAACA 2679
 |||||
 Db 819 sSerTrpAsnProGInuGlyThr 826
 RESULT 3
 ABU04775
 ID ABU04775 standard; protein: 839 AA.
 AC ABU04775;
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0295254P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOs INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 PT MPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134bp; English.
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 2.7e-303 Length: 839
 Score: 2792.00 Matches: 557
 Percent Similarity: 79.35% Conservative: 100
 Best Local Similarity: 67.27% Mismatches: 166
 Query Match: 53.93% Indels: 6
 DB: 6 Gaps: 4
 US-09-396-985b-46 (1-2951) x ABU04775 (1-839)
 QY 208 ATGATGCTCCCTCCGCTCCGCTAGCATGCTGATGACGACTG--TTCTTCTCCCTGC 264
 |||||
 Db 1 MetMetSerLaseTrpArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 265 CTGACACACGAGAGCTTGAATCCCTGCATAGAGGATGTTCTTAATTTACCTCAATGC 324
 |||||
 Db 21 ValArgProGInuSerTrpGInuProCysValGInuValProAsnIleThrTyrGInuCys 40
 QY 325 ATGATCAGAAACTCGCAAAAGTCCCTGATGACATTCCTTTCACCAAGACATATGAT 384
 |||||
 Db 41 MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAATAAGCTATAGCTTCCCAATTTTTCAGAACTT 444
 |||||
 Db 61 LeuSerPheAsnProLeuAsnTrpGInuGlySerTyrSerPheSerPheProGInuLeu 80
 QY 445 CAGTGCTGATTTATTCACAGTGTGAAATGAAACATTTGAACAGACAGGATGCGATGCG 504
 |||||
 Db 81 GInValLeuAsnLeuSerThrArgGInuIleGInThrIleGluAspGlyAlaTyrGInuSer 100
 QY 505 TTACACCACTCTCAAACTTGATCTGACAGAAACCTTATCCAGATTTCCTCCACGA 564
 |||||
 Db 101 LeuSerHisLeuSerThrLeuIleLeuThrGInuAsnProIleGInSerLeuAlaLeuGly 120
 QY 565 AGTTTCTCGGACATAAGATTAGACAATCTGCGTGGCTGGAGCAAAATTGGGCTCT 624
 |||||
 Db 121 AlaPheSerGlyLeuSerSerLeuGInuLysLeuValAlaValGInuThrAsnLeuAlaSer 140
 QY 625 CTGAAAGCTTCCCTATTTGACAGCTTATTAACCTTAAGAACTCAATGTGCTCAAT 684
 |||||
 Db 141 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
 QY 685 TTTATACATTCCTGTATAGTTTACCTGCATATTTTCCAACTGACGAACCTATGATG 744
 |||||
 Db 161 LeuIleGInSerPheLysLeuProGInuTyrPheSerAsnLeuThrAsnLeuGInuHisLeu 180
 QY 745 GATCTTTCTTATACATATATTCAACTATTAACGTGACAGACTTACAGTTTACAGGAA 804
 |||||
 Db 181 AsnLeuSerSerAsnLysIleGInSerIleTyrCysThrAsnLeuArgValLeuHisGln 200
 QY 805 AATCCACAAGTCAATCTCTTTAGACATGCTTTGAACCAATGATGACTTCAATCAAGAC 864
 |||||
 Db 201 MetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsnPheIleGInPro 220
 QY 865 CAAGCTTTACAGGAATTAAGCTTCATGACCTTGAAGAGTATTTTAATAGCTCA 924
 |||||
 Db 221 GlyAlaPheLysGInuIleArgLeuHisLysLeuThrLeuArgAsnPheAspSerLeu 240
 QY 925 AATATATGAAAACCTGCTCAAAACCTGGCTGTTTACAGCTCCATCGGTGATCTTG 984
 |||||
 Db 241 AsnValMetLysThrCysIleGInuGlyLeuAlaGlyLeuGInuValHisArgLeuValLeu 260
 QY 985 GGAGATTTAAAGATGAAGAAAGATCTGAAATTTTGAACCCCTATCAATGGAAGAGCTA 1044
 |||||
 Db 261 GlyGInPheArgAsnGInuLysAsnLeuGInuLysPheAspLysSerAlaLeuGInuGlyLeu 280
 QY 1045 TGTGATGTGACATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
 |||||
 Db 281 CysAsnLeuThrIleGInuGInuPheArgLeuAlaTyrLeuAspLysTyrLeuAspAspIle 300

QY 1105 GTTAAAG--TTCCATTCCTGGCGAATGTTCTGCAATGTCCTGGCAGGCTATCATATA 1161
 :::::::::::::::::::::
 Db 301 ILAapreubheanCysleuThrAsnValSerSerSerleuValSerValThrIle 320
 QY 1162 AAATATTTAGAAAGATGTTCTTAAACATTTGCAATGGCAATCTTATCATCATAGATGT 1221
 :::::::::::::::::::::
 Db 321 GLAArgValIlyAspPheSerTyrAsnPheGlyTyrPdlInHlsleuGluLeuValAsnCys 340
 QY 1222 CAACTAAG-CAGTTTCCAACTCGGATCTACCCCTTTTAAAGTTGACTTTAAGCATAG 1280
 :::::::::::::::::::::
 Db 341 LysPheGlyInPheProInLeuLysleuLysSerleuLysArgleuInrPheInrSer 360
 QY 1281 AACAAAGGCTCTACGATTTTAAAAAAGTGCCCTCAACAGCTCAGCTATCATAGATTT 1340
 :::::::::::::::::::::
 Db 361 AsnIlyGlyIlyAsnAlaPheSerGluValAspLeuProSerleuGluPheLeuAspLeu 380
 QY 1341 AGTGAAGAAATGCACTGAGCTTTAGTGGTGGCTGTTCTTATTTCTGATTTGGGAACAACAGC 1400
 :::::::::::::::::::::
 Db 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerInSerAspPheGlyThrThrSer 400
 QY 1401 CTGAGCACTTTAAGCTCAGCTTCAATGGTGCCATCATATATGAGTCAATTTCAATGGT 1460
 :::::::::::::::::::::
 Db 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1461 CTAGAAGAGCTGCAGACCTGGAATTTTTCAGCACTTATTAATAAGGCTCAGAGATT 1520
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 Db 421 LeuGluInleuGluInHlsleuAsp-PheGluInHlsSerAsnLeuLysGluMetSerGluP 440
 QY 1521 CTGAGCTTTTATCTCTTAAAAAGCTTACTTATCTTGAACATCTCTTATCTTACACCA 1580
 :::::::::::::::::::::
 Db 440 eSerValPheLeuSerleuLysArgAsnLeuIleTyrLeuAspIleSerHlsThrHlsThrAr 460
 QY 1581 AATTGACTTCGATGCTATATTTCTTGGCTGACAGCTCAACACATTAATAAATGGCTGG 1640
 :::::::::::::::::::::
 Db 460 GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGluValLeuLysMetAlaGly 480
 QY 1641 CAATCTTTTCAAGACACACCTTTCAAAATGTCCTTGGCAACACACAACTTGAACATT 1700
 :::::::::::::::::::::
 Db 480 YAsnSerPheGluInleuAsnPheLeuProAspIlePheThrGluLeuLysAsnLeuThrP 500
 QY 1701 CCTGATCTCTTAAATGTCATTTGCAACAAATATCTTGGGGGGTATTGACACCTCCA 1760
 :::::::::::::::::::::
 Db 500 eLeuAspLeuSerGlnCysGlnleuGluInleuSerProThrAlaPheAsnSerLeuSe 520
 QY 1761 TAGACTTCAATTTAATATATGAGTCACAAATCTTATGTTTGGATCATCCCATTA 1820
 :::::::::::::::::::::
 Db 520 rSerleuGluValleuAsnMetSerHlsAsnAsnPhePheSerleuAspInrPheProIly 540
 QY 1821 TAAACAGCTGTATCTCCCTCAGCACTTGTGATGTCAGTTTCAATGCAATAGACATCT- 1878
 :::::::::::::::::::::
 Db 540 rLysCysleuAsnSerleuGluInValleuAspTyrSerleuAsnHlsIleMetThrSerIly 560
 QY 1879 -AAAGGAATCTGCAACATTTTCCAAAGAGCTTACGCTTTTCAATTTTCAACAATTC 1937
 :::::::::::::::::::::
 Db 560 sLysGlnGluLeuGlnHlsPheProSerSerleuAlaPheLeuAsnleuThrGlnsAs 580
 QY 1938 TGTGCTTGATATGTAATGTAACATGAAATTCCTGCACTGGGATGAGAGAGAGAGT 1997
 :::::::::::::::::::::
 Db 580 pPheAlaCysThrCysGlnHlsGlnSerPheleuGlnTrpIleLysAspGlnArgGlnle 600
 QY 1998 CTGTGGAATGTTGAACAAATGACATGTGCAACACCTGTAGAGATGAATACCTCTTATG 2057
 :::::::::::::::::::::
 Db 600 uLeuValGluValGluArgMetGluCysAlaInrProSerAspLysGlnIlyMetProVa 620
 QY 2058 GTTGGATTTTAAATATCTACCTGTTATATGTAACAAGACATCATCATGTGTCAAGGGT 2117
 :::::::::::::::::::::
 Db 620 lLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValle 639
 QY 2118 CAGTGTGATTTGGTATCCAGTGTGATTTGATATATGATATACCTCATATTTTCAACCTG 2177
 :::::::::::::::::::::
 Db 639 uSerValleuValValSerValValAlaValleuValTyrLysPheThrPheHlsleuWe 659
 QY 2178 ACTTATTTGCTGGCTGTAAAAAGTACAGCAGAGAGAGAAAGCATCTATGATCATTTTGAT 2237

Db 659 tLeuLeuAlaGlyCysIleLysTyrGlyLysArgGluAsnIleTyrAspAlaPheValIle 679
 QY 2238 CTACTGTGATCGAATGAGACCTGGGTGGAATAGCTGGTGAAGAAATTTTGAACAAG 2297
 :::::::::::::::::::::
 Db 679 eTyrSerSerGlnAspGluAspTyrValArgAsnGluLeuValLysAsnleuGluGlu 699
 QY 2298 AGTGCCCGCTTTCACTCTGCGCTTCACTACAGAGACTTATCTCTGTGTAGCCATTCG 2357
 :::::::::::::::::::::
 Db 699 yValProProPheGlnleuCysleuHlsTyrArgAspPheIleProGlyValAlaIleAl 719
 QY 2358 TGGCAACATCATTCAGAAAGCTTCCAGAAAGCCGAAAGTTATTTGTGTAGTCTAG 2417
 :::::::::::::::::::::
 Db 719 aAlaAsnIleIleHlsGluGlyPheHlsLysSerArgLysValIleValIleValSerG 739
 QY 2418 ACACTTTATTCAGAGCCGCTTGGTGTATCTTTGAATATGATATTTGCTCAAACTGGCAGTT 2477
 :::::::::::::::::::::
 Db 739 nHlsPheIleGlnSerArgTyrCysIlePheGluTyrGluIleAlaGlnThrTrpGlnP 759
 QY 2478 TCTGACAGCCGCTGGCATCATCTTCAATGTCCTTGAAGAGTTGAGAGCTCTGCT 2537
 :::::::::::::::::::::
 Db 759 eLeuSerSerArgAlaGlyIleIlePheIleValleuGlnLysValGluLysThrleu 779
 QY 2538 GAGGACAGAGTGAATTTGATCGCTTCTTACAGAAACACCTTACCTGGAATGGAGGA 2597
 :::::::::::::::::::::
 Db 779 uArgGlnGlnValGluLeuTyrArgleuLeuSerArgAsnThrTyrleuGluTrpGluAs 799
 QY 2598 CAATCTCTGGGAGGACACATCTTTCGAGAAAGACTTAAATAATGCCCTTATGATGAGAA 2657
 :::::::::::::::::::::
 Db 799 pSerValleuGlyArgHlsIlePheThrArgArgleuArgLysValleuLeuAspIly 819
 QY 2658 AGCTCGAATCTGAGCAACA 2679
 :::::::::::::::::::::
 Db 819 sSerTrpAsnProGluGlyThr 826
 RESULT 4
 ADCT8785.
 ID ADCT8785 standard; protein; 839 AA.
 AC ADCT8785;
 XX 01-JAN-2004 (first entry)
 DT XX
 DE Human PRO protein #7.
 XX
 KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.
 OS Homo sapiens.
 PN MO2003034984-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002WC-US033070.
 XX
 PR 19-OCT-2001; 2001US-0340083P.
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Gurney AL;
 DR WPI; 2003-481990/45.
 DR N-PSDB; ADCT8784.
 XX
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX
 PS Claim 12; SEQ ID NO 14; 327bp; English.
 CC
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

SO Sequence 839 AA:

Alignment Scores:

Pred. No.:	2,76-303	Length:	839
Score:	2792.00	Matches:	557
Percent Similarity:	79.35%	Conservative:	100
Best Local Similarity:	67.27%	Mismatches:	166
Query Match:	53.93%	Indels:	6
		Gaps:	4

US-09-396-985B-46 (1-2951) x ADC78785 (1-839)

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Qy 208 ATATGCTCCCTGGCTCTCTGCTAGATGACATG---TTCTTCTCTGC 264
Db 1 MetMetSerAlaSerAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
Qy 265 CTGACACGAGGAGCTTGAATCCCTGATAGAGTAGTCTTATATTAATTAACCTACATGC 324
Db 21 ValArgProGluSerTyrGluProCysValGluValAlaProAsnIleThrTyrGlnCys 40
Qy 325 ATGATCAGAAACTCAGCAAGATCCCTGATGACATTCCTTCTCAACCAAGACATAGAT 384
Db 41 MetCyluLeuAsnProPheTyrIleProAsnLeuProPheSerThrIlyAsnLeuAsp 60
Qy 385 CTGAGCTTCAACCCCTTGAAGATTTTAAAGCTTATAGCTTCTTCCAAATTTTCAAACTT 444
Db 61 LeuSerPheAsnProLeuArgH1leuGlySerTyrSerPhePheSerPheProGluLeu 80
Qy 445 CAGTGGCTGATTTATCCAGGTGAGAAATGAAACAATTTGAAGACAAGGACATGGCATGCC 504
Db 81 GluAlaLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
Qy 505 TTACACGACCTCTCAAACTTGATCTGACAGAAACCTATCCAGATTTTCCCCAGA 564
Db 101 LeuSerH1leuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
Qy 565 AGTTCTCTGAGCTTACCAAGTTTGAACATCTGGTGGCTGAGACAAATTTGGCTCT 624
Db 121 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValIleGluThrAsnLeuAlaSer 140
Qy 625 CTAAAGAGCTCCCTATTTGACAGCTTATTAAGAAACCTCAATGGTGGCTCACAAT 684
Db 141 LeuIlyAsnProIleGlyH1leuIlySerThrLeuIlySerGluLeuAsnValAlaH1Asn 160
Qy 685 TTTATACATCTCTGATGATCTGACATATTTTCAATCTGACGAACTAGTACATGTG 744
Db 161 LeuIleGlnSerPheIlySerLeuProGluTyrPheSerAsnLeuThrAsnLeuGluH1Ser 180
Qy 745 GATCTTTCTTATTAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
Db 181 AspLeuSerSerAsnIlySerIleGlnSerIleTyrCysThrAspLeuArgValLeuH1Gln 200
Qy 805 AATCACAAGTCATCTCTCTTGAACATCTGATGACATTTGAACCAATGATGATCTCAAGAC 864
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
Qy 865 CAACCTTTTCAAGAAATTAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 924
Db 221 GlyAlaPheIlySerGluIleArgLeuH1IlySerLeuThrLeuAsnGluAsnPheAspSerLeu 240
Qy 925 AATATTAATGAAGAACTTGCCTTCAAAACCTGGCTGGTTTACAGTTCATCGGTTGATCTTG 984
Db 241 AsnValMetIlySerThrCysIleGlnIlyLeuAlaGlyLeuGluValH1AspArgLeuValLeu 260
Qy 985 GGAAATTTAAAGTGAAGAAATCTGAAATTTTGAACCTCTATCATGGAAGACTA 1044
Db 261 GlyIlyPheArgAsnGluIlyAsnLeuGluIlySerPheAspIlySerAlaLeuGluGlyLeu 280
Qy 1045 TGTGATGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
  
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Db 281 CysAsnLeuThrIleGlnIlyPheArgLeuAlaTyrLeuAspIlyTyrIlyLeuAspAspIle 300
Qy 1105 GTTAAG---TTCCATGCTGGGGAAGTTTCTGCAATGCTCTGGCAGAGTATCATATA 1161
Db 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValIleIle 320
Qy 1162 AATATCTAGAAAGATGTTCTTAAACATTTCAAAATGCAATCTTATCAATCATTAAGATGT 1221
Db 321 GluArgValIlyAspPheSerTyrAsnPheGlyTyrGlnH1SerLeuGluLeuValAsnCys 340
Qy 1222 CAACATAAG-CAGTTTCAACTCTGATCTTACCTTTCTTAAAGTTTGAATTAACATATG 1280
Db 341 LysPheGlyGlnPheProThrLeuIlySerLeuIlySerLeuIlyArgLeuThrPheThrSer 360
Qy 1281 AACAGAGGCTCATGATTTTAAAGAGGCGCTTCAAGCTCCAGCTCATAGATCTT 1340
Db 361 AsnIlyGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
Qy 1341 AGTAGAAATCAGTCACTGAGCTTATGAGTGGCTGTTCTTATTTCTGATTTGGACAACAGC 1400
Db 381 SerArgAsnIlyLeuSerPheIlySerGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
Qy 1401 CTGAGACCTTGAACCTCAGCTTCAATGTGTCATCATTAATGAGTCCAAATTTCAATGGT 1460
Db 401 LeuIlyTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
Qy 1461 CTGAAAGAGCTGACAGACCTCGATTTTTCAGACCTCTACTTTAAAGAGTTCACAGATT 1520
Db 421 LeuGlnIleuGluH1SerLeuAsp-PheGlnH1SerAsnLeuIlyGlnMetSerGluPhe 440
Qy 1521 CTCAGGCTTCTTATCCCTTGAAGGCTTCTTCAATCTTGAATCTTATTAATTAACCA 1580
Db 440 eSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerH1SerH1SerThrArg 460
Qy 1581 AATGACTTGATGATGATATTTCTGGCTTGAACAGTCTCAACATTAATAATGGCTGG 1640
Db 460 GValAlaPheAsnGlyIlyPheAsnGlyLeuSerSerLeuGluValLeuIlyMetAlaGly 480
Qy 1641 CAATCTTTCAAAAGACACACCTTTCAAATGCTTTCGAAACAAACAACAACTTGACAT 1700
Db 480 yAsnSerPheGlnIlyAsnLeuPheProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
Qy 1701 CTTGATCTTCTTAAATGTCATTAATGTCACAAATATCTTGGGGGTATTTGACACCTTCA 1760
Db 500 eleuAspLeuSerGlnCysGlnLeuGluIlyLeuSerProThrAlaPheAsnSerLeuSe 520
Qy 1761 TAGACTTCAATTAATTAATTAATGATGACAAATCTATGTTTGGATTCATCCATTA 1820
Db 520 rSerLeuGlnValLeuAsnMetSerH1AsnAsnPhePheSerLeuAspThrPheProTy 540
Qy 1821 TAAACAGCTTATTCCTCAGCAGCTCTGATTTGACGTTTCAATCGCATAGACATCT-- 1878
Db 540 rIlySerCysLeuAsnSerLeuGlnValLeuAspIlySerLeuAsnH1SerLeuThrSerIly 560
Qy 1879 -AAGGAATLCTGCAACATTTTCAAGAGCTTACCTTCTTCAATCTTCTTCAACATTC 1937
Db 560 sIlySerGlnIlyLeuGlnH1SerPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsn 580
Qy 1938 TGTGCTTGTATATGTAACATCAGAAATTTCTGCAAGTGGGTCAAGAACAGAGAGATT 1997
Db 580 pPheAlaCysThrCysGluH1SerGlnSerPheLeuGlnIlyIleLysAspGlnArgGlnLe 600
Qy 1998 CTGCGTAATGTTGAACAAATGACATGTGCAACACCTGTGAGATGAATACCTCCCTTACT 2057
Db 600 uLeuValGluValGluArgMetGluCysAlaThrProSerAspIlySerGlnIlyMetProVa 620
Qy 2058 GTTGATTTTAATTAATTTCTCTGTATATGATGATGATGATGATGATGATGATGATGATGAT 2117
Db 620 lLeuSerLeu--AsnIleThrCysGlnMetAsnIlySerH1IleGlyValSerValIle 639
Qy 2118 CAGTGTGATTTGTGTATCCACTGTAGCATTTTGTGATATACACTTCTATTTTCACTGAT 2177
  
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Db 639 uservalleva1valserVala1aValleuVal1TrylasePheH1sLeuMe 659
QY 2178 ACTTATGTCGGCTGTAAGAAAGTACAGAGAGGAAAGATCATGATCATTTGGAT 2237
Db 659 ctLeuVala1aG1yCys1leuYrtyrG1yArgG1yG1aSn1leYrtyrSp1aPheVal11 679
QY 2238 CTACTCGAGTCAGATGAGATCGGTGAGAAATGAGCTGTAAGATTTAGAGAGG 2297
Db 679 eYrtyrSerSerG1aSp1aG1uSp1rVala1aGaaG1uLeuVal1aSn1leuG1uG1 699
QY 2298 AGTGCCTTCCTTCACTTCCTGCTTCACTACAGAGATTTATTCCTGCTGATGCATTC 2357
Db 699 yVal1ProProPheG1uLeuYrtyrG1aSpPhe1leProG1yVala1a1a1eal 719
QY 2358 TGCCAACTATCATCCAGAGAGCTTCCAGAGAGCGGAGAGTTATGTTGATGATGCTAG 2417
Db 719 aa1aAaSn1le1leH1sG1uG1yPheH1sYrtyrG1yVala1leVala1aVala1SerG1 739
QY 2418 ACACTTATTCAGAGAGCGTGTGTATCTTGAATATGAGATTCGCAACATGAGCAGTT 2477
Db 739 nh1sPhe1leG1uSer1rgrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 759
QY 2478 TCTGAGAGAGCGCTCTGTCATCATCTTCTTCTTGAAGAGTTGAGAGAGTCCCTGCT 2537
Db 759 eLeuSerSerArg1aG1y1le1lePhe1leValleuG1uLeuVala1G1uYrtyrtyrtyr 779
QY 2538 GAGGACAGAGTGAATTTGATGCTTCTTCTTGAAGAGAGAGTCCCTGAGAGAGGAG 2597
Db 779 uArgG1uG1aVala1G1uLeuYrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 799
QY 2598 CAATCTCTGGGAGAGAGATCTTCTGAGAGAGAGTAAAGTCCCTATTTGATGAGAG 2657
Db 799 pSerValleuG1yA1rG1s1le1lePhe1rPArG1aG1uLeuArg1ySa1a1eLeuMeSpG1y 819
QY 2658 AGCCTCGAATCTGAGAGAGCA 2679
Db 819 sSerTrpAsnProG1uG1yThr 826
RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX ADD48826;
AC
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
KM Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN MO2003016475-A2.
XX
XX 27-FEB-2003.
PD
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAF05316.
DR

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
Alignment Scores:
Pred. No.: 2,7e-303 Length: 839
Score: 2792.00 Matches: 557
Percent Similarity: 79.35% Conservative: 100
Best Local Similarity: 67.27% Mismatches: 166
Query Match: 53.93% Indels: 6
DB: 7 Gaps: 4
US-09-396-985b-46 (1-2951) x ADD48826 (1-839)
QY 208 ATGATCCTTCCTCGCTCCTGCTGAGACTGTGATGACGACG--TTCTTCCTCGC 264
Db 1 MetMetSerAlaSerArgLeuAlaG1yThrLeu1leProAlaMetAlaPheLeuSerCys 20
QY 265 CTGACACCGAGAGCTTGAATCCCTGATAGAGGTGTTCTTAATTTACCTACCAATGC 324
Db 21 ValArgProG1uSerTrpG1uProCysVala1G1uVala1ProAsn1leH1rtyrG1uCys 40
QY 325 ATGATCAGAAACTCAGAAAGTCCCTGATGACATCTTCTTCAACCAAGACATATGAT 384
Db 41 MetG1uLeuAsnPheYrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 60
QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGAGTATAGCTTCTTCAATTTTTCAGACTT 444
Db 61 LeuSerPheAsnProLeuArgH1sLeuG1ySerTySerPheSerPheProG1uLeu 80
QY 445 CAGTGGCTGATTTATCCAGGTGTGAATTTGAAACATTTGAAGACAGCATGGCATGGC 504
Db 81 G1uVala1aSn1leuAsnPheYrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 100
QY 505 TTACACCACTCTCAACTGATGATGACAGAGAAACCTATCCAGAGTTTTCCTCCAGCA 564
Db 101 LeuSerH1sLeuSerThrLeu1leu1leu1leu1leu1leu1leu1leu1leu1leu1leu 120
QY 565 AGTTTCTTGAGACTTAAAGATTGACAACTGCTGCTGCTGAGAGCAAAATTTGGCTCTT 624
Db 121 AlaPheSerG1yLeuSerSerLeuG1uYrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 140

QY	625	CTAGAAGGCTTCCCATTTGGAACAGCTTTTAACTTTAAAGGAACTGAATGGCTCAACAT	684
Db	141	LeuGluAsnProIleuYhiSleuYsthrLeuYsGluLeuAsnValAlaHisn	160
QY	685	TTTATACATTCCTGTAGTTACCTGCATATATTTTTCAACTGCAACCACTAGTACATGTG	744
Db	161	LeuIleGlnSerPheYleuProGluYrPheSerAsnLeuThrAsnLeuGluHiSleu	180
QY	745	GATCTTTCTTTAACTATATTTCAAACTATTTACTGTCAACGACTTACAGTTTCTACGTAA	804
Db	181	AspLeuSerSerAsnYhiIleGlnSerIleYrCysThrAspLeuArgValLeuHiSglN	200
QY	805	AATCCACAAGTCAACTCCTTTTGACATGCTTTTGAACATGCTTGAACCAATGACTTCATTCAAAC	864
Db	201	MetProLeuLeuAsnLeuSerLeuAsnProMetAsnPheIleGlnPro	220
QY	865	CAAGCCTTTCAGGGAAATTAAAGCTCCATGAACCTGACTTAAAGAGTAAATTTTAAATGTGCA	924
Db	221	GlyAlaPheYleuYsGluIleArgLeuHiSrySleuThrLeuAlaGluAsnAsnPheAspSerLeu	240
QY	925	AATATATGAAAACCTGGCTTCAAAAACCTGGCTGTTTACAGCTCACTCGGTGATCTTG	984
Db	241	AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHiSargLeuValLeu	260
QY	985	GGAGAAATTTAAAGATGAAGAAGAAATGTGAAATTTTGAACCTGTATCATGAGAGACTA	1044
Db	261	GlyGluPheArgAsnGluGlyAsnLeuGluYsPheAspYsSerAlaLeuGlnGlyLeu	280
QY	1045	TGTGATGTGACCATTTGATGAGTACAGTTACATATCAATAAATGATTTTTCAGATGATTT	1104
Db	281	CysAsnLeuThrIleGluGluPheArgLeuAlaYrLeuAspYrYrYrLeuAspSrrIle	300
QY	1105	GTTAAG--TTTCCATTCGCTTGGCGCAATGTTTCTGCAATGCTCTGCGACAGTATCTATA	1161
Db	301	IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	320
QY	1162	AAATATCTAGAAGATGTTCTTAAACATTTCAATATGCAATCTTATCAATCATTAAGATGT	1221
Db	321	GluArgValYleuAspPheSerYrAsnAsnGlyTrpGlnHiSleuGluLeuValAsnCys	340
QY	1222	CACCTAAG-CAGTTTCCAACTCTGCATCTACCTTTCTTAAAGTTGACCTTAACTATG	1280
Db	341	LysPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrSer	360
QY	1281	AACAAAGGCTTATCAGTTTAAAAAAGATGGCCCTCAACAGCTCAGCATCTATGATCTT	1340
Db	361	AsnYsGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAsnPro	380
QY	1341	AGTGAATGACACTGACGCTTATAGTGTGGCTGTTCTTATTTGATTTGGGAACAAACAGC	1400
Db	381	SerArgAsnGlyLeuSerPheYleuGlyCysSerGlnSerAsnArgPheGlyThrThrSer	400
QY	1401	CTGAGACACTTGAACCTCAGCTTCAATGTCGCCATCATTTATGATGCCAATTTACATGGGT	1460
Db	401	LeuYsYrYleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly	420
QY	1461	CTAGAAGAGCTGACACCTGATTTTTTACACACTTAACTTAAAGAGGTCACAGATT	1520
Db	421	LeuGluGlnLeuGluHiSleuAsp-PheGlnHiSerAsnLeuYsGlnMetSerGluPhe	440
QY	1521	CTCAGCGTCTTATCCCTTGAAGAGCTTACTTACCTTGACATCTTTATATCAACCA	1580
Db	440	SerValPheLeuSerLeuAspAsnLeuIleYrLeuAspIleSerHiSthrHiSthrArg	460
QY	1581	AATTGACTTCGATGGTATATTTCTTGGCTTGACCAAGTCTCAACACATTTAAATGGCTGG	1640
Db	460	GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuYsMetAlaG1	480
QY	1641	CAATTCCTTCAAGAACAAACCCCTTTCAAAATGCTTTTGCAAAACAAACAACTTGACATT	1700
Db	480	YAsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe	500

QY	1701	CTGTGATCTCTTAAAGTCAATTTGAGAAACAAATCTTGGGGGATATTGGACACCTTCCA	1760
Db	500	elueApleuSerGlnCysGlnleuGlnleuSerProThraIaPheAmsSerLeuSe	520
QY	1761	TAGACTTCATTAATTAATAGACTCAACAACATCTATTGTTTGGATTCATCCCATTA	1820
Db	520	rSerleuGlnValLeuAmsMetSerIaSaenAenPhePheSerleuAmsPThrPheProTy	540
QY	1821	TAAACAGCTGATTTCCCTCAGACACTTTGATTCAGATTCAATGGCATAGACATCT--	1878
Db	540	rLysCysleuAmsSerleuGlnValleuAAsPyrSerleuAmsnIleMetThrSerLy	560
QY	1879	-AAAGSAATCTGCAACATTTTCCAAAGAGCTAGACCTTCTCAATCTTTACATATTC	1937
Db	560	sLysGlnGlnleuGlnIinhIspheProSerSerleuAaIaPheleuAmsleuThrGlnAmsA	580
QY	1938	TGTTGCTTGTAATATAGTGAACATCAGAAATTCCTGACATGGGTCAAGACAAGACAGATT	1997
Db	580	pPheIaIaCysThrCysGlnIeGlnSerPheleuGlnTrpIleLysAAspGlnAArgGlnle	600
QY	1998	CTTGCTGAATGTTGAACAAATGACATGTGCAACCTGTAGAGATGAATTCCTCTTAAGT	2057
Db	600	uLeuValGlnValGlnAurGmetGlnCysAlaIthrProSerAAspLysGlnGlyMetProVa	620
QY	2058	GTTGGATTTTAATAATTTCTACCGCTGTTATATGTAACAACAATCATCAGCTGCAGAGCT	2117
Db	620	lLeuSerleu--AsnIleThrCysGlnMetAAsnLysThrIleIleGlnValSerValle	639
QY	2118	CAGGTGATATGTGGTATCCACTAGACATTTCTGATATACCATCTTCATTTTCACCTGAT	2177
Db	639	uSerValleuValIaSerValIaAaIaValleuValTyLysPheTyrrhehIleSleuMe	659
QY	2178	ACTTATTTCTGGCTGTAAAAAGTACACAGACAGAGAAGAAACATCTATGATSCATTTTGAT	2237
Db	659	lLeuLeuAlaGlyCysIleLysTyrrGlyAArgGlnGlnAAsnIleTyraAspIaPheValIl	679
QY	2238	CTACTCGAATGCAAAATATAGACATCGGTGGAGAAATAGACTGTGAAGAAATTTAGAAGAGG	2297
Db	679	eTyrrSerSerGlnAAspGlnAAspTrpValAArgAAsnGlnleuValIyAAsnleuGlnGlnI	699
QY	2298	AGTACCCCGCTTTCACCTCGCTTCACTACATACAGAGACTTATATCTGTGTAGCCATTGC	2357
Db	699	yValProPheGlnleuCysleuHisTyrrAAspPheIleProGlyAlaIaIeAl	719
QY	2358	TGCCAATCATCTCAGAAAGCTTCCACAAGAGCCGGAAGATTATGTGGTAGTGTCTAG	2417
Db	719	aIaAAsnIleIleHisGlnGlyPhehIleSlySerAArgLysValIleValIaValIaSerGI	739
QY	2418	ACACTTATTTACAGACCCGTGTGGTATCTTTGAATATAGATTGCTCAAAACATGGCAGTT	2477
Db	739	nHisPheIleGlnSerAArgTrpCysIlePheGlnTyrrGlnIleAlaGlnIthrTrpGlnPh	759
QY	2478	TCTGAGAGAGCGCTCTGGAGCATATCTTCATTTGCTTGAAGAGTTGAAGAAGCCCGCT	2537
Db	759	eIeueSerSerAArgIaGlyIleIlePheIleValleuGlnLysValGlnuSerThrLeuLe	779
QY	2538	GAGGACAGCAGATGGAATTTATGAGCTTCTTACACAGAAACCTTACCTGGAATGGAGAGA	2597
Db	779	uArgGlnGlnValaGlnleuTyrrArgleuAmsSerAArgAsnThrTyrrleuGlnIurpGlnAe	799
QY	2598	CAATCTCTGGGGAGGACATCTTTCTGGAGAGACATTAAAAATGCCCTATTGGATGGAAA	2657
Db	799	pSerValleuGlnIaArgHisIleIlePheTrpArgLeuAArgLysAlaIeueAmspGlyLy	819
QY	2658	AGCCTGAATCTCGAGCAACA 2679	
Db	819	sSerTrpAAsnProGlnGlnTyrr 826	
RESULT 6			
ID AAM86361 standard; protein; 837 AA.			
XX AAM86361, AAM86361,			

Db 4425 LeuAap -PheGlnHisSerAsnLeuValGlnMetSerCyluPheSerVal1PheLeuSerLe 444

QY 1539 TGAAGAAGTACTTAACTTGAACATCTCTTAATCTAACAACAAATGACCTTGATGGTAT 1539B

Db 444 uArgAsnLeuIleTyrLeuAAsp1LeSerHisThrHisArgValAlaPheAsnGly11 464

QY 1599 ATTTCTTGCGCTGACCACTGTCAACAACATTTAAATGGCTGGCAATTTCTTCAAGAACA 1655E

Db 464 ePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAs 484

QY 1659 CACCCTTTCAATGTCTTTGGCAACAACAACAAACTGACATTTCCGTGATCTCTTAATG 1718

Db 484 nPheLeuProAsp1IlePheThrGlnLeuAlaArgAsnLeuThrPheLeuAAspLeuSerGlnCy 504

QY 1719 TCAATTTGAACAATAATCTTGCGGGGGATTTTGACACCCCTCCATAGACTTCAATTAATA 1778

Db 504 sGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSerLeuGlnValLeuAs 524

QY 1779 TATGAGTCAACAATCTTAATGTTTGGATTCATCCATTAATTAACAAGCTGTATTCCT 1838B

Db 524 mMetSerHisAsnAsnPhePheSerLeuAAspThrPheProTyrLysCysLeuAsnSerLe 544

QY 1839 CAGACCTGTATTTGCACTTTCAATCGCATGAGACATCT--AAAGGAATATGCAACA 1895S

Db 544 uGlnValLeuAAsp1TyrSerLeuAsnHisAlaLeuThrSerLysLysGlnGluLeuGlnHis 564

QY 1896 TTTTTCAAAGAGCTAGACCTTTCTTCAACTTACTTAACAATCTGTGCTGTATATGCA 1955S

Db 564 sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCyThrCysGly 584

QY 1956 ACATCAGAAATTCCTGACAGTGGGTCAAGAAACAGAAAGAGTTCTTGGAATGTTGAACA 2015S

Db 584 uHisGlnSerPheLeuGlnTyrP1LeLysAAspGlnArgGlnLeuLeuValGlnValuAr 604

QY 2016 AATGACATGTGCCAACACCTGTAGAGATGAATACCTCCTTAGCTGTGAATTTAATAATTC 2075S

Db 604 gMetGlnCysAlaThrProSerAAspLysGlnGlyMetProValLeuSerLeu--Asn11 623

QY 2076 TACCTGTATATGTACAAGACAATCATCATGTGTGACAGTGTGATGATGGTATGTC 2135S

Db 623 eThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSerValLeuValSer 643

QY 2136 CACTGTAGCAATTTGTATATACCACTTATATTTTCACTGTATACTTATGTGTGCTGTAA 2195S

Db 643 rValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCys11 663

QY 2196 AAAGTACAGCAGAGAGAAAGCACTTAAGCACTTAATTTGTATCTAATGATCAGAAAGA 2255S

Db 663 eLysTyrLysArgGlyGlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspG1 683

QY 2256 GGACTGGGTGAGAAATAGCTGTGTAAAGAAATTTAGAAAGAGAGAGCCCGCTTCACT 2315S

Db 683 uAspTyrValArgAsnGlnLeuValLysAsnLeuGlnIleGlyAlaProProPheGlnLe 703

QY 2316 CTGCTCTTCACTACAGAGACTTATATCTGTGTAGCCATGTCTGTGCAACATCATCCAGGA 2375S

Db 703 uCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAsnIleIleHisG1 723

QY 2376 AGGCTTCCACAAGAGCCGGAAGGTATTTGTGTAGTGTCTAGACACTTTATTCAGAGCCG 2435B

Db 723 uGlyPheHisLysSerArgLysValIleValValValSerGlnHisPheIleGlnSerAr 743

QY 2436 TTGGGTGTCTTTGAATATAGATTGCTCAAAACATGGAGATTTTCAGACAGCCGCTGG 2495S

Db 743 gTyrCysAllePheGlnTyrGlnIleAlaGlnThrTyrPheLeuSerSerArGlyAlaG1 763

QY 2496 CATCATCTTCAATGTCTTGAAGAAGGTGAGAAGTCCCTGTGTAGGCAAGAGGTGAATT 2555S

Db 763 yIleIlePheIleValIleGlnGlnLysValGlnLysThrLeuAAspGlnGlnValGluLe 783

QY 2556 GTATGTGCTTTTAGACAAACACTTACTGTGAATGGAGACAGCAATCTCTTGGGGAGGCA 2615S

Db	783	UTYrArgLeuSeuSerArGAsnThrTYrLeuclUlrPglUuaPSeVallLeuclYlrRgh	803
QY	2616	CATCTTTCGGAGAAACTTAAAAAAGCCCTATTGGATGGAAGAAAGCCTCGAATCTGAGCA	267
Db	803	lePheTrpArGArGLeuArGylAlaLeuSeuAspGlylYSerTrPAAsnProclUgl	823
QY	2676	AACA 2679	
Db	823	YThr 824	
RESULT 7			
ID	AAE16102	standard; protein; 837 AA.	
XX	AAE16102;		
AC	AAE16102;		
XX	26-MAR-2002	(first entry)	
DT			
XX			
DE	Human DNAX Toll like receptor (DTRLR) 4 #2.		
XX			
KW	Human; DNAX Toll like receptor; DTRLR; therapy; immunological disorder;		
KM	interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200190151-A2.		
PD			
XX	29-NOV-2001.		
XX			
PF	23-MAY-2001; 2001WO-US016766.		
XX			
PR	25-MAY-2000; 2000US-0207558P.		
XX			
PA	(SCHE) SCHERING CORP.		
PI			
XX	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;		
XX			
DR	WPI; 2002-083085/11.		
XX	N-PSDB; AAD26292.		
XX			
PT	New DNAX Toll like receptor (DTRLR) proteins, useful for treating		
PT	conditions exhibiting abnormal expression of the receptors of their		
PT	ligands, particularly abnormalities manifested by immunological		
PT	disorders.		
XX			
PS	Claim 3; Page 41; 297pp; English.		
XX			
CC	The invention relates to mammalian receptor proteins, e.g., primate,		
CC	human DNAX Toll like receptor (DTRLR) protein and their corresponding		
CC	nucleic acids. The DTRLR is useful for treating conditions exhibiting		
CC	abnormal expression of the receptors of their ligands. Such abnormality		
CC	is manifested by immunological disorders. In particular, the DTRLR is		
CC	useful for treating various disease or disorders associated with abnormal		
CC	expression or abnormal triggering of response to a ligand. The DTRLR is		
CC	also useful as an immunogen for the production of antisera or antibodies		
CC	specific, e.g., capable of distinguishing between other interleukin (IL)-1		
CC	receptor family members, for the DTRLR or its various fragments. The		
CC	purified DTRLR can be used to screen monoclonal antibodies or antigen-		
CC	binding fragments. The antibodies are useful for screening expression		
CC	libraries for particular expression products. These are useful for		
CC	detecting or diagnosing various immunological conditions related to		
CC	expression of DTRLR or cells that express it. The present sequence is		
CC	human DTRLR4 protein. The DTRLR4 gene is located on chromosome 9q32-33.		
CC	Note: The present sequence SEQ ID NO 26 is stated to be similar to the		
CC	sequence shown in page 240-243 (AAE16116). However these sequences differ		
CC	at several locations		
XX			
XX			
XX	Sequence 837 AA;		
Alignment Scores:			
Pred. No.:	4,19e-301	Length:	837
Score:	2772.50	Matches:	554
Percent Similarity:	79.56%	Conservative:	100

Best Local Similarity: 67.40% Mismatches: 162
 Query Match: 53.55% Indels: 7
 DB: 5 Gaps: 5
 US-09-396-985b-46 (1-2951) x AAIE102 (1-837)

QY 226 CTGGCTAGAGCTGTGATCATGGCACTG---TTCTTCTCTGCTGCTGACCAAGGAGTGTG 282
 Db 6 LeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysValArgProGlnuSerTrp 25
 QY 283 AATCCCTGCATAGAGGTAGTCTCTTAATATTAATCTTACCAATGCATGATCGAATCACTGAC 342
 Db 26 GluProCysValGlu---ValProAsnIleThrTrpGlnCysMetGluLeuAsnPheTrp 44
 QY 343 AAGTCCCTGATGATCTCTTCTTCAACCAAGACATAGATCTGAGCTTCAACCCCTG 402
 Db 45 LysIleProAsnLeuProPheSerThrLysAsnLeuAsnLeuSerPheAsnProLeu 64
 QY 403 AAGATCTTAAAGGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCC 462
 Db 65 ArgHisLeuGlySerTrpSerPhePheSerPheProIleuGlnValLeuAsnLeuSer 84
 QY 463 AGGTGTAATTTGAACATTTGAAGACAGGCGATGCGATGCTTACCACTTCTCAAC 522
 Db 85 ArgCysGluIleGlnThrIleGluAspGlyAlaTrpGlnSerLeuSerHisLeuSerThr 104
 QY 523 TTGATTAATGACAGAAACCTATCCAGATTTTCCCAAGAAAGTTTCTGACCTTAC 582
 Db 105 LeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSer 124
 QY 583 AGTTTACACATCTGTGCTGTGAGACAAATTTGCGCTCTTACAAAGCTTCCCTATT 642
 Db 125 SerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSerLeuGlnuAsnPheProIle 144
 QY 643 GGACAGCTTTATACCTTAAAGAACTCAATGTGCTCAACATTTTATACATCTCTGTAAG 702
 Db 145 GlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheLys 164
 QY 703 TTACCTGATATTTTCCATCTGACGACCTAGTACATGAGATCTTCTTATATATAT 762
 Db 165 LeuProIuTrpPheSerAsnLeuThrAsnLeuGlnuHisLeuAsnLeuSerSerAsnLys 184
 QY 763 ATTCAACATATTAATCTCAACGACTTACAGTTTCTAGTGAATAATCCACAAAGCTCAATCTC 822
 Db 185 IleGlnSerIleTrpCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeu 204
 QY 823 TCTTTAAGACATGTCTTTGAACCCCAATGACTTCACTTAACAACAAAGCTTTCAGGGAAAT 882
 Db 205 SerLeuAsnLeuSerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGlnIle 224
 QY 883 AAGCTCATGACAGCTCTTAGAGGTAAATTTTAATAGCTCAATATATATGAAACCTTGC 942
 Db 225 ArgLeuHisLysLeuThrLeuArgAsnAsnAsnAsnAsnAsnAsnValMetLysThrCys 244
 QY 943 CTTCAAAACCTGCTGCTTTTACAGCTCATGCTGCTTGAATCTTGAGAGATTTAAAGATGAA 1002
 Db 245 IleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValIleuGlnGluPheAsnArgAsnGln 264
 QY 1003 AGGAATGTGAATTTTGAACCTCTATATCAAGAGACATGAGATGTGATGCCATTTGAT 1062
 Db 265 GlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGln 284
 QY 1063 GAGTTCAAGCTTAAATATCAAAATGATTTTTCAGATGATATGTTAAG---TTCCATATGC 1119
 Db 285 GluPheArgLeuAlaTrpLeuAspLysTrpLeuAsnAspIleIleAspLeuPheAsnCys 304
 QY 1120 TTGGCAATGTTTCTGCAATGCTCTGCGAGGTGATCTATAAATATCAAGATGTT 1179
 Db 305 LeuThrAsnValSerSerPheSerLeuValSerValThrIleGlnuGlyValLysAspPhe 324
 QY 1180 CTTAAACATTTCAATGCGCAATCTTTATCAATCATTAAGATGTCACATTAAG-CAGTTTCA 1238
 Db 325 SerTrpAsnPheGlyTrpGlnHisLeuGlnLeuValAsnCysLysPheGlnGlnPhePro 344

QY 1239 ACTGTGATCTACCCCTTTCTTAAAGTTTGACTTTAATATGACAAAGGCTTATCAAGT 1298
 Db 345 ThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAla 364
 QY 1299 TTTAAAGGAGGACCTTACCAAGTCTCAGCTTATCTTGAATCTTATAGTAAATGACCTGAC 1358
 Db 365 PheSerGlnValAspLeuProSerLeuGlnPheLeuAsnLeuSerArgAsnGlyLeuSer 384
 QY 1359 TTTAGTGGTGGCTGTCTTATCTGATTTTGGGAAACAAACAGCTGACCTTACGACCTC 1418
 Db 385 PheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeuLysTrpLeuAsnLeu 404
 QY 1419 AGCTTCAATGAGTGGCCCTCATTAATGAGTGCATTAATTCAGGTGCTGAGAGGCTGACGAC 1478
 Db 405 SerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeuGlnuGlnLeuGlnuHis 424
 QY 1479 CTGGATTTTTCAGACTCTTATTAATAAGGCTCAGAAATTTCTCAGCCTTCTTATCCCT 1538
 Db 425 LeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerIle 444
 QY 1539 TGAAGGCTAATCTTACCTTGAACATCTCTTATATCAACCAAAATTTGACTGATGTAAT 1598
 Db 444 ValArgAsnLeuIleTrpLeuAsnProIleSerHisThrHisThrArgValAlaPheAsnGlyAl 464
 QY 1599 ATTCTTGGCTTGACAGCTCTCAACACATTAATAAGGCTGCGCAATTTCTTCAAGACAA 1658
 Db 464 ePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnuLys 484
 QY 1659 GACCTTTCAATGCTCTTTGCAAAACAAACAACTTGAATCTCTGATCTTCTTAAATG 1718
 Db 484 nPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeuAsnLeuSerGlnCys 504
 QY 1719 TCAATTTGAACAAATATCTTGGGGGATTTTGAACCCCTCAATGACCTTCAATATTAAT 1778
 Db 504 GlnLeuGlnuGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnuAlaLeuAs 524
 QY 1779 TATGATCAACAACATCTATTTGTTGGATTCATCCATTTATTAACAGCTGATTTCCCT 1838
 Db 524 nMetSerHisAsnAsnPhePheSerLeuAsnProTrpTrpCysLeuAsnSerIle 544
 QY 1839 CAGCACTTTGATTTGACATTTCAATGCAATGACATCT--AAAGAAATCTGCAACA 1895
 Db 544 GlnValLeuAspTrpSerLeuAsnHisIleMetCysTrpLysGlnuGlnuGlnuHis 564
 QY 1896 TTTTCCAAAGAGCTTACCTCTTCAATCTTATCAATTTCTGTTGCTGTATATGTA 1955
 Db 564 ePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGln 584
 QY 1956 ACATCAAGAAATTCCTGACAGTGGGTCAAGGACAGAGCAAGTCTTGAGTGAATGTGAACA 2015
 Db 584 uHisGlnSerPheLeuGlnTrpIleLysAspGlnuGlnuGlnuLeuValGlnuValGlnuArg 604
 QY 2016 AATGACATGTGCAACCTGTAGAGATGAATACCTCTTATGTTGATTTTAATATTC 2075
 Db 604 GmetGlnCysAlaThrProSerAspLysGlnuGlnuMetProValLeuSerLeu--AsnIle 623
 QY 2076 TACCTGTATATGTAACAAGCAATCATCAAGTGTGACAGTGTGACAGTGTGATTTGGTATC 2135
 Db 623 eThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSerValLeuValAlaIse 643
 QY 2136 CACTGTGATCTTGTATATACACTTATTTTCACTGATCTTCACTTATGCTGCTGATA 2195
 Db 643 ValValAlaValLeuValTrpLysPheTrpPheHisPheMetLeuLeuAlaGlySerIle 663
 QY 2196 AAGATCAGCAGAGAGAAAGCATCTATGATGCAATTTGTGATCTGATCGACATGAATGA 2255
 Db 663 eLysTrpGlyArgGlyGlnuAsnIleTrpAspAlaPheValIleTrpSerSerGlnuAsp 683
 QY 2256 GGACTGGGTGAAGAAATGAGCTGTGAAGAAATTTGAAGAAAGAGTGGCCGCTTCACT 2315
 Db 683 uAspTrpValArgAsnGlnuLeuValLysAsnLeuGlnuGlnuGlnuValProProPheGlnu 703

PD 29-NOV-2001.
 XX 23-MAY-2001; 2001MO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI; 2002-083086/11.
 DR N-PSDB; AAD26306.
 XX
 XX New DNAX Toll like receptor (DTRL) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS Claim 3; Page 240-243; 297pp; English.
 XX
 XX The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTRL) protein and their corresponding
 CC nucleic acids. The DTRL is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTRL is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTRL is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTRL or its various fragments. The
 CC purified DTRL can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTRL or cells that express it. The present sequence is
 CC human DTRL4 protein, alternative version. The DTRL4 gene is located on
 CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
 CC be similar to the sequence shown in page 41 (AAE16102). However these
 CC sequences differ at several locations
 XX
 XX Sequence 837 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2,566-300 Length: 837
 Score: 2765.50 Matches: 553
 Percent Similarity: 79.44% Conservative: 100
 Best Local Similarity: 67.27% Mismatches: 163
 Query Match: 53.42% Gaps: 7
 DB: 5
 US-09-396-985b-46 (1-2951) x AAE16116 (1-837)
 QY 226 CTGGCTAGAGCTGTGATGAGCACTG--TTCTTCTCTGCTGACACGAGAGCTTG 282
 Db 6 LeuAlaGlyThreuleuIleProAlaMetAlaPheIleuSerCysValaArgProGluSerTrp 25
 QY 283 AATCCCTGCTAGAGGAGTAGTCTTAATATTAATCTACCAATGATGATCGAAACTCAGC 342
 Db 26 GluProCysValaGlu--ValProAsnIleThrTyrlncysmetGluIleuAsnPhetyr 44
 QY 343 AAGTCCCTGATGATCTCTTCTTCAACGAGACATAGATGAGCTTCAACCCCTTG 402
 Db 45 LysIleProAsnIleuProPheSerThrLysAsnIleuAspLeuSerPheAsnProIleu 64
 QY 403 AAGATCTTAAAGAGTATAGCTTCTCAATTTTTCAGACATTCAGTGGCTGATTTATCC 462
 Db 65 ArgHisIleuGlySerTrpSerPhePheSerPheProIleuGlnValIleuAspLeuSer 84
 QY 463 AGGTGTAATTTGAACATATTGAAGACAGAGCATGCGATGCTTACACCTCTCAAC 522
 Db 85 ArgCysGluIleIleGlnIleIleGlnAspGlyAlaTyrlncysIleuSerHisIleuSerThr 104
 QY 523 TTGATACTGACAGGAACCTATCCAGAGTTTTCCTCCAGAGAGTTTCTCTGAGACTACA 582

Db 105 LeuIleuThrGlyIleuProIleuGlnSerIleuAlaIleuGlyAlaPheSerGlyLeuSer 124
 QY 583 AGTTTAGACAAATGTGGTGGCTGGAGACAAAATTTGGCCCTCTTAAAGCTCCCTATT 642
 Db 125 SerLeuGlnIleuValAlaValGluThrAsnIleuAlaSerIleuGlnIleuPheProIle 144
 QY 643 GGACAGCTTATTAACCTTAAAGAACTCAATGTGGCTCACAAATTTTATACATTCCTGTAAG 702
 Db 145 GlyHisIleuLysThrIleuLysGluIleuAsnValAlaHisAsnIleuIleGlnSerPheLys 164
 QY 703 TTAAGTCAATATTTTTCATCTGACGAACCTAGTACATGTGATTTTCTTATTAATCTAT 762
 Db 165 LeuProGluIleuPheSerIleuThrAsnIleuGlnHisIleuAspLeuSerSerAsnLys 184
 QY 763 ATTCGAACATATATCTGTCAACAGCTTACAGCTTCTACGTAATTCACCAAGCATCTTC 822
 Db 185 IleGlnSerIleuLysThrIleuLysValIleuHisGlnMetProIleuLeuAsnIleu 204
 QY 823 TCTTTAGACATGTCTTGAACCAATGACTTTCATTCAGACCAAGCTTTCAGGGAAT 882
 Db 205 SerLeuAspLeuSerLeu--*ProMetAsnPheIleGlnProGlyAlaPheLysGluIle 224
 QY 883 AAGCTTCATGAACTGACTCTAAGAGGTAATTTTATAGCTCAATATTAATGAACACTGTC 942
 Db 225 ArgLeuHisIleuLysThrIleuLysAsnValAlaAspSerIleuAsnValMetLysThrCys 244
 QY 943 CTTCGAACCTGCTGCTGCTTACACGCTTCATCGCTGATCTTGGAGAAATTTAAAGATGA 1002
 Db 245 IleGlnGlyIleuAlaGlyIleuGluValHisArgIleuValIleuGlyIleuPheArgAsnGlu 264
 QY 1003 AGGAATCTGGAATTTTGAACCCCTATCACTGGAAGGACTAGTATGATGACATTTGAT 1062
 Db 265 GlyAsnIleuGlnIleuPheAspLysSerAlaIleuGlnGlyLeuLysAsnIleuThrIleuGlu 284
 QY 1063 GAGTTCAAGGTTTACATATCAATGAATGATTTTTCAGATGATATTTGTAAG--TTCCATGTC 1119
 Db 285 GluPheArgLeuAlaIleuLysAspGlyTrpIleuAspAspIleIleAspLeuPheAsnCys 304
 QY 1120 TTGGCAATGTTTCTGCAATGTCTCTGCGACAGGTATCTATTAATAATATCTAGAAGATGTT 1179
 Db 305 LeuThrAsnValSerSerPheSerIleuValSerValThrIleuGluArgValIleuAspPhe 324
 QY 1180 CTTAAACATTTTCAAAATGGCAATCTATCAATCATTAAGATGCACTAAG--CAGTTTCCA 1238
 Db 325 SerTrpAsnIleuLysIleuGlnHisIleuGluIleuValAsnCysLysPheGlyIleuPhePro 344
 QY 1239 ACTCTGATCTACCTCTTCTTAAAGTTTGAATTAATCAATGAAACAAAGGCTTATCACT 1298
 Db 345 ThrIleuLysIleuLysSerIleuLysArgIleuThrPheThrSerAsnLysGlyIleuAla 364
 QY 1299 TTTAAAAAAGTGCCCTTACCAAGTCTACAGCTATCTAGATCTTATGTAAGAAATGCACTGAGC 1358
 Db 365 PheSerGluValAlaAspLeuProSerIleuGlnPheLeuAspLeuSerArgAsnGlyLeuSer 384
 QY 1359 TTATAGTGGTGGCTGTTCTTATTTCTGATTTTGGGAAACAAAGCTGAGACACTTAAGACCTC 1418
 Db 385 PheLysGlyCysPheSerGlnSerIleuAspPheGlyThrThrSerIleuLysTrpIleuAspLeu 404
 QY 1419 AGCTCAATGAGGCCATCTTATGAGTCAATTTTCAATTTTCAAGGCTTGAAGAGCTGACAGAC 1478
 Db 405 SerPheAsnGlyValIleuThrMetSerSerAsnIleuLysGlnIleuGlnIleuGlnHis 424
 QY 1479 CTGGATTTTTCAGACCTCTTATTAAGAGGTACAGAAATTTCTCAGCGTTCTTATCCCT 1538
 Db 425 LeuAsp-PheGlnHisSerAsnIleuLysGlnMetSerGluPheSerValPheLeuSerIle 444
 QY 1539 TGAAGAGCTTACTTATCTGACATCTCTTATATCAACCAAAATTTGACTGATGTAT 1598
 Db 444 ValArgAsnIleuLysIleuAspIleuSerHisThrHisIleuArgValAlaPheAsnGlyIle 464
 QY 1599 ATTTCTTGCTTGCACAGCTCTCAACACATTAATAAATGCTGCGCAATTTCTTCAAAACAA 1658


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Db      464 ePheAmGlyLeuSerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAs 484
QY      1659 GACCCCTTCAAAAGTCTTTGGCAACAACAACATTCGACCTTCGATTCCTTCAAAAG 1718
Db      484 nPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCy 504
QY      1719 TCAATGGAAACAATATCTTGGGGGGATTTGACACCCCTCCATAGACTTCATTAATTA 1778
Db      504 sGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSerLeuGlnValLeuAs 524
QY      1779 TATGAGTCAACAACATCTATGTTTGGATTCATCCATTAATCAACAGCTGATTCCT 1838
Db      524 nMetSerHisAsnAspPheSerLeuAspThrPheProTyrLeuGlyCysLeuAsnSer 544
QY      1839 CAGCAGCTTTGATGGAGTTTCAATGCGCAGACATCT--AAAGGAATATTCGACAA 1895
Db      544 uGlnValLeuAspTyrSerLeuAsnHisLeuMetThrSerLysLeuGlnGlnGln 564
QY      1896 TTTTCCAAAGAGTGGAGCTTTCTTCAATCTTAACATTCGTTGTTGTTATATGTA 1955
Db      564 sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysG 584
QY      1956 ACATCAGAAATTCCTCGAGTGGGTCAAGAACAGAACAGCTTCGTGATGTTGAACA 2015
Db      584 uHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeuValGluValGluAr 604
QY      2016 AATGACATCTGCAACCTCTAGAGATGAATACCTCTTGTTGTTGATTTAATAATTC 2075
Db      604 gMetGluCysValThrProSerAspLysGlnGlyMetProValLeuSerLeu--Asn 623
QY      2076 TACCTGTTATATGTACAGACAATCATCATGATGTCAGTGCAGTGTGATGTTGATAC 2135
Db      623 eThrCysGlnMetAsnLysThrIleLeuGlyValSerValLeuSerValLeuValLys 643
QY      2136 CAGCTGAGCACTTCTGATATACCACTTTATTTTACCTGATATCTTCTGAGCTGTA 2195
Db      643 rValValAlaValLeuValLysLysPheTyrPheHisLeuMetLeuLeuAlaGlyS 663
QY      2196 AAGTTCAGAGAGAGAAAGCACTGATGCACTTGTGATCTGATCTGAGTCAAGATGA 2255
Db      663 eLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleLysSerSerGlnAsp 683
QY      2256 GGACTGGGTGAGAAATGAGCTGGTAAAGATTTAGAAAGAGAGTGCCTTCCTTCACT 2315
Db      683 uAspTrpValArgAsnGluLeuValLysAsnLeuGlnGlyValProPheGlnLe 703
QY      2316 CTGCTCTTCACTACAGACCTTTATCTCTGTTGATGACCATTCGCCAACATTCACAGA 2375
Db      703 uCysLeuHisIleTyrArgAspPheIleProGlyValAlaIleAlaAsnIleIleHis 723
QY      2376 AGGCTTCCACAAGACCGGAAGGTTATTTGGTGAAGTGTACAGACATTTATTCAGAGCC 2435
Db      723 uGlyPheHisLysSerArgLysValIleValValSerGlnHisPheHisIleGlnSer 743
QY      2436 TTGGTATGATCTTGAATATGATGATGCTCAAACTGACGATTCCTGAGCCGCTGTGG 2495
Db      743 gTrpCysIlePheGlnTyrGlnIleAlaGlnIleThrGlnPheLeuSerSerArgAla 763
QY      2496 CATCATCTTCATGTTCTTGAAGAGTTGAAGATTCCTCTGAGGACGAGGTGAAT 2555
Db      763 yIleIlePheHisLeuValLeuGlnLysValGlnLysThrLeuLeuArgGlnGlnVal 783
QY      2556 GTATCGCTCTTGAAGAGAAACCTACCTGGAATGGGAAGAGCAATCTCTGGGAGAGCA 2615
Db      783 uTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSerValLeuGlyArg 803
QY      2616 CATCTTTCGAGAGAACTTAAATAGCCCTATTTGATGAGAAAGCCCTGATCTGAGCA 2675
Db      803 sIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGln 823
QY      2676 AACA 2679
Db      823 yThr 824

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RESULT 10
AD057791
ID AD057791 standard; protein; 795 AA.
AC AD057791;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS Macaca mulatta.
XX
FH Key Location/Qualifiers
FT Misc-difference 635
FT /label= Lys, Asn
XX
XX MO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003MO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI; 2004-400726/37.
XX
XX N-PSDB; AD057789, AD057790.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 12; 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents rhesus monkey TLR4.
XX
SQ Sequence 795 AA;
XX
Alignment Scores:
Pred. No.: 1,64e-296 Length: 795
Score: 2731.50 Matches: 541
Percent Similarity: 80.15% Conservative: 97
Best Local Similarity: 67.96% Mismatches: 154
Query Match: 52.76% Indels: 5
DB: 8 Gaps: 3
US-09-396-985B-46 (1-2951) x AD057791 (1-795)
QY 298 GTAGTCTTAATATTACTTACCAATGATGATGACAAAGTCCCTGATGAC 357
Db 1 ValValProAsnIleThrTyrGlnCysMetGluLeuAsnPheTyrTrpIleProAspAsn 20
QY 358 ATTCTTCTTCAACAAGAACATGATGATGAGCTTCAACCTCTGAAAGATCTTAAAGC 417
Db 21 LeuProPheSerThrTyrAsnLeuAspLeuSerPheAsnProLeuArgHisLeuGlySer 40

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QY	418	TATAGCTTCCTCCAAATTTTTCAGAACTTCAGTGGCTGGAAATTTATCCAGGTGGAAATTTGA	477
Db	41	TTTTTTTTTTT:::	60
QY	478	ACAAATGGAAGACAGGCAATGGCATGGATGGCTTACACCACTTCCAACTTGATCTGACAGGA	537
Db	61	ThrlIeGIuaSpGIyAlaTyrGIlnSerIeuSerHlSleuSerThrlleuHleuHrGIy	80
QY	538	AACCTTATCCAGAGTTTTTCCCAGGAAGTTCTCTGGACCTAACCAATTAGACATCTG	597
Db	81	AsnProIIeGIlnSerIeuAlaIeuDlYAlaPheSerGIYleuSerSerIeuDlYleu	100
QY	598	GTGGCTGTGGAGACAAATTTGGCTCTCTCAGAAAGCTTCCATTTGGACAGCTTAACC	657
Db	101	ValAlaValGIuThrAsnIeuAlaSerIeuGIuaPheProIIeGIYHlSleuYsThr	120
QY	658	TTAAAGAACTCAATGCTGGCTCACAAATTTATACATCTCTGTAAGTTACCTGCATATTTT	717
Db	121	LeuYsGIuIeuAsnValAlaHlAsnIeuIleGIlnSerPheYleuProGIuYrPhe	140
QY	718	TCCAAATCGACGAACCTGATACATGGATCTTCTTAACTATATTCAACTTACT	777
Db	141	SerIeuAsnIuThrAsnIeuGIuHlSleuAspIeuSerSerAsnYleIleGIlnsnIleYr	160
QY	778	GTCAACGACTTAACAGTTTCTACGTGAAGAAATCCACAAAGTCAATCTCTTTAGACATGCT	837
Db	161	CysYsAspIeuGIuValIeuHlSglIlnMetCProIeuSerAsnIeuSerIeuAspIeuSer	180
QY	838	TTGAACCCCAATTTGACTTCTATTCACACCAAGCTTTCAGGGAATTAAGCTCCATGACTG	897
Db	181	LeuAsnProIIeAsnPheIleGIlnProGIYAlaPheYsGIuIleArGIuHlSlyIeu	200
QY	898	ACTCAAGAGGTAATTTTATATGCTCAATATTAATGAAGAACTTGCTTCAAAACTGGCT	957
Db	201	ThrlleuArGIserAsnPheAspAspIeuAsnValMetYsThrCysIleGIlnIleuAla	220
QY	958	GCTTTACACGTCATCGCTGATCTTGGAGAGAAATTTAAAGTAAGAAATCTGGAAAT	1017
Db	221	GIleuGIuValHlSArGIleuValIeuGIuIlePheArGIuAsnGIuArGIuAsnIeuDlY	240
QY	1018	TTTGAACCTCTATACAGGAAGGACATATGTGATGACATTTGATGATTCAGGTTACA	1077
Db	241	PheAspYsSerSerIeuGIuGIuIleuYsAsnIeuHlIleGIuIlnPheArGIleuHr	260
QY	1078	TATACAAATGATTTTTCAGATGATATTTGTAAG--TTCCATTTGGCTGGCAATTTTCT	1134
Db	261	TyrIleuAspYrYrYrIleuAspAsnIleIleAspIeuPheAsnYleuAlaAsnValSer	280
QY	1135	GCAATGTCTGGCAGGCTGTATCTATAAAATATCTAGAAGATGTTCTTAAACATTTCAA	1194
Db	281	SerPheSerIeuValSerValSerIleYsArGIuValGIuAspPheSerTyrAsnPheArG	300
QY	1195	TGGCAATCTTATCATCATTAAGATGATGAACCT--AAGCAGTTTCCAACTCTGATCTAAC	1253
Db	301	TrpGIlnHlSleuGIuIeuValaAsnYsYsPheGIuGIuIlnPheProHlIleuGIuIeuGIu	320
QY	1254	TTTCTTAAAGATTGACTTTTAACTATGAACAAAGGCTATCATGCTTTTAAAAAGTGCC	1313
Db	321	SerIeuYsArGIleuHrPheThrlaAsnYsGIuAsnAlaPheSerGIuValAsp	340
QY	1314	CTACCAAGTCACGATCTCTGATCTTATGTAAGAAATGACATGAGCTTATAGTGGCTGT	1373
Db	341	LeuProSerIeuGIuIlnPheIeuAspIeuSerArGIuAsnGIYleuSerPheYleGIYCyAsYs	360
QY	1374	TCTTATTTCTGATTTTGGGAACAAACAGCTGACCACTTAGACTTCAGCTTCAATGTGACC	1433
Db	361	SerGIlnSerArPheGIYThrThrSerIeuYrYrIleuAspIeuSerPheAsnAspVal	380
QY	1434	ATCATTTATGATGGCAATTTTCATGAGGTCTTAAAGAGTCGACGACACTTGGAATTTTTCAGA	1493
Db	381	IlleHrMetSerSerAsnPheIeuGIuIeuGIuYsIeuGIuHlSleuAsp--PheGIlnHl	400

QY	1494	CTCACTTAAAAAGGGTCACAGAAATTCCTGACGCTTCTATTCCTTGAAAAAGTACCTTTA	155
DB	400	SSerAsnLeuysgInmetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTy	420
QY	1554	CCTTGACATCTCTTATATCTAAACACAAAATGACTCGATGATATATTTCTTGCGCTTAC	1613
DB	420	RLeuAspIleSerHisThrHisStrHisArgValAlaPheAsnIleYIlePheAspGlyLeuIle	440
QY	1614	CAGTCTCAACACATTAAAAATGGCTGGCAATCTTTTCAAAGACAACACCTTTTCMAATGT	1673
DB	440	uSerLeuIysValIleuIyswMetAlaGlyAsnSerPheGlnIuAsnPheLeuProAspG1	460
QY	1674	CTTTGCAAAACACAAACAACTTGACATTCCTGATCCTCTTCAATGATCAATTGGACAACAT	1733
DB	460	ePheThrAspLeuIysAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIle	480
QY	1734	ATCTTGCGGGGATATTTGACACCCCTCCATAGACTTCAATTAATTAATATAGAGCAACAA	1792
DB	480	uSerProThrAlaPheAspThrLeuAsnIuysLeuGlnValIleuAsnMetSerHisAsnAs	500
QY	1794	TCATATGTTTGGATTCATCCATTAATMAACAGCTGTATTCCTCCAGACACTTGTATGTG	1853
DB	500	nPhePheSerLeuAspThrPheProTyIysCysLeuProSerLeuGlnValIleuAspTy	520
QY	1854	CAGTTTCAATGCGATAGACATCTTAAAGA--ATACTGCAACATTTTCCAAAGACTCT	1910
DB	520	rSerLeuAsnHisIleMetThrSerAsnAsnGlnIleuGlnHisPheProSerSerIle	540
QY	1911	AGCCTTCTTCACTCTTCTTAAACATTCCTGTTGTTATATATGTAACATCGAATTCCT	1970
DB	540	uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheIle	560
QY	1971	GCAGTGGGTCAAGACAGACAGACAGCTTCTTGCGAATGTTGACAAATGACATGTGCAC	2030
DB	560	uGlnTTrpIleIysAspGlnArgGlnLeuLeuValGlnAlaGlnIuArgMetGlnCysAlaTh	580
QY	2031	ACCTGTAGAGATGAATACCTCTTGAAGTTTGATTAATTAATTCATCTGTATATGTA	2090
DB	580	rProSerAspIysGlnGlyMetProValIleuSerIle--AsnIleThrCysGlnMetAs	599
QY	2091	CAAGACATCATCAGTGTGTCAGTGTGTCAGTGTATTTGGTATTCACCTGAGACATTTCT	2156
DB	599	nIysThrIleIleGlyValSerValPheSerValLeuValSerValValAlaValIle	619
QY	2151	GATATACCACTCTCATTTTCCACCTGATCACTTATGCTGCGCTGTAAAAAGTACACAGAG	2210
DB	619	uValTyIlyPhePheTyRheHisIleuMetLeuLeuHisGlyCysIle**TyRtyIArgG1	639
QY	2211	AGAAAGCATCTATGATSCATTTGTGATCTACTGAGTCAGAAATGAGACCTGGGTAGAAA	2270
DB	639	yGluAsnIleTyRAspAlaPheValIleTyRSerSerGlnAspGlnAspTrpValArgAs	659
QY	2271	TGAGCTGTGAAGAATTTAAGAAAGAGAGTCCCCGCTTTCACCTGTGCTTCACTACAG	2330
DB	659	nGluLeuValIysAsnLeuGlnGlyValProProPheGlnIleuCysLeuHisTyRAr	679
QY	2331	AGACTTATTCCTGCTGTAGACATTTGCTGCAACATCATCCAGAGAGAGCTTCCACAAGAG	2390
DB	679	gAspPheIleProGlyValAlaIleAlaIleAsnIleIleHisGlnGlyPheHisIysPSe	699
QY	2391	CCGGAAGGTTATGTGTAGTGTCTAGACACTTATTCAGAGCCGTTGTGTATCTTTGA	2450
DB	699	rArgIysValIleValValIleSerGlnHisPheIleGlnSerArgTrpCysIlePheG1	719
QY	2451	ATATGAGATGTCCTCAACATGAGAGTTTCGAGAGCCGCTGCGCAATCATCTTCATGT	2510
DB	719	uTyRglnIleAsnIleThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVa	739
QY	2511	CCTTGAGAGGTTGAGAAAGTCCCTGCTGAGGACAGAGTGAATGTATGAGCCTCTTAG	2570
DB	739	IleuGlnIysValGlnIuysThrIleuLeuArgGlnGlnIuValGlnIuTyRArgLeuIeuse	759
QY	2571	CAGAAACACTTACCTGGAATGGAGAGCAATCCTCTGGGAGGACACATCTTTGGAGAG	2630

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|||||
Db      759 rAGsAnThrTyLeuGIuTrpGIuaSpSerValLeuGIyGlnHisIlePheTrpArgAr 779
QY      2631 ACTTAAATAATGCCCTATTGATGGAGAAAGCGCTGATCCCTGAGCAA 2676
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      779 gLeuArgLySaIaLeuLeuAspGIyArGSetTrpAsnProGIuGln 794

RESULT 11
AD057803
ID AD057803 standard; protein: 808 AA.
XX
AC AD057803;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PE 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; AD057801, AD057802.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 24; 11pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Alignment Scores:
Pred. No.: 2,15e-296 Length: 808
Score: 2730.50 Matches: 541
Percent Similarity: 80.18% Conservative: 98
Best Local Similarity: 67.88% Mismatches: 154
Query Match: 52.74% Indels: 5
DB: 8 Gaps: 3

US-09-396-985B-46 (1-2951) x AD057803 (1-808)
QY      298 GTAGTCTCTAATATTACTCCATGCATGCATGAGAAACTCAGCAAGTCCCTGATGAC 357
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 ValAlaProAsnIleThrTyrgInCysWeGIuLeuAsnPheTyLySIIleProAspAsn 20
QY      358 ATTCCTTCTTCACCAAGAACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAAAGC 417
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...|||
Db      21 LeuPProPheSerThrIySaSnLeuAsnLeuAspLeuSerPheAsnProLeuArGHisLeuGIySer 40
QY      418 TATAGCTCTCCCAATTTTTCAGAACTTCAGTGGCTGATTTTATCCAGGTGATAATTGAA 477
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      41 TySerPhePheSerPheProGIuLeuGlnValLeuAsnLeuSerArgGylGlnIleGln 60
QY      478 ACAATTGAAGACAAAGCATGGCATGGCTTACACCACTCTCAAACTGTATCTGACAGGA 537
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ThrIleGIuAspLyAlaTyrgInSerLeuSerHisLeuSerThrIleLeuThrGIy 80
QY      538 AACCTTATCCAGAGTTTTCCTCCAGAGAGTTTCTCTGACTATCAACAAGTTTAGCAATTCG 597
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 AsnProIleGlnSerLeuAlaLeuGIyAlaPheSerGIyLeuSerSerLeuGlnLySleu 100
QY      598 GTGGCTGTGGAGACAAATTGGCGCTCTAGAAAGCTCCCTATTTGAGACGCTTATTAAC 657
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      101 ValAlaValaGIuThrAsnLeuAlaSerLeuGIuAsnPheProIleGIyHisLeuLySthr 120
QY      658 TTTAAAGAACTCAATGTGGCTCACAATTTTATCATCTCTGTAAAGTTTACCTGCATATTTT 717
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 LeuLySGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLySleuProGIuTyrPhe 140
QY      718 TCCAAATCTGACGAACCTAGTACATGTGATCTTTCTTATTAATTAATTCAACTATTACT 777
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      141 SerAsnLeuThrAsnLeuGIuHisLeuAspLeuSerSerAsnLySleuIleGlnSerIleTy 160
QY      778 GTCAAGACCTTACAGTTTCTACGCTGAAATCCCAAGTCAATCTCTTTAGACATGTC 837
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      161 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
QY      838 TTGAACCAATTAATGACTTCATTCAGAACCAAGCCTTTCAGGAAATTAACTCCATGAAC 897
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 LeuAsnProMetSerAsnHeIleGlnProGIyAlaPheLySGlnIleArgLeuHisLySleu 200
QY      898 ACTCTAAGAGGTAATTTTATATAGCTCAATATATATGAAAACTTGCTTCAAAACCTGGCT 957
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      201 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLySerCysIleGlnLyLeuAla 220
QY      958 GGTTCACGCTGCATGGTTGATCTTGAGGAGATTTTAAAGATTAAGAAAGAACTGGAATT 1017
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      221 GlyLeuGlnValaHisArgLeuValaLeuGIyGlnPheArgAsnIuGlnLeuAsnLeuGIyLyS 240
QY      1018 TTTGAACCTCTATCATGAGAGACTATGATGATGACCATTTGATGATTCAGTTTAA 1077
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 PheAspLySerSerAlaLeuGIuGIyLeuCySaSnLeuThrIleGIuGlnPheArgLeuAla 260
QY      1078 TATACAAATGATTTTTCAGATGATATTGTTAAG--TTCCATGCTTGGCGAATGTTTCT 1134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      261 TyrLeuAspTyrgTyrlLeuAspAspIleIleAspLeuPheAsnCySleuThrAsnValSer 280
QY      1135 GCATGTCTCTGGCAGGTGATGATCTATTAATAATATCTGAAGAAGTTTCTCTAAAC 1194
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      281 SerPheSerLeuValSerValInThrIleLySerValLySAspPheSerTyraSnPheGIy 300
QY      1195 TGGCAATCTCTATCATCATTAATGATGATGCACTAAG--CAGTTTCCAACCTCGATCTAAC 1253
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 TyrgIleHisLeuGIuLeuValLyCySlySAspPheGIyGlnPheProThrLeuLySleuLyS 320
QY      1254 TTTCTTAAAGATTGACTTAACTATGACAAAGGCTCTATCAGTTTAAAAAAGTGCC 1313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      321 SerLeuLyArgLeuThrPheThrSerAsnLyGIyGIyAsnAlaPheSerGIuValAsp 340
QY      1314 CTACCAAGTTCAGCTATCTAGATCTTATGTAAGAAAGCACTGAGCTTTAGTGGTGTCT 1373
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      341 LeuProSerLeuGIuPheLeuAspLeuSerArgAsnGIyLeuSerPheLySlyCySAsp 360
QY      1374 TCTTATCTGATTTGGGAACAAACAGCTGAGCACTTGAACCTCAGCTCAATGTGTC 1433
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361 SerGIleSerAspPheGIyThrThrSerLeuLyTyrlLeuAspLeuSerPheAsnGIyVal 380
QY      1434 ATCATTAATGATGCCAATTTTCATGGGTCTGAAGAGCTGACAGCTGATTTTTCAGCA 1493
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 381 ILethrMetSerSerAsnPhelLeuGluInLeuGluIleuAsp-PheGlnI 400
 QY 1494 CTCTACTTTAAAGAGGTCAGACAAATCTCAGCGTCTTATCCCTTGAAAGACTTCTTA 1553
 Db 400 sSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTy 420
 QY 1554 CTTTGACATCTCTTATATCTAACACCAAAATGACTTCGATGATATTTCTTGCGCTTAC 1613
 Db 420 rLeuAspIleSerIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSe 440
 QY 1614 CAGCTGACACATTAATAAATGCTGCAATCTTTCAAGACAAACACCTTCAAAATGT 1673
 Db 440 rSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPhelProAspI 460
 QY 1674 CTTTGCAACACCAACAACTTGACATTCCTGATCCCTTCAATGATTTGGAACAAAT 1733
 Db 460 ePheThrGluLeuArgAsnLeuIleThrPheLeuAspLeuSerGlnGluLeuGluIle 480
 QY 1734 ATCTTGAGGGGTATTTGACACCTCCATAGACTTCATTAATTAATATGATGACAA 1793
 Db 480 uSerProThrAlaPheAsnSerLeuSerSerLeuGluValLeuAsnMetSerIleAsnAs 500
 QY 1794 TCATTTGTTTGGATTCATCCCATTTAACACAGCTGATTCCTCAGACCTTGATTG 1853
 Db 500 nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGluValLeuAspTy 520
 QY 1854 CAGTTCAATCGCTAGACATCT---AAAGAAATCTGGAACATTTTCCAAAGATCT 1910
 Db 520 rSerLeuAsnHisIleMetThrSerLysLysGlnGluLeuGlnHisPheProSerSerLe 540
 QY 1911 AGCCTTCTCAATCTTACTAACATTTCTGTTGATATGATGATGACAAATGATTCCT 1970
 Db 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleSerPheLe 560
 QY 1971 GCAGTGGGTCAAGAACAGAAAGAGTCTTGATGATGATGACAAATGACATGTGCAAC 2030
 Db 560 uGlnTrrPrlLysAspGlnArgGlnLeuValGluValGluArgMetGluCysAlaIle 580
 QY 2031 ACCGTGAGAGTGAATACCTCCCTAGTGGATTTAATTAATCTCACTGTTATATGTA 2090
 Db 580 rProSerAspLysGlnGlyMetCProValLeuSerLeu--AsnIleThrCysGlnMetAs 599
 QY 2091 CAAGACATCATCATGAGTGTGAGTGTGAGTGTGATGATGATTCATGACATTTCT 2150
 Db 599 nLysThrIleIleIleGlyValSerValLeuSerValLeuValSerValAlaAlaValle 619
 QY 2151 GATATACACTTCTATTTTCACTGATCTTATTTGCTGCGCTGTAAGAAAGTACAGAGG 2210
 Db 619 uValTyrLysPhePheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArg 639
 QY 2211 AGAAGCATCTATGATGATCTGATCTGATCTGAGTCAAGATGAGACAGCGGTGAGAAA 2270
 Db 639 yGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrrValaArgAs 659
 QY 2271 TGAGCTGGTAAAGAAATTTAGAGAGAGAGTCCCGCTTACCTGCTTCACTACAG 2330
 Db 659 nGluLeuValLysAsnLeuGlnGlyValProPheGlnLeuCysLeuHisTyrArg 679
 QY 2331 AGACTTATTCCTGCTGATGACATTCCTGTCGCAACATCATCAGAGAGCTTCCACAGAG 2390
 Db 679 gAspPheIleProGlyAlaIleAlaIleAlaAsnIleIleHisGluGlyPheHisLysSe 699
 QY 2391 CCGGAGGTATATGCTAGTGTCTAGACACTTATTCAGAGCGGTGGTATCTTGA 2450
 Db 699 rArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrrCysIlePheG 719
 QY 2451 ATATGAGATTGCTCAACATGACAGTCTTGAGACAGCGCTGCGCATTCATCTCATGT 2510
 Db 719 uTyrGlnIleAlaGlnThrTrrPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
 QY 2511 CTTTGAGAGGTGAGAGTCCCTGCTGAGCAGACAGGTGGAATGTATGCGCTTCTAG 2570
 Db 739 lLeuGlnLysValGluTyrThrLeuLeuArgArgGlnValGluLeuTyrArgLeuLeuSe 759

QY 2571 CAGAAACACTTACCTGATGAGAGCAATCTCTGGGAGGACATCTTGTGAGAG 2630
 Db 759 rArgAsnThrTyrLeuGlnTrrPheGlnAspSerValLeuGlyArgHisIlePheTrrArgAr 779
 QY 2631 ACTTAAATGCTTATTTGATGAGAAAGCTCGAATCTTGACCAACA 2679
 Db 779 gLeuArgLysAlaLeuLeuAspGlyLysSerTrrAsnProGluGlyThr 795
 RESULT 12
 ADOS7797
 ID ADOS7797 standard; protein; 801 AA.
 AC ADOS7797;
 DT 12-AUG-2004 (first entry)
 XX
 DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
 XX
 KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KW sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
 XX
 OS Saimiri sciureus.
 OS
 FH Key Location/Qualifiers
 FT MISC-difference 14
 FT /label= Leu, Phe
 XX
 PN WO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Meslier W;
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADOS7795, ADOS7796.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 18; 11pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antisthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents squirrel monkey TLR4.
 XX
 SQ Sequence 801 AA;
 Alignment Scores:
 Pred. No.: 3,58e-296 Length: 801
 Score: 2728.50 Matches: 542
 Percent Similarity: 79.17% Conservative: 89
 Best Local Similarity: 68.01% Mismatches: 162
 Query Match: 52.70% Indels: 5
 DB: 8 Gaps: 3
 US-09-396-985B-46 (1-2951) x ADOS7797 (1-801)

OY	298	GTAGTCTCTAATATTTACTTACCAATGATGATGACAAACCTCAGCAAGTCCCTGATGAC	357
Db	1	ValValProdanValThrTyrGlnCysMetGluLeuAsn**TyrValLeProAspAsn	20
OY	358	ATTCCTCTTCAACCAAGACATAGATGTGAGCTTCAACCCCTTGAAGATCTTAAAAAGC	417
Db	21	IleProPheSerThrLysAsnLeuAspLeuSerPheAsnProLeuAlaGlnIleGlySer	40
OY	418	TATAGCTTCCCAATTTTTCAGAACTTCAGTGGCTGCAATTTATCCAGGTGTAATGAA	477
Db	41	HisSerPhePheAsnPheProGluLeuGlnValLeuAspLeuSerArgCysAspIleGln	60
OY	478	ACAATTGAAGACAAAGCATGGCATTGGCTTACACCACTCTGCAAACTTGATCTGACGGA	537
Db	61	ThrIleGluAspGlyAlaTyrGlnSerLeuSerMetHisLeuSerThrLeuIleLeuThrGly	80
OY	538	AACCCCTATCCAGAGTTTTCSSCAAGAGTTTCTGTGACATGACAAAGTTTACCAATCTG	597
Db	81	AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu	100
OY	598	GTGGCTGTGAGACAAATTTGGCCCTCTAGAAACCTTCCCTATTTGACACATTTAAAC	657
Db	101	ValAlaValGluThrHisLeuLeuSerLeuGluAsnProIleGlyHisLeuLysThr	120
OY	658	TTAAAGAACTCATATGTGGCTCACAATTTTATCACTCTCTGAATTACCTGCAATTTT	717
Db	121	LeuLysAspLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPhe	140
OY	718	TCCAACTGACGAACTTGTACATGTGAGTCTTTTATCTATGTAACATTAATTA	777
Db	141	SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerAspAsnIleGlnAsnIleTyr	160
OY	778	GTCAACGACTTACAGTTTCTACGTGAACATCCACAAAGTCAATCTCTTTAGACATGTCT	837
Db	161	CysLysAspLeuGlnValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer	180
OY	838	TTGAACCAATGACTTCATTCACAGACCAAGCTTTTCAGGGAAATTAAAGCTCCATGACTG	897
Db	181	LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeu	200
OY	898	ACTCTTAAGAGTATTTTAATAGCTCAATAATATGAAGAACTGGCTTCAAACTGGCT	957
Db	201	ThrLeuAspAsnAspPheAspSerLeuAsnAlaMetLysThrCysIleGlnGlyLeuAla	220
OY	958	GGTTTAAACAGTCCATCGGTGATCTTGGGAGAAATTTAAAGAAAGAAATCTGGAATTT	1017
Db	221	GlyLeuGlnValHisArgLeuValLeuGlyLeuPheAspGlnArgAsnIleGluAsp	240
OY	1018	TTTGAACCTCTATCATGAGAAAGCATATGTGATGACCATTTGATGAGTTCAAGTTAA	1077
Db	241	PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleAsnGluPheArgLeuAla	260
OY	1078	TATACAAATGATTTTTCAGATGATTTGTGAAG--TTCCATGTCTTGGCCAAATGTTCT	1134
Db	261	TyrLeuAspAspPheLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnValSer	280
OY	1135	GCATGTCTCTGGCAGGTGATCTATCTTAAAAATATCTGAAGAAGATGTTCTAAATTTCA	1194
Db	281	SerPheSerLeuValAsnValHisIleLysValGlyValGluAspPheSerTyrAsnPheArg	300
OY	1195	TGGCAATCTTATCATCATTTAGATGTCA-ACTAAGACATTTTCCAACTGTGATCTACC	1253
Db	301	TyrGlnHisLeuGlnLysValAsnValPheGlnGlnPheProProLeuLysLeuLys	320
OY	1254	TTTCTTTAAAAAGTTTGACTTAACTATGAAACAAGGCTCATAGTTTTAAAAAGTGGCC	1313
Db	321	SerLeuLysArgLeuThrPheThrAlaAsnLysGlyArgAsnHisPheSerGluValAsp	340
OY	1314	CTACCAAGCTCAGCAATCTAGATCTTGTGTAATAATGCACTGAGCTTTAGTGGTGGCTGT	1373
Db	341	LeuProSerLeuGlnPheLeuAspLeuSerAspGlnGlyLeuSerPheLysGluCysCys	360

QY	1374	TCCTATTCTGATTTGGGAACAAACGCTTGAGACCTTAACCTCAGCTTCATGTGCC	1433
Db	361	SeGlnSerIserPheGlyThrThrSerLeuIysrTyLeuAspLeuSerPheAsnAspVal	380
QY	1434	ATCATTTTGAAGTGCATTTTCAATGGCTGTGAAGAGGTGGAGACCGTGAATTTTTCAGCA	1493
Db	381	IleThrMetGlySerAsnPheLeuGlyLeuGluGlnLeuGlnIshLeuAsp-PheGlnIsh	400
QY	1494	CTCTACTTTAAAAAGGTCACAGAAATTTCTAGCGCTTTATCCCTTGAAGAAAGCTTTTA	1553
Db	400	sSerAsnLeuIserGlnMetSerGlnPheSerValPheLeuSerLeuIshArgAsnIleTy	420
QY	1554	CCTTGACATCTCTTATACTTAACACCAAAATTTGACTTGGATGGTATATTTCTTGCTTGAC	1613
Db	420	rLeuAspIleSerIshThrIshIshArgValAlaPheAsnGlyIlePheAsnGlyLeuPhe	440
QY	1614	CAGTCTCAACACATTAATAAATGGCTGGCAATTTCTTCAAAAGACAAACCCCTTCAAAATG	1673
Db	440	eSerLeuIysValLeuIysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuGlnAspI1	460
QY	1674	CTTTGCAAAACCAACAACTTGACATTTCTGGATCTCTTGAATGCAATTTGGAAACAAT	1733
Db	460	ePheThrAspLeuAsnAsnLeuIlePheLeuAspLeuSerGlnGlnLeuGlnIsh	480
QY	1734	ATCTTGGGGGGATTTTGAACACCCCTCCATAGACTTCAATTTATTAATATGATGCACAA	1793
Db	480	uSerProThrAlaPheAspSerLeuProGlyLeuArgIleLeuAsnMetSerIshAsnAs	500
QY	1794	TCCTATGTTTGGATTCATCCCATTTTAAACACACTGATATTCCTCGACACTCTGTGATTG	1853
Db	500	nPhePheAlaLeuAspIshPheProTyIshIshLeuIysSerLeuGlnValLeuAspTy	520
QY	1854	CAGTTTCAATGCGCATAGACATCTAAAGG--ATACTGCAACATTTTCCAAAGCTT	1910
Db	520	rSerLeuAsnIshIleGlyThrSerIshAsnGlnGlnLeuGlnIshPheProSerSerIsh	540
QY	1911	AGCCTTCTTCAATCTTACTTAACAATTCGTGCTGTTGATATGATGAAACATCAAAATTCCT	1970
Db	540	uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIshGlnSerPheIsh	560
QY	1971	GCAAGGGGTCAAGAAACAAGACAGCTTCTTGCTGAATGTGAACAATGACATGTGCAAC	2030
Db	560	uGlnIshIleIysAspGlnArgGlyLeuValGlnValGlnIshMetGlnCysValAlsh	580
QY	2031	ACCTGTAGAGATGAAATACCTCCCTTAAGTGTGATTTTAATTAATCTACCTGTTATATGTA	2090
Db	580	rProLeuAsnArgIysGlyIleProValLeuSerLeu--AsnIleThrCysGlnMetIsh	599
QY	2091	CAGAACAATCATAGTGTGTCAAGTGTGATGTGATGTGTGATTCACATGTAACAATTTCT	2156
Db	599	rIshThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValIsh	619
QY	2151	GATATACACCTTATTTTCACTGATACCTTATATGCTGGCGGTGAAGTAACACAGAGG	2210
Db	619	uValIshIshPheIshPheIshIshMetLeuLeuAlaIshIshIshIshIshIshIshIshIsh	639
QY	2211	AGAAACACATCATGATTTTGTGATCTTACAGTGCAGATGACAGATGACGCTGGTACAGAA	2270
Db	639	yGlnAsnIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIsh	659
QY	2271	TGAGCTGTGAAGATTTTGAAGAAGAGAGTCCCGCTTCACTCTGCTTCACTACAGG	2330
Db	659	ngIshLeuValIshAsnLeuGlnGlnGlnIshIshIshIshIshIshIshIshIshIshIshIsh	679
QY	2331	AGACTTTATCTGTGTATAGCATTTGCTGGCCCAACATCTCAAGAAAGCTTCCCAAGAG	2390
Db	679	gAspPheIleProGlyValAlaIleAlaIshAsnIleIshIshIshIshIshIshIshIshIshIsh	699
QY	2391	CCGGAAGGTTATGTGTAGTGTCTAGACATTTATTCAGACCGCTTGATATCTTTGA	2450
Db	699	rArgIshValIleValIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIsh	719
QY	2451	ATATAGATTGCTCAACATGGCAGATTTCTGAGACGCGCTTGCGATCATCTTCATTTG	2510

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Db      719  utryctluilealaglnthrtfnglnphelusersearaglailellellepheileva 739
Qy      2511 CCTGAGAGGTTGAGAGTCCCTGCTGAGGACAGAGTGAATTTGATCCCTTTAG 2570
Db      739  lileglnlysevalgluylsSerleuLeuAarglInglInValgluLeuYrAargleuLeuSe 759
Qy      2571 CAGAAACACTACCTGAGATGGAGACATCTCTGGGAGGACATCTTCTGAGAG 2630
Db      759  rArgAsnthrYrleuGlutPrGluAaspSerValleuGlYarGhlstlePheTPrAargAr 779
Qy      2631 ACTTAAATGSCCTATTGATGAGAAAACCTCGAATCTTGAGCAACA 2679
Db      779  glEuArGylsalaleuLeuAaspGlyArGPrOTrPAsnProGlutGlyThr 795

RESULT 13
AD057782 standard; protein; 808 AA.
XX
AC      AD057782;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KM      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
OS      Pan troglodytes.
XX
PN      WO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PF      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Meesler W;
XX
DR      WPI: 2004-400726/37.
DR      N-PSDB: AD057780, AD057781.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1; SEQ ID NO 3; 111pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX
SQ      Sequence 808 AA;

Alignment Scores:
Pred. No.:      6,056-296      Length:      808
Score:          2726.50      Matches:     541
Percent Similarity: 80.05%      Conservative: 97
Best Local Similarity: 67.88%      Mismatches:  155
Query Match:    52.67%      Indels:      5
DB:              8      Gaps:         3

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US-09-396-985b-46 (1-2951) x AD057782 (1-808)
Qy      298  GTAGTCTCTAATATTACCTTACCAATGATGATGATCAGAAATCAGCAAAAGTCCCTGATGAC 357
Db      1    ValValProAsnIleThrYrGlnCyseMeGlulEuAsnBheYrYrIleProAspAsn 20
Qy      358  ATTCCCTCTTCAACCAAGAACATAGATCTAGGCTTCAACCCCTTGAAGATCTTAAAAAGC 417
Db      21  LeuProPheSerThrYrAsnLeuAaspLeuSerPheAsnProLeuAarghlstleuGlySer 40
Qy      418  TATAGCTTCTCAATTTTTCAGAACTTCAGTGCGCTGGATTATTCAGGTGTGAATTGAA 477
Db      41  TySerPhePheSerPheProGluLeuGlnValleuAaspLeuSerAargGluIleGln 60
Qy      478  ACAATTGAAGCAAGGATGCGATGGCTTACACCACTCTCAAACTTGATGACAGCA 537
Db      61  ThrIleGluAaspGlyAlaYrGlnSerLeuSerHisleuSerThrLeuIleuThrGly 80
Qy      538  AACCCCTACAGAGTTTTCCTCCAGGAAGTTCTCTGGAATTAACAAGTTTGAACAATCTG 597
Db      81  AsnProIleGlnSerleuAlaleuGlyAlaPheSerleuYleuSerSerleuGlnLysleu 100
Qy      598  GTGGCTGTGAGACAAAAATTGGCTCTTGAAGAGCTTCCCTATTGGACAGCTTATTAAC 657
Db      101  ValAlaValGluThrAsnleuAlaSerleuGluAsnBheProIleGlyHisleuYleThr 120
Qy      658  TTTAAAGAACTCAATGTGGCTGCAATTTATATCTTCTGTAAAGTTACCTGCAATTTT 717
Db      121  LeuLysGluLeuAsnValAlaHisAsnleuIleGlnSerPheYrleuProGluYrPhe 140
Qy      718  TCCAATCTGACGAACCTAGTACATGTGATCTTCTTATATATATATTAATTAACAATTA 777
Db      141  SerAsnleuThrAsnleuGluHisleuAaspLeuSerSerAsnYslleGlnSerIleYr 160
Qy      778  GTCACAGACTTACAGTTTCTACGTGAATTCACAAAGTCAATCTCTTTAGACATGCT 837
Db      161  CysThrAaspLeuAryValleuHisGlnMeProleuLeuAsnleuSerleuAaspLeuSer 180
Qy      838  TTGAACCAATTTGATCTTCAATTAAGACCAAGCCTTTCAGGAAATTAAAGCTTCATGA 897
Db      181  LeuAsnProMetAsnBheIleGlnProGlyAlaBheLysGluIleAargleuHisLysleu 200
Qy      898  ACTCTAAGAGTAAATTTTATAGCTCAATATATATGAATGAACCTTGCTCAAAACCTGG 957
Db      201  ThrLeuAryAsnAsnBheAaspSerleuAenValMetCysThrYrIleGlnYleuAla 220
Qy      958  GGTTTACAGCTCCATCGGTTGATCTTGGGAGATTTAAAGATGAAGAAATCTGGAATT 1017
Db      221  GlyleuGluValHisAargleuValleuGlyGluPheAryAsnGluGlyAsnleuGluLys 240
Qy      1018  TTTGAACCTCTATCATGAGAGGACTATGTGATGACCATGATGATGATTCAGGTTAACA 1077
Db      241  PheAspSerSerAlaleuLeuGluGlyLeuCyAsnleuThrIleGluGluPheAargleuAla 260
Qy      1078  TATTAACAATATTTTTCAGATGATGATTTTAAAG---TTGCATGTCTGGGGAATGTTCT 1134
Db      261  TyLeuAspYrYrYrleuAspAspIleIleAaspLeuPheAsnYslleuThrAsnValSer 280
Qy      1135  GCATGTCTCTGCGAGGTGATCTATTAATAATATCTTGAAGATGTTCTTAAACATTTCA 1194
Db      281  SerPheSerleuValSerValThrIleYrSerValLysAaspPheSerYrAsnPheGly 300
Qy      1195  TGGCAATCTTATCAATCATTAATGATGACAACTAAG---CAGTTTCAACTGTGATCTAAC 1253
Db      301  TrpGlnHisleuLeuValleuValencyLysPheGlyGlnBheProThrleuLysleuLys 320
Qy      1254  TTTCTTAAAGTTTGACTTTAATATGAACAAGGCTATCATGTTTAAAGAGTGGCC 1313
Db      321  SerleuLysAryGleuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluValAasp 340
Qy      1314  CTACCAAGTCTCAGTATCTAGATCTTAGAGAAAGCACTGAGCTTATGATGTGCTGTG 1373

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Db      341  LeuProSerLeuGluIupheLeuAspLeuSerArgAsnGlyLeuSerPheGlyCysCys 360
Qy      1374  TCTTATTCTGATTTGGGAAACAAGCCTGAGACATTAGACCTCAGCTTCAATGTCGCC 1433
Db      361  SerInSerAspPheGlyThrThrSerLeuIysThrLeuAspLeuSerPheAsnGlyVal 380
Qy      1434  ATCATTTGAGTGGCAATTTTCATGAGTGTAGAGAGTGCAGACCTCGAATTTTTCAGCA 1493
Db      381  IleThrMetSerSerAsnPheLeuGlyLeuGluIuInleuGluIuIleuAsp-PheGlnI 400
Qy      1494  CTCTACTTTAAAAAGGCTCACAGAAATCTCAGCGTCTTATCCCTTGAAGAACTACTTTA 1553
Db      400  SerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArgLeuIleTy 420
Qy      1554  CCTTGACATCTCTTATCTAACAACCAAAATTGACTTGAGTGTATTTTCTTGCGCTTGC 1613
Db      420  rLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 440
Qy      1614  CAGTCTCAACACATTTAAAAATGGCTGGCAATTTCTTCAAGACAAACACCTTCAAAATG 1673
Db      440  rSerLeuGluValLeuIysMetAlaGlyAsnSerPheGlnIuAsnPheLeuProAspI 460
Qy      1674  CTTTGCAAAACAACAACCTTGACATTCCTTGATCCTTCAATGTCATTTGAAACAAT 1733
Db      460  ePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIle 480
Qy      1734  ATCTTGGGGGGTATTTGACACCCCTCCATGACCTTCAATTTAAATGATGATCAACA 1793
Db      480  uSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAs 500
Qy      1794  TCTATTGTTTGTGATTCATCCCATTTAAACACAGTGTATCCCTTCAGACCTTGTATTG 1853
Db      500  nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 520
Qy      1854  CAGTTTCATGCGATAGACATCT--AAAGAAATACAGCAATTTCCAAAGAGTCT 1910
Db      520  rSerLeuAsnHisIleMetThrSerLysGlnGluLeuGlnHisPheProSerSerLe 540
Qy      1911  AGCCTTCTTCAATCTTACTAACAATTCGTGCTTGTATGTATGTGAACATCGAAATCT 1970
Db      540  uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 560
Qy      1971  GCAGTGGGTCAAGACAGAAAGAGATTTCTGTGTAATTTGAACAAATGACATGTGCAC 2030
Db      560  uGlnThrIleLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGluCysAlaTh 580
Qy      2031  ACTGTAGAGATGAATACCTCCTAGTGTGATTTTAATTAATCTACTGTTATATGTA 2090
Db      580  rProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAs 599
Qy      2091  CAAAGACATCATCAGTGTGTGAGTGTGATGTGATGTGATTCACCTGATAGCATTTCT 2150
Db      599  nLysThrIleIleGlyValSerValLeuSerValLeuValSerValAlaValAlaVal 619
Qy      2151  GATATACCATCTTATTTTACCTGATCTTATTTGCTGGCTGTAAAAAGTACAGACAGG 2210
Db      619  uValTyrIleLysPheTyrPheHisIleMetLeuLeuAsnIleGlyIleLysTyrGlyArg 639
Qy      2211  AGAAAGCATCTATGATGATTTGTGATCTACTCGATCGAATGAGAGACTGGGTGAGAAA 2270
Db      639  yGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAs 659
Qy      2271  TGAAGTGTGAAGAAATTTAGAAAGAGAGTCCCGGCTTTCACTCTGCTTCACTACAG 2330
Db      659  nGluLeuValLysAsnLeuGlnGluGlyValProProPheGlnLeuCysLeuHisTyrAr 679
Qy      2331  AGACTTTATTCCTGGTGTAGGCAATGTGCGCAACATCATCCAGAAAGCTTCCCAAGAG 2390
Db      679  gAspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSe 699
Qy      2391  CCGAAGGTTATTTGTGTAGTGTCTAGACATTTATTCAGAGCCGTTGGTGTATCTTGA 2450
Db      699  rArgLysValIleValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 719

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Qy      2451  ATATGAGATTGCTCAACATGGCAGTTTCTGAGCAGCCGCTGGCATCTTCAATGT 2510
Db      719  uTyrGluIleAlaGlnThrThrPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
Qy      2511  CCTTGAAGAGTTTGAAGAAGTCCCTGCTGAGGACAGAGTGAATTTATCGCTTTTGA 2570
Db      739  lleGlnLysValGlnLysThrLeuLeuArgArgGlnValGluLeuTyrArgLeuLeu 759
Qy      2571  CAGAAACACCTTACCTGGAATGGAGAGACAATCCTCTGGGGAGACATCTTCTGAGAG 2630
Db      759  rArgAsnThrTyrLeuGlnTyrPheGluAspSerValLeuGlyArgHisIlePheThrArg 779
Qy      2631  ACTTAAAAATGCGCTTATGATGAGAAAGCTCGAATCCTGAGCAACA 2679
Db      779  gLeuArgLysAlaLeuLeuAspGlyLysSerThrAsnProGluGlyThr 795

RESULT 14
AD057800
ID      AD057800 standard; protein; 795 AA.
AC
XX      AD057800;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS      Papio hamadryas.
XX
PN      W02004042365-A2.
XX
PD      21-MAY-2004.
XX
PF      03-NOV-2003; 2003W0-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
XX
WP1; 2004-400726/37.
DR      N-PSDB; AD057798, AD057799.
DR
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Disclosure; SEQ ID NO 21; 111pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The method, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents hamadryas baboon TLR4.
XX
SQ      Sequence 795 AA;
XX

Alignment Scores:
Pred. No.: 2,83e-295
Score: 2720.50
Percent Similarity: 79.65%
Best Local Similarity: 67.84%
Length: 795
Matches: 540
Conservative: 94
Mismatch: 158

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Db      699  ranglyvalillevaivalserginhiisnellcginserhrgtrpysilepnecl 719
Qy      2451  ATATGAGATTGCTCAAAACATGGCAGTTTCTGAGCAGCCCTCTGGCATCATCTTCATTGT 2510
Db      719  ufyglnuilaaglnhrtrpginpheusersearaglaiglylellepnelelva 739
Qy      2511  CCTTGAGAGGTTGAGAGTCCCTGAGGAGCAGAGTATGATGAGCCCTCTTAC 2570
Db      739  lileglnlyvalglnystrleuvalrglnvalglnleutyraargleuuse 759
Qy      2571  CAGAAACACCTACCTGAGATGAGAGCAATCCCTGGGAGCAGCATCTTCTGAGAG 2630
Db      759  rargserthrtyrleuclutrpgluapservalleuclglnhiislepnetpargar 779
Qy      2631  ACTTAAAAATGCCCTATTGATGAGAAAACCTCGAATCTTGAGCA 2676
Db      779  gleuarglyalaileuvalapglayargsertrpaspnproglunglu 794

RESULT 15
AD057785 ID AD057785 standard; protein; 808 AA.
XX
AC AD057785;
XX
DT 12-AUG-2004 (first entry)
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN MO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
PS WPI; 2004-400726/37.
DR N-PSDB; AD057783, AD057784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;

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Alignment Scores: 6.38e-294 Length: 808
Pred. No.: 2708.50 Matches: 538
Score:

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Percent Similarity: 79.80% Conservative: 98
Best Local Similarity: 67.50% Mismatches: 157
Query Match: 52.32% Indels: 5
DB: 8 Gaps: 3

US-09-396-985b-46 (1-2951) x AD057785 (1-808)
Qy      298  GTAGTCCCAATATTTACCTACCAATGATGATCAGAAATCAGAAAGTCCCTGATGAC 357
Db      1  ValValProkasmlethrtyrlnyrmwgluvalasnpheyrlyslleproabapn 20
Qy      358  ATTCTCTTCAACCAAGAACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGC 417
Db      21  leupropheSerthrlyasnpheuserPheasnpheuserPheasnpheuserPheasnpheuser 40
Qy      418  TATAGCTTCCCAATTTTCAAGACTTCAGTGCCTGATTTATCCAGGTGATAATGAA 477
Db      41  TysSerPhePheSerPheProgluvalleuvalasnpheuserargygluilegln 60
Qy      478  ACAATTGAAGACAAAGGATGAGTGGCTTACACCTCTCAAACTTGATGACAGCA 537
Db      61  ThrilegluhsppolyalatyrglnserleuserHleuserThrleuileuthrgly 80
Qy      538  AACCTATCCAGAGTTTTCCTCCAGAGATTTCTCTGACATACAAATTTAGCAATCTG 597
Db      81  AsnProileglnserleuvalleuvalasnpheSerlyleuserSerleuvalleu 100
Qy      598  GTGCTGTGAGACAAATTTGGCTCTTGAAGAGTCCCTTGGACAGCTTATAAC 657
Db      101  ValAlaValAlaGluThrAsnleuvalasnpheSerleuvalasnpheProileglnysleuysr 120
Qy      658  TTAAGAAATCTCAATGTGGCTCACAATTTATCATCTCGTAGTACCTGATATTTT 717
Db      121  leuylsleuvalasnpheValahisnleuileglnSerPheylsleuProgluTyrrpe 140
Qy      718  TCCAACTGACGAACCTAGTACATGATCTTCTTATATCATATTAATTAATTAAT 777
Db      141  SerAsnleuThrAsnleuGluTyrlleuapleuserSerAsnlyleleuSerleuTy 160
Qy      778  GTCAAGCATTTACAGTTTCTGACGTAATCCCAAGTCAATCTCTTGAACATGTCT 837
Db      161  CysThrAspleuvalleuHleuHleuMetProleuvalasnpheuserleuapleuser 180
Qy      838  TTGAACCAATTTGATCTTCAAGACCAAGCTTTCAGGAGTATTAAGCTCCATGACTG 897
Db      181  leuAsnProMetThrPheileglnProgluAlaPheylsleuileargleuHsluysleu 200
Qy      898  ACTTAAGAGTAAATTTATAGCTCAATATATATGAAAACTTGCTTCAAACTGGCT 957
Db      201  ThrleuarghsnAsnpheasnpheSerleuvalasnpheSerleuvalasnpheSerleuvalasnphe 220
Qy      958  GGTTCACAGTCCATGAGTTGATCTTGGGAGATTTTAAGATGAAGATCTGGAAT 1017
Db      221  GlyleuGluValAlaArgyleuvalleuGlnlyPheargAsnlyleuvalleuGlnly 240
Qy      1018  TTTGAACCCCTCATGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1077
Db      241  PheAspysSerAlaileuGlnlyleuysAsnleuThrileuGlnlyPheargleuAla 260
Qy      1078  TATACAAATGATTTTTCAGATGATATGTTAAG---TTCCATGCTTGGGAAATGTTCT 1134
Db      261  TyrlleuAspysTyrlleuAspysPheileleleAspleuPheAsnlyleuThrAsnValser 280
Qy      1135  GCATGCTCTTGGCAGGTGATCTATTAATATCTGAAGATGTTCTTAAACATTTCAA 1194
Db      281  SerPheSerleuvalasnpheValThrileglnArgyleuvalasnpheSerTyranphegln 300
Qy      1195  TGGCAATCCTTATCATCATTAATGATGATGATGATGATGATGATGATGATGATGAT 1253
Db      301  TrpGlnHlsleuGlnleuvalasnpheCyslyspheGlnPheProThrleuysleuys 320
Qy      1254  TTTCTTAAAGATTGACTTAACTATGACAAAGGCTTCACTGTTTAAAAAGTGCC 1313

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Db 321 SerLeuYsArGLeuThrPheThrSerAsnLysGlyAlaAsp 340
 QY 1314 CTCAAGATCTCAGCTATCTGATCTTAGTAAGATGCACTGAGCTTAGTGCGCT 1373
 Db 341 LeuTrSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysAs 360
 QY 1374 TCTTATTCGATTTGGGAACAACAGCTGAGACCTTAGACCTCAGCTTCATGTGCC 1433
 Db 361 SerGlnSerAspPheGlyThrThrSerLeuYsTrLeuAspLeuSerPheAsnGlyVal 380
 QY 1434 ATCATATGATGCCAATTTATGAGGTGTAGAAAGCTGCAACCTTGATTTTTCAGCA 1493
 Db 381 IleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAsp-PheGlnHis 400
 QY 1494 CTCTACTTAAAGGGGTCAAGAAATTCAGCGCTTATCCCTTGAAAGCTACTTTA 1553
 Db 400 SSerAsnLeuYsGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTy 420
 QY 1554 CCTTGACATCTCTTATATCTAACACCAAAATGACTGCTGATATTTCTTGCTTGAC 1613
 Db 420 rLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSe 440
 QY 1614 CAGTCTCAACACATTAATAATGCTGCAATTCCTTCAAGACAACACCTTCAAAATG 1673
 Db 440 rSerLeuGluValLeuYsMetAlaGlyAsnSerPheGlnGlnHisPheLeuProAspI 460
 QY 1674 CTTTGCAAAACACAAACAACTTGATCCCTGATCCCTTCAAAATGCAATTTGGAACAAT 1733
 Db 460 ePheThrGluLeuArgAsnLeuTrnPheLeuAspLeuSerGlnCysGlnLeuGlnLe 480
 QY 1734 ATCTTGGGGGGTATTTGACACCTTCATAGACTTCATTAATTAATATGAGTCAACA 1793
 Db 480 userProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAs 500
 QY 1794 TCTATTGTTTGGATTCATCCCATTAATACACAGCTGATTCCTCAGACCTTGTGATG 1853
 Db 500 nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuArgValLeuAspTyr 520
 QY 1854 CAGTTTCAATGCGATGAGACATCT--AAAGAAATCTGCAACATTTTCCAAAGACTCT 1910
 Db 520 rSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSerLe 540
 QY 1911 AGCCTTCTTCATCTTACTTAACAATTCGTTGTATGTATATGATGACATGAAATTCCT 1970
 Db 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLe 560
 QY 1971 GCAGTGGGTCAAGACAGAAAGAGCTTCTTGATGATGTTGAACAAATGACATGTGCAC 2030
 Db 560 uGlnTrpIleLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGlnCysAlaThr 580
 QY 2031 ACCGTGAGAGTGAATACCTCCTTAGTGGATTTTAATATATTCCTGTTATATGTA 2090
 Db 580 rProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAs 599
 QY 2091 CAAGACAATCATCATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 2150
 Db 599 nLysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLe 619
 QY 2151 GATATACACTTCTATTTTCACTGATATCTATGCTGCTGTAAAAAGTACAGACAGAGG 2210
 Db 619 uValIlyLysPheTyPheHisLeuMetLeuLeuAlaGlyCysIleLysTyGlyArgG 639
 QY 2211 AGAAGATCTATGATGATGATTTGATCTACTGAGTCAGATGAGATGAGATGAGATGAG 2270
 Db 639 yGluAsnValIlyAspAlaPheValIleTySerSerGlnAspGlnAspTrpValArgAs 659
 QY 2271 TGAAGTGTAAAGATTTAAGAAAGAGAGGCGCGCTTCACTGCTGCTTCACTACAG 2330
 Db 659 nGluLeuValIlyAsnLeuGlnGlyValProProPheGlnLeuCysLeuHisTyArg 679
 QY 2331 AGACTTATTCCTGCTGATGAGCATGCTGCCAATCATCATCAGGAAGGCTTCCACAAGAG 2390
 Db 679 gAspPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSe 699

QY 2291 CCGAAGATTATTTGGTATGATGCTAGACATTTATCAGAGCGCTGATCTTGA 2450
 Db 699 rArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheG 719
 QY 2451 ATATGATATGCTCAACATGAGCATGTTCTGAGCAGCGCTCGGCATCATCTTCATGT 2510
 Db 719 uTyArgIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
 QY 2511 CCTTGAGAAGGTTGAGAAGTCCCTGCTGAGCAGCAGAGTGAATGATGATGCTTCTTAG 2570
 Db 739 lLeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyArgLeuLeuSe 759
 QY 2571 CAGAAACACCTACCTGGAATGGAGAGCAATCCCTGAGGAGGACATCTTCTGAGAGAG 2630
 Db 759 rArgAsnThrTyLeuGlnTrpGlnAspSerValLeuGlyArgHisIlePheTrpArgAr 779
 QY 2631 ACTTAAATAATGCCCTATTTGATGAGAAAGCCTGGAATCCTGAGCAACA 2679
 Db 779 gLeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThr 795

Search completed: March 29, 2005, 17:03:32
 Job time : 193.387 secs

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Qy      355 GACATTCCTCTTCAACCAAGAAATGATGTGAGCTTCAACCCCTTGAAGATCTTAAA 414
Db      .....|||
56 AsnLeuProPheSerThrIlysaAsnLeuAspLeuSerPheAsnProLeuAlaPheGlnIleuGly 75
Qy      415 AGCATATGCTTCTCCATTTTTCAGACTTCAGTGGCTGGATTATTCAGGTGTAAT 474
Db      |||||.....|||
76 SerTyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerAlaGlySerGlnIle 95
Qy      475 GAAACAAATTGAAGCAAGGATGGCATGGCTTACACACCTCTCAAACTTGATTAAGTACA 534
Db      .....|||
96 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerIleuSerThrIleLeuThr 115
Qy      535 GGAACCTTATCCAGAGCTTTTCCCAAGAAATTTCTGTGACATTAACAAGTTTAAAGCAAT 594
Db      .....|||
116 GlyAsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 135
Qy      595 CTGGTGGCTGTGAGAGCAAAATGGCTCTAGAAAGCTTCCCTATTTGACAGCTTATA 654
Db      .....|||
136 LeuValAlaValAlaGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlnIleuLys 155
Qy      655 ACCTTAAAGAAATGCAATGGCTGCTCACAAATTTTATACATTTCTGTGAATTAAGTTCGACAT 714
Db      .....|||
156 ThrLeuLysGluLeuAsnValAlaAsnLeuIleGlnSerPheLysLeuProGluTyr 175
Qy      715 TTTTCCAAATCGACGAACTAGTACATGGATGCTTTCTTATATCATATTAATTAAGCAATAT 774
Db      .....|||
176 PheSerAsnLeuThrAsnLeuGlnIleuAspLeuSerSerAlaLysIleGlnSerIle 195
Qy      775 ACTGTCAACGACTTACAGTTTCTACGTGAATCCAGAAATCCAGACATCTCTTTAGACATG 834
Db      .....|||
196 TyrCysThrSerAspLeuArgValIleuIleGlnMetProLeuLeuAsnLeuSerLeuAspLeu 215
Qy      835 TCTTTGAACCCCAATGTGACTTCATTCAAAGACCAAGCTTTGACGGGATTTAAAGTTCATGAA 894
Db      .....|||
216 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuIleLys 235
Qy      895 CTGACTTAAAGAGTAATTTTAAAGCTCAAAATTAATGAAGAAATTCCTTCAAAACCTG 954
Db      .....|||
236 LeuThrLeuAlaArgAsnAsnPheAspSerLeuAsnValMetCysThrCysIleGlnGlyLeu 255
Qy      955 GCTGTGTTTACACGTCATCGGTGATCTTGGAGAAATTTAAAGATGAAGAAAGATCTGAAA 1014
Db      .....|||
256 AlaGlyLeuGlnValIleHisArgLeuValLeuGlyGlnPheArgAsnGlnGlyAsnLeuGln 275
Qy      1015 ATTTTGAACCTTCATCAGGAAGAAGATATGATGATGACATTCATGATGATGATGATGAT 1074
Db      .....|||
276 LysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeu 295
Qy      1075 ACATATACAAATGATTTTTCAGATGATATGTTAAG---TTCCATTCCTGGGCAATGTT 1131
Db      .....|||
296 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 315
Qy      1132 TCTGCAATGTCTCTGGAGAGGTGTATCTATAAATATCTAGAAAGATGTTTCCAAACATTTG 1191
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316 SerSerPheSerLeuValSerValThrIleGlnArgAllyAspPheSerTyrAsnPhe 335
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Qy      1251 CCCCTTTTAAATTTGACATTTTAAAGTATGAACAAGGCTATCAAGTTTAAAAAAGTG 1310
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356 LysSerLeuLysAspGlyLeuThrPheThrSerAsnLysGlyAlaAsnAlaPheSerGlyVal 375
Qy      1311 GCCCTTACCAAGTCTCAGCTATCTAGATCTTATGAAATGCACTGAGCTTATGAGTGCG 1370
Db      .....|||
376 AspLeuProSerLeuGlnPheLeuAspLeuSerIleArgAsnGlyLeuSerPheLysGlyCys 395
Qy      1371 TGTTCATTATCTGATTTGGGAAACAACAGCTTGAGACATTTGACCTCAGCTTCAATGTT 1430

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Db      396 CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 415
Qy      1431 GCCATCATTAATGAGTCCCAATTTTCAATGGGCTAGAGAGCTGACAGCCTGATTTTCA 1490
Db      |||||.....|||
416 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnMetLeuIleHisLeuAsp-PheG 435
Qy      1491 GCACTCTACTTTTAAAAAGGCTCACAGAAATTTCTCAGGCTTTTATCCCTTGAAGAAAGTACT 1550
Db      |||||.....|||
435 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAspLeuIle 455
Qy      1551 TTACCTTGACATCTCTTATCTAACAACCAAAATTTGACTTGATATTTCTTGCTT 1610
Db      .....|||
455 eTyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLe 475
Qy      1611 GACCACTTCAACACATTTAAATAGCTGGCAATTTCTTCAAGAACCAACCTTTCAAA 1670
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475 UserSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAs 495
Qy      1671 TGTCTTTGCAAAACAACAACAAATTTGACATTTCTGATCTCTTAAATGTCATTTGAAACA 1730
Db      .....|||
495 PilePheThrGlnLeuAspArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 515
Qy      1731 AATATCTTGGGGGGGTATTGACACCTCCATAGACTTCAATTTTAAATATGATGACACA 1790
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515 HisSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAs 535
Qy      1791 CAATCTATGTTTGTGATTTGATCCCATTAATTAACAGCTGATTTCCCTCAGACACTTTGA 1850
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535 HisAsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAs 555
Qy      1851 TTGCACTTTCATTCGATAGACACATCT--AAAGAAATAGTGAACATTTTCCAAAGAG 1907
Db      .....|||
555 pTyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerse 575
Qy      1908 TCTAGCTTCTTCAATCTTACTAACAATTTCTGCTGTGATATGTGAACATGAAATT 1967
Db      .....|||
575 rLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPh 595
Qy      1968 CCTGACAGTGGGTCAAGAACAGAAAGAGTTCTTGGAATGTGGAACAAATGACATGTGC 2027
Db      .....|||
595 eLeuGlnThrPrlLeuLysAspGlnArgGlnLeuLeuValGluValGlnArgMetCysVal 615
Qy      2028 AACACCTGTAGAGATGAATACCTCTTATGTTGATTTTAAATTAATTTACCTGTTATAT 2087
Db      .....|||
615 aThrProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMet 634
Qy      2088 GTACAAAGACATATCATCAGTGTGTCAAGTGTGATGATGATGATGATGATGATGATGAT 2147
Db      .....|||
634 tAsnLysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaVal 654
Qy      2148 TCTGATATACCACTTCATTTTCACTGATTAATTTGCTGGCTGTGAAAAAGTACAGCAG 2207
Db      .....|||
654 lLeuValTyrLysPheTyrPheHisLeuMetCysLeuAlaGlyCysAlleLysTyrGlyArg 674
Qy      2208 AGGAAAGACATCTATGATGATGATGATGATCTAATGATGATGATGATGATGATGATGATG 2267
Db      .....|||
674 gGlyGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspIlePheValAla 694
Qy      2268 AAATGACCTGTAAAGAAATTTGAAGAAGAGAGTCCCGCTTTCACACTCTGCTTCACTA 2327
Db      .....|||
694 gAsnGlnLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysValMetHisTyr 714
Qy      2328 CAGAGACTTATTCCTGGGTAGACATGCTGTGCAACATGATCATCAGGAAGGCTTCCACA 2387
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734 sSerArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePh 754
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754 eGlnTyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIle 774

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QY 2508 TGTCTTGAGAGGTTGAGAGTCCCTGAGGAGGAGGATTTGATCCCTCT 2567
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 QY 2628 AAGACTTAAATGCTTATGATGAGAAAGCTCGAATCTGAGCAAA 2679
 Db 814 gArGLeuArglySAlaLeuLeuAspGlyLySerTPrAsnPrGluGlyThr 831
 RESULT 2
 US-08-514-014-4
 Sequence 4, Application US/08514014
 Patent No. 5707829
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John
 APPLICANT: Kelleher, Kerry
 APPLICANT: Carlin, McKenough
 TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 NUMBER OF INVENTION: ENCODED THEREBY
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Genetics Institute, Inc. -- Legal Affairs
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/514,014
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: G16000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 661 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-514-014-4
 Alignment Scores:
 Pred. NO.: 4.59e-53 Length: 661
 Score: 579.50 Matches: 185
 Percent Similarity: 47.54% Conservative: 124
 Best Local Similarity: 28.46% Mismatches: 305
 Query Match: 11.19% Indels: 37
 DB: 1 Gaps: 16
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 Db 28 CysIleGlyuylsGluAlaAsnlyThrTyraGlyuylsGluValLeuGlyLeuSerGluIle 47
 QY 349 CCGATGACATCTCTTCTTCAACCAAGAACATAGATCTGACCTTCAACCCCTGAAGATC 408
 Db 48 ProAspThrLeuProAsnThrThrGluPheLeuGlnPheSerPheAsnPheLeuProThr 67

QY 409 TTAAGAGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGCAGTATTCACAGGTG 468
 Db 68 IleHisAsnArgThrPheSerAlaGlyLeuMetAsnLeuThrPheLeuAspLeuThrArgCys 87
 QY 469 GAAATGAAACAAATGAGAACAGGACATGGCATGGCTTACCAACCTTCAAACTTGATA 528
 Db 88 GlnIleAsnThrPheIleGlnAspThrPheGlnSerHisIleGlnLeuSerThrLeuVal 107
 QY 529 CTGACAGGAACCTTATCCAGAGTTTTCCTCCAGAAAGTTTCTGACTGACCTTAAAGTTTA 588
 Db 108 LeuThrGlyAsnProLeuIlePheMetAlaGluThrSerLeuAsnGlyProlySerLeu 127
 QY 589 GACATCTGGTGGCTGGAGACAAATGCGCTCTGAGAAAGCTTCCTATGACAG 648
 Db 128 LysHisLeuPheLeuIleGlnThrGlyIleSerAsnLeuGlnPheIleProValHisAsn 147
 QY 649 CTATTAACCTTAAAGAACTCAATGGGCTCACAAATTTTATACATTCCTGTAAGTTACCT 708
 Db 148 LeuGlnAsnLeuGlnSerLeuTyrlLeuGlySerAsnHisIleSerSerIleLysPhePro 167
 QY 709 GCATATTTTCCATCTGACGAACCTTAGTACATGTGATCTTTCTTATACCTATATTCAA 768
 Db 168 LysAspPhePro--AlaArgAsnLeuLysValLeuAspPheGlnAsnAlaIleHis 186
 QY 769 ACTATTAAGTGTCAACGACCTTACAGTTTCTACGTGAAGAAATCCACAAAGTCATCTCTTTA 828
 Db 187 TyrlIleSerArgGluAspMetArgSerLeuGln--AlaIleAsnLeuSerLeu 204
 QY 829 GACATGCTTTTGAACCAATGACCTTATTCATTCACAGCAACCTTTCAGGAAATTAAGCTC 888
 Db 205 AsnPheAsnGlyAsnAsnValLysGlyIleGluLeuGlyAlaPheAspSerThrValPhe 224
 QY 889 CATGACCTGACTTAAGAGTTAATTTTATAGCTCAATATTAAGAAACTTGCTTCA 948
 Db 225 GlnSerLeuAsnPheGlyGlyThrProAsnLeuSerValIlePheAsnGly--LeuGln 243
 QY 949 AACCTGGCTGTTTACACGTCACGCTGATGCTGAGCAATTTTAAAGATGAAGAAAG 1008
 Db 244 AsnSerThr-----ThrGlnSerLeuThrPheGlyThrPheGlnAsp 260
 QY 1009 CTGAAATTTTGAACCTCTATCATGAGAGCAATGATGATGACATGATGATGATTC 1068
 Db 261 GluAspIle--SerSerAlaMetLeuLysGlyLeuCysGluMetSerValGlnSerLeu 279
 QY 1069 AGGTAAACATATACAAATGATTTTTCAGAT--GATATGTTAAGTTCCATGGCTGGCG 1125
 Db 280 AsnLeu--GlnGlnHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThr 298
 QY 1126 AATGTTTCGCAATGCTCTGCGAGGATGATCTAATAAATATAGTAAGAAAGTGTCCATA 1185
 Db 299 GlnLeuGlnGluLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSerGlyMetLys 318
 QY 1186 CATTT-----CAATGCAATCTCTATCATCAT-----TAG 1217
 Db 319 GlyLeuAsnLeuLeuLysIleValLeuSerValAsnHisPheAspGlnLeuCysGln 338
 QY 1218 ATGTCAATAGAGATTTTCAACTGAGATCTACCTTTTAAAGTTGACTTTAACT 1277
 Db 339 IleSerAlaIleAsnPheProSerLeuThrHisLeuTyrlLeuArgIleAsnValLys 358
 QY 1278 ATGAACAAAGGCTATCAATTTTAAAGAGGCGCTTACCAAGTCTGACCTATGAT 1337
 Db 359 LeuHisLeuGlyAlaGlyCysLeuGlnLys-----LeuGlyAsnLeuGlnThrLeuAsp 376
 QY 1338 CTATGAGAAATGACCTGACCTTATGATGAGCTGTCTTATCTGATTTGGAGAACAAAC 1397
 Db 377 LeuSerHisAsnAspIleGlyAlaSerAspCysCysSerLeuGlnLeuLysAsnLeuSer 396
 QY 1398 AGCCTGACACTTAAAGCTGACCTTCAATGATGATGATC--ATTATAGTGGCAATTTTC 1454
 Db 397 HisLeuGlnThrLeuAsnLeuSerHisAsnGlnProLeuGlyLeuGlnSerGlnAlaPhe 416

[illegible]

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833_823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Alignment Scores:
Pred. No.: 4,59e-53 Length: 661
Score: 579.50 Matches: 185
Percent Similarity: 47.54% Conservative: 124
Best Local Similarity: 28.46% Mismatches: 305
Query Match: 11.19% Indels: 37
                Gaps: 16
                2

US-09-396-985B-46 (1-2951) x US-08-833-823-4 (1-661)
QY      TGCATGAGGTGATTCCTAATATTAACCTACCAATGCATGCATGAAGAATCAGCAAAATC   348
DB      CysIIleGIuIsegluAlahsnlyrThryTrasnycsgluabntnugylLeuSerGIuile 47

QY      CCTGATGACATTCCTTTCTTCAAACAAGAACATAGATCGATGCCATCCCTTGAAATC   408
DB      ProAspThrIeuProAsnthrThrgIuhPheIeuGIuPheSerPheAsnPheIeuProThr 67

QY      TTAATAAGCTATAGCTTCTCCAAATTTTCAAGACTTCAGTGGCTGGAATTTATCCAGGT   468
DB      ILeHisAsnArgThrPheSerArgIeuMetAsnPheIeuThrPheIeuAspIeuThrArgCys 87

QY      GAATTTGAACAATGGAAGACAAGGCATGGCATGGCTTACACCACTCTCAAACTTGATA   528
DB      GIuIleAsnTrpIleHISgluAspThrPheGlInserHisHisGIuIleuSerThrIeuVal 107

QY      CTGACAGAAACCCTTATCCAGAGATTTTTCCCAGAGATTTCTGTGACCTAACAAAGTTTA   588
DB      LeuThrGIuAsnProIeuIlePheMetAlaGIuThrSerIeuLysAsnGIuProIySerIeu 127

QY      GACAATCTGGTGGCTGTGGAGACAACAATTTGGCTCTTAGAAAACCTTCCCTATTGGACAG   648
DB      LysHisIleuPheIeuIleGIuThrGIuIleSerAsnIleuGIuPheIleProValHisAsn 147

QY      CTTATTAACCTTAAGAAATCAATAGTGGCTCAAAATTTTATACATTCCTGTAAACTTACT   708
DB      LeuGIuAsnIeuGIuSerIeuIyrIeuGIuSerAsnHisIleSerSerIleLysPhePro 167

QY      GCATATTATTCCCATGCTGACGAACCTAGTACATGAGCATCTTTCTTATACATAATTATCAA   768
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QY      ACTATTACTGTCAACGACTTACAGTTTCTAGCGTAAAAATCCAAGTCATCTCTTTTA     828
DB      TyrIleSerArgGIuIuSpmetArgSerIeuGIuGIN-----AlaIleAsnIeuSerIeu 204

QY      GACATGCTTTGAACCAATTCATCTTACAAAGCAAGCCTTTACAGGAATTAACTC       888
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Db	205	AenPheAenGIYAAsnAsnValLysGlyIleGluLeuGlyAlaPheAspSerThrValPhe	224
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OY	949	AACCTGGCTGGTTTACAGCTCCATGGCTGATCTGGGGAGAAATTTAAAGATGAAGAAGAT	1008
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Db	261	GluAspIle---SerSerAlaMetLeuLysGlyLeuCyGluMetSerValGlnSerLeu	279
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Db	280	AsnLeu---GlnGlnIleArgPheSerAspPrlLeuSerSerThrThrPheGlnLysPheThr	298
OY	1126	AATGTTTCTGCAATGCTCTGGCAGAGTGTATCTATAAAATATCTAGAAGATGTTCTTAA	1189
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OY	1186	CATT-----CAATGGCAATCCCTATCAATCAT-----TAG	121
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OY	1218	ATGTCACTAAGCAGTTTCCACTCTGGATCTACCTTTCTTAAAGTTTGACTTTAACT	1277
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OY	1278	ATGAACAAGGCTCATACGTTTAAAAAAGGGCCCAACAAGCTCTAGCATTTACAT	1333
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OY	1338	CTTAGTAATAATGACACTAGCTTAAAGTGTGGTCTTTCTTATTTGATTTGGGAACAAC	1397
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OY	1398	AGCTGAGACACTTAAGCTCAGCTTCAATGGTGGCATC---ATTATGATGGCCAAATTC	1455
Db	397	HISleuGlnThrLeuAsnLeuSerThrAsnGlnProLeuGlyLeuGlnSerGlnAlaPhe	416
OY	1455	ATGGGTCTAGAAGAGCTCAGAGCTGGATTTTACAGACTCTATTAAAAAGGCTAC	1514
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OY	1575	CACCAAAATTAAGTTCGATGTATATTTCTTGACTTGAACAGTCTCAACATTTAAAT	1634
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OY	1635	GGCTGGCAATCTTTCAAAAGACACACCTT-----TCAATAGCTTTGGAACACAC	1688
Db	476	uLysGlyAsnHisPheGlnAspGlyThrIleThrLysThrAsnLeuLeuGlnThrValG1	496
OY	1689	AAATCTCAATCCCGAATCCCTTAATATGTCAAATTTGAACAATAATCTGGGGGATTT	1748
Db	496	ySerLeuGlnValLeuIleLeuSerSerCyGlyLysLeuSerIleAspGlnGlnAlaPhe	516
OY	1749	TGACACCTCCATAGACTTCAATTAATTAATATAGTACACAACATCTATTTG-----TT	1802
Db	516	eHisSerLeuGlyLysMetSerHisValAspLeuSerHisValAsnSerLeuThrCyAspSe	536
OY	1803	TTTGATTTCA---TCCCAATTAAACAGCTGATTTCCCTCAGACACTTTGATTTGCAGTTT	1858
Db	536	rIleAspSerLeuSerHisIleuLysGlyIleTyI-----LeuAsnLeuAlaAl	552
OY	1860	CAATGGCAATGAGACATTAAGCAAAAGAAATCTGGAACATTTTCCAAAGATCTAGCTTCTT	1919
Db	552	AsnSerIleAsnIleIleSerProValGluLeuProIleLeuSerGlnGlnSerThrI1	572

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1-
QY      1920 CAATCTTAACAAATTCCTGCTGTGTATATGTGAACATCAAGAAATTCCTGCAGTGGG 1975
Db      572 eashnuserh1sasnProleuaspCystrhCysersasn1eh1spheLeuthr1ptply 592
QY      1980 CAAGGACAGAGACAGTCTTGCTGTGAATGTGTGAACAAATGACATGTGCAACACCTGTAGA 2035
Db      592 rlysgclnslnleuth1slyslsleuaglugsylsecdlgnlurthrCysalaaenproprose 612
QY      2040 GATGAAT-----ACCTCCTTAGNGTGTGATTTTAATAATTCACCTGTATAT 2087
Db      612 rleuarglyVallylsleuserasrVallylsleuserCysglyl1erhral1a1egly11 632
QY      2088 GTACAAAGACATCATCATGTGTGTGACAGTGCTAGTGTGATTTGTGTATCCATGTAGCAT 2144
Db      632 ephpeheleu1levalPheleuLeuLeu1a1leuLeuPhehealVallylSty 652
QY      2148 TCTGATATACCACTTCAATTTTACCTG 2175
Db      652 rleuenuargTrplystYrgh1n1stle 661

RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavodny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB0601QC
; CURRENT APPLICATION NUMBER: US/09/982.308B
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,153
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.:      1,9e-40      Length:      784
Score:          463.00      Matches:      218
Percent Similarity: 41.64%      Conservative: 133
Best Local Similarity: 25.86%      Mismatches:  317
Query Match:      8.94%      Indels:      176
DB:              4          Gaps:      34

US-09-396-985B-46 (1-2951) x US-09-982-308B-23 (1-784)
QY      337 CTCGCAAAAGTCCTGTATGATTCCTTCAACCAAGAAACATATCTGAGCTTCAAC 396
Db      43 leuanser1leProserGlyLeuthrGlu1aVallysser1leuaspLeuserAsn1sn 62
QY      397 CCCTTGAAGATCTTAATAAGCTATAGCTTCCCAATTTTTCAGAACTTCAGTGCCTGAT 456
Db      63 Arg1lethrTyrl1eSerAsn-----SerAsp 71
QY      457 TTATTCAGAGTGCTGAAATTTGAAACAATGAAGACAAAGCAGTGCCTTACACCACTTC 516
Db      72 leu1nhr1gCysVal-----Asn1eu 78
QY      517 TCAAACTTGATCTGACAGGAACCCATTCACAGATTTTCCCGAGGAAGTTTCTCTGGA 576

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QY	2533	TAGAAAGTCCCTGCTAGCAGACAG---GTGGAATTGTTATCGGCTTCTTACGAGAAACAC	2579
Db	740	eEluYsYsYsAlaIlePrIoGlnArghcYsYsYsLeuAAGlyIleMeTsnhrIySth	760
QY	2580	CTACTGGAATGGGAGACGACATCTCTGGGGAGCGACATCTTGTGAGAAAGCTTAAAA	2639
Db	760	rTyLeuGlnTrrPrIoMeTAspIuAlaGlnArghGlnGlyPhetrrValAsnLeuArghAl	780
QY	2640	TGCCCCA 2646	
Db	780	aAlaIle 782	
<p>RESULT 5 US-09-949-016-8799 Sequence 8799, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: C1001307 CURRENT APPLICATION NUMBER: US/09/949, 016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241, 755 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/237, 768 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231, 498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSeq for Windows Version 4. 0 SEQ ID NO 8799 LENGTH: 775 TYPE: PRT ORGANISM: Human US-09-949-016-8799</p>			
<p>Alignment Scores: Pred. No.: 2,36e-34 Length: 775 Score: 406.50 Matches: 207 Percent Similarity: 39.88% Conservative: 118 Best Local Similarity: 25.40% Mismatches: 288 Query Match: 7.85% Indels: 203 DB: 4 Gaps: 33</p>			
<p>US-09-396-985B-46 (1-2351) x US-09-949-016-8799 (1-775)</p>			
QY	337	CTCAGCAAAAGTCCTGATGACATTCCTTCTTACCAACAAGACATAGATCTGACCTTCAAC	396
Db	78	LeuAAserIlePrIoSerGlyLeuThrIuAlaValIySerLeuAsnSerIAsn 97	
QY	337	CCCTTGAAGACTTTAAAAAGCTATAGACTTCTCCAAATTTTCAGAACTTCAAGTGCGTGAT	456
Db	98	ArgIleThrIyIleSerAsn-----SerAsp 106	
QY	457	TTATCCAGGTGGAATTAACAATTTGAAGACAAGCATGGCATGGCTTTACACACCTTC	516
Db	107	LeuGlnArghCysVal-----AsnLeu 113	
QY	517	TCMAACTGTATACGTACAGAGAAACCTTATCAGAGTTTTCGCCAGAAATTTCTCTGA	576
Db	114	GlnAlaIleValLeuThrSerGngIyIleAsnThrIleGlnIuAspSerPheSer 133	
QY	577	CTAAACAAGTTTGAACAATCTGGTGGCTGTGGAGACAAATTTGGGCTCTTGAAGAACTTC	636
Db	134	LeuGlySerLeuGlnIleuAsnSerTyAsnTyIleuSerAsnLeuSerSer 153	
QY	637	CCTATTGACACACTTATACCTTTAAAGAAACCAATGAGTGAGCTACACATTTTATACATTC	696
Db	154	TrpPheIySPrIoLeuSerSerLeuThrPheLeuAsnLeuGlyAsnProTyIySthr 173	
QY	697	TGTAAAGTACCTGCATATTTTTCCAATCTGACGACACCTTATACATGTCGATCTT-----	750

Db	174	LeuGluGluThrSerLeuPheSerHisLeuThrIleuGluIleLeuArgValGlyAsn	193
Qy	751	-----TCCTATACTATATTCAAACTATTACTGTCAACGACTTACAGTTTCTACGTGA	804
Db	194	MetAspThrPheThrIleYsIleGlnArgGlyAspPheAlaGlyLeuThrPheLeuGluGlu	213
Qy	805	AATCCACAAAGTCATCTCTCTTTAGACATGCTTTGAACCCCAATTGACTTCATTCAACAC	864
Db	214	-----LeuGluIleAspAlaSerAspLeuGlnSerTyrGluPro	226
Qy	865	CAAGCTTTCAGGGAATT-----AAGCTTCATGA	894
Db	227	LysSerLeuYsSerIleGlnAsnValSerHisLeuIleLeuHisIleMetYsGlnHisIle	246
Qy	895	CTGACTCTAAGAGGTAAATTTTAATAGCTCAATATTAATGAAGACTTGCTTCA	948
Db	247	LeuLeuGluGluIlePheValAspValThrSerSerValGlu---CysLeuGluIleuArg	265
Qy	949	-----AAGCTGGCTGTTTACAGTCCATCGGTGATCTTGGAGAAATTTAAAGAT---	999
Db	266	AspThrAspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu	285
Qy	1000	-----GAAGGAATCTGGAAATTTTGAACCTGTATCATGTGA	1038
Db	286	IleIleYsYsPheThrPheArgAsnValYsIleThrAspGluSerLeuPheGlnValMet	305
Qy	1039	-----GCACTATGTAGTGTGACCATTTGATGAGTTCCAGTTCA	1077
Db	306	LysLeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsn	325
Qy	1078	TATACAAATGATTTT-----TCAGATGATATTGTTAACTTCATGCTTGCCGAAGTT	1131
Db	326	GlyValGlyAsnPheArgAlaSerAspAsn-----	335
Qy	1132	TCGTCAATGTCTCGGACGTGTATCTATAAATCTAGACAGATGTTCCAAACATTTCC	1191
Db	336	-----AspArgValIleAspProGly	342
Qy	1192	AAATGGCAATCTTATCAATCATTTAGATGTCAACCTAGCTTTCAACTCTG---GAT	1247
Db	343	LysValGluThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyrAsp	362
Qy	1248	CTACCTCTTTCTTAAAGTTGACTTTAATCTATGACAAAGGCTCATCAGTTTAAAAA	1307
Db	363	LeuSerThrLeuTyrSerLeuThrGluArgValYsArgIleThrValGluAsnSerYs	382
Qy	1308	GTG-----GCCCTACCAAGTCTCAGTATCTAGATTTT	1340
Db	383	ValPheLeuValProCysYsLeuLeuSerGlnHisIleuYsSerLeuGluTyrLeuAspLeu	402
Qy	1341	AGTAGAATGACGTG-----AGCTTTAGGTGGTGGCTGT-----TCTTAATCT	1382
Db	403	SerGluAsnLeuMetValGluGluTyrLeuYsAsnSerAlaCysGluAspAlaIlePro	422
Qy	1383	GATTGGGAAACAAACAGCTGAGA-----CACTTA---GACCTCAGCTTCAATGGTGCC	1433
Db	423	SerLeuGlnThrLeuIleLeuArgGlnAsnHisIleuHisIleSerLeuGluTyrThrGlyGlu	442
Qy	1434	ATCATTTATGAGTGCCAATTTTCATGGGTCTAGAAAGCTGCAGCACCTGAGATTTTCA	1493
Db	443	ThrLeuLeuThr-----LeuYsAsnLeuThrAsnIleAspIleSer---Iy	457
Qy	1494	CTTACCTTTAAAAAGGTCACAGAAATCTCAGCGTCTTATCCCTTGAAAGCTACCTTA	1553
Db	457	AsnSerPheHisSerMetProGluThrCysGlnIleP-----ProGluYsMetLeuTyr	475
Qy	1554	CTTTGACATCTCTTATCTACACCAACAAATTTGACTTGATGTATATTTCTTGACTGAC	1613
Db	475	IleuAsnLeuSer-----SerThrArgIleHis-----	484
Qy	1614	CAGTCTCAACACATTAATAATGCTGGCAATTTCTTTCAAGACAAACCCCTTTCAAAATGT	1673

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Db 485 -----SerValThrGlyCysIleProIysThrLeuGluIleuAspVa 499
QY 1674 CTTTGAACACCAACCAACTTGACATCTCGATCCTTTAAATGTCATTTGAAACAAT 1733
    ||| ||| ||| ||| |||
Db 499 lSeAsnAsnAsnLeuAsnLeuPheSerLeuAsn----- 510
QY 1734 ATCTTGGGGGATATTTGACACCTCCATAGACTTCATTAATTAATAATGAGTCAACA 1793
    ||| ||| ||| ||| |||
Db 511 -----LeuProGlnLeuIleuGlyIleSerArgAsnIly 523
QY 1794 TCTATTGTTTGGATTCAATCCCATTTAAACAGCTGATATTCCTCGACACTCTTGATTG 1853
    ||| ||| ||| ||| |||
Db 523 sLeuMetThrLeuProAspAla-----SerLeuLeuProMetLeuLeuValLeuIly 541
QY 1854 CAGTTTCAATCGCATAGACACA-----TCTAAAGAAATCTGCACATTTTCCAAAGAGTCT 1910
    ||| ||| ||| ||| |||
Db 541 eSeArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe--HisThrIle 560
QY 1911 AGCCTTCTTCAATCTTAAACAATCTGTGCTTGTATATGTGACATCGAATAATCCT 1970
    ||| ||| ||| ||| |||
Db 560 ulysThrLeuGlnIleGlyIleAsnAsnPheIleCysSerCysGlu-----PheIle 577
QY 1971 GCAGTGGGTCAAGAACAGACAGCGTTCTTGCTGAATGTT-----GACA 2015
    ||| ||| ||| ||| |||
Db 577 uSerPheThrGlnGlnGln--GlnAlaLeuAlaValLeuIleAspTrpProAlaAs 596
QY 2016 AATGACATGTGACACACCTGTAGAGATGAAATACCTCTAGTGTGTGATTTTAAATATTC 2075
    ||| ||| ||| ||| |||
Db 596 nTyLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSe 616
QY 2076 TACCTGTATATGTACCAAGACAAATCATAGTGTGTCAGTGTGATGTGTGATTC 2135
    ||| ||| ||| ||| |||
Db 616 rValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeu----- 633
QY 2136 CACTGTAGCATTTTGTATATACCACTTCTATTTTCACTGATACTTTATGCTGGC----- 2190
    ||| ||| ||| ||| |||
Db 634 -----PheLeuLeuIleLeuLeuThrGlyValLe 643
QY 2191 -TGTAAAGATAC----- 2202
    ||| ||| ||| ||| |||
Db 643 uCysHisArgPheHisGlyLeuTrpTyrMetLeuMetCysTrpAlaTrpLeuGlnAlaIly 663
QY 2203 -----ACGAGAGAGAAAGCATCTATGATGATGATTTGTGATCTA 2240
    ||| ||| ||| ||| |||
Db 663 sArgLysProArgLysAlaProSerArg--AsnIleCysTrpAspAlaPheValSerTyr 682
QY 2241 CTCGATGCAGATAGAGACTGGGTGAGAAATGAGCTGTGTAAGATTTAGAGAGAGAGT 2300
    ||| ||| ||| ||| |||
Db 682 rSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGlnGlnLeuGluAsnPheAs 702
QY 2301 GCCCGGCTTCACTGCTGCTCTCACTACAGAGACTTATTTCTGGTGTAGCCATTGCTGC 2360
    ||| ||| ||| ||| |||
Db 702 nProProPheLysLeuCysLeuHisLysArgAspPheIleProGlyLysTrpIleIleAs 722
QY 2361 CAACATCATCCAGAGAGGCTTCCACAGAGCCGAGAGGTTATTTGTGATGCTGTAGACA 2420
    ||| ||| ||| ||| |||
Db 722 pAsnIleIle--AspSerIleGlyLysSerHisLysThrValPheValLeuSerGluAs 741
QY 2421 CTTTATTCAGAGCCGCTGTGTATCTTTGAATATGAGATGCTCAACATGCGAGTTTCT 2480
    ||| ||| ||| ||| |||
Db 741 nPheValLysSerGluTrpCysLysTyrGlnLeuAspPheSerHisPheArgLeuPheAs 761
QY 2481 GAGAGCCGCTGTGACATCTTCACTGTGCTTGAAGAGTT 2523
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Db 761 pGluAsnAsnAspAlaAlaIleLeuIleLeuLeuGlnProIle 775

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/ TITLE OF INVENTION: THEREFOR
/ FILE REFERENCE: MEI-019
/ CURRENT APPLICATION NUMBER: US/09/063,950C
/ CURRENT FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 605
/ TYPE: PR1
/ ORGANISM: Papilio hamadryas
US-09-063-950-5

Alignment Scores:
Pred. No.: 2,32e-21 Length: 605
Score: 285.50 Matches: 144
Percent Similarity: 36.06% Conservative: 94
Best Local Similarity: 21.82% Mismatches: 240
Query Match: 5.51% Indels: 183
DB: 3 Gaps: 17

US-09-396-985b-46 (1-2951) x US-09-063-950-5 (1-605)

QY 301 GTTCTTAATATTACCTACCAATGCATGATCAGAAACTCAGCAAGTCCCTGATGACATT 360
    ||| ||| ||| ||| |||
Db 53 ValAsnGlnLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspGlyIle 72
QY 361 CTTTCTTCAACCAAGAACATATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGACTAT 420
    ||| ||| ||| ||| |||
Db 73 ProGlyGlyThrGlnAlaLeuTrpLeuAspSerHisAsnLeuSerIleProProAla 92
QY 421 AGCTTCCAAATTTTTCAGAACTTCAGTGGCTGAGATTTATCCAGTGTGAAATTTGAAACA 480
    ||| ||| ||| ||| |||
Db 93 AlaPheArgAsnLeuSerSerLeuAlaPheLeuAsnLeuGlnGlyGlnLeuGlySer 112
QY 481 ATTGAAGACAGGCAAGCAAGGCTTACACCACTTCAAACTTGATATCGACAGAAAC 540
    ||| ||| ||| ||| |||
Db 113 LeuGlnProGlnAlaLeuLeuGlyLeuGluAsnLeuCysHisLeuHisLeuGluArgAsn 132
QY 541 CCTATCCAGAGTTTTCCTCCAGGAAGTTTCTGTGACTAACAGATTTTGAACAATCTGGTG 600
    ||| ||| ||| ||| |||
Db 133 GlnLeuArgSerLeuAlaValGlyThrPheAlaTyrThrProAlaLeuAlaLeuGly 152
QY 601 GCTGTGGAGCAAAATTTGGCTCTTGAAGAGCTTCCATTGAGACATTATTAACCTTA 660
    ||| ||| ||| ||| |||
Db 153 LeuSerAsnAsnArgLeuSerArgLeuGluAsp----- 163
QY 661 AAGAACTCAATGTGGCTCAAAATTTATATCATTTCTGTAGTTACTGCAATATTTTCC 720
    ||| ||| ||| ||| |||
Db 164 -----GlyLeuPheGlu 167
QY 721 AATCTGCAACCACTAGATGATGAGATCTTTTATATCTATATTCAAACTATTAAGTCTG 780
    ||| ||| ||| ||| |||
Db 168 GlyLeuGlyAsnLeuTrpAspLeuAsnLeuGlyTrpAsnSerLeuAlaVal----- 184
QY 781 AAGCACTTACAGTTTCTACGTGAAATCCAAAGTCAATCTCTTTTGAACATGCTTTTG 840
    ||| ||| ||| ||| |||
Db 184 ----- 184
QY 841 AACCAATTCATCTTCAATCAAGCAAGCTTTCAGGGAATTT--AAGTTCATGAACAG 897
    ||| ||| ||| ||| |||
Db 185 -----LeuProAspAlaAlaPheArgGlyLeuGlyGlyLeuArgGlnLeu 199
QY 898 ACTCTAAGAGTAATTTTATAGCTCAATATATATGAAACTTGCTCAAAACCTGGCT 957
    ||| ||| ||| ||| |||
Db 200 ValLeuAlaGlyAsn----- 204
QY 958 GATTACACGTCATCGGTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGAATAT 1017
    ||| ||| ||| ||| |||
Db 205 -----ArgLeuAlaTyr 208
QY 1018 TTGAACCTCTTATCATGAGAGACATATGTGATGACCAATTGATGATTCAGGTTTACA 1077
    ||| ||| ||| ||| |||
Db 209 LeuGlnProAlaLeuPheSerGlyLeuAlaGlnLeuArg----- 221

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RESULT 6
US-09-063-950-5
/ Sequence 5, Application US/09063950C
/ Patent No. 6225085
/ GENERAL INFORMATION:
/ APPLICANT: Holzman, Douglas A.
/ TITLE OF INVENTION: NOVEL TRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES

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QY 1078 TATCAATATGATTTTCAGATGATATGTTAAGTTCCATGCTGGCAATGTTCTGCA 1137
 Db 222 -----GluLeuAspLeuSerArg 227
 QY 1138 ATGCTCTGGCAGGTGATCTATAAATATCTAGAGATGTTCTTAACATTTGCAATGG 1197
 Db 228 AsnIleuArgIleIleValIleAsnValPheAlaGlnLeuPro-----ArgLeu 244
 QY 1198 CAATCCTTATCAATCATTAAGTGCACATAAGCTTTCCAACT-----CTGAT 1247
 Db 245 GlnIleuLeuTyrLeuAspArgAsnLeuIleAlaIleValAlaProGlyAlaPheLeuGly 264
 QY 1248 CTACCCCTTTCTTAAAGTTTACTTTTAACTTGAACAA-----GGCTATGAGTTT 1301
 Db 265 LeuIleValIleuArgIlePheLeuAspLeuSerIleAsnArgValAlaGlyLeuLeuGlnAsp 284
 QY 1302 AAAAAGTGGCCCTACCAAGTCTCAGCTATCTAGATCTTACTAGAAATGCACTGAGCTTT 1361
 Db 285 ThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeuSerIleAsnAlaIleAlaSer 304
 QY 1362 AGTGTGGCTCTTCTTATCTGAT-----TTGGGAACAAC 1397
 Db 305 LeuArgProArgTyrThrPheGluAspLeuIlePheLeuGlnLeuGlnIleAsn 324
 QY 1398 AGCCTGAGACACTTACACCTCAGCTCAATGTCATCATTAAGTGCATTTGATG 1457
 Db 325 ArgIleArgGlnLeu-----AlaGluArgSerPheGln 335
 QY 1458 GGTCTAGAGAGCTGACGACACCTGATTTTTCAGCACTCTTCTTAAAGGTCACAGA 1517
 Db 336 GlyLeuGlnGlnLeuGlnValLeu-ThrLeuAspIleAsnGlnLeuGlnVal---Ly 354
 QY 1518 ATTCTCAGCGCTTCTTATCCTTGAAGACTTACTTACCTGACATCTCTTACTTAAACAC 1577
 Db 354 sValGlyAlaPheLeuGlyLeuThrAsnValAlaIleMetAsnLeuSerGlyAsnCysLe 374
 QY 1578 CAAATTTGACTGATGATGATATTTCTTGCTTGCACGATCTCAACATTAATAAATGGC 1637
 Db 374 uArgAsnLeuProGlnValPheArgGlyLeuGlyLeuIleAsnIleLeu 394
 QY 1638 TGGCAATTCCT----- 1647
 Db 394 uGlySerCysLeuGlyArgIleArgProIleThrPheAlaGlyLeuSerGlyLeuArg 414
 QY 1648 -----TTCAAGACACACCCCTTCAATGCTTTGCAACACA-----AC 1668
 Db 414 GlnPheLeuIleAspAsnGlyLeuValGlyIleGlnGlnSerLeuTyrGlyLeuAl 434
 QY 1689 AAACCTGACATTCCTGATCCTCTTAATATGATCAATGGAACAATATCTGGGGGATTT 1748
 Db 434 aGlnLeuLeuGlnLeuAspLeuIleSerAsnGlnLeuThrIleLeuProIleGlnLeuPhe 454
 QY 1749 TGACACCCCTCATGACTTCAATATTAAATATGATGATGACACAACATCTATTGTTTGA 1808
 Db 454 eGlnGlyLeuGlyLeuGlnGlyLeuLeuLeuSerIleAsnArgLeuAlaGlnLeuPhe 474
 QY 1809 TTATCCCATTAACAACAGCTGATTCCTCAGACACTCTTGATGACATTGCAATTCGCAT 1868
 Db 474 cAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspValSerIleAsnArgLe 494
 QY 1869 AGAGACATCTAAAGATATCTGCAACATTTCCAAAAGTCTGACCTTCTTCATCTTAC 1928
 Db 494 uGlnAlaLeuProGlySerLeuLeuAlaSerLeuGlyArgGlnArgTyrLeuAsnLeuArg 514
 QY 1929 TAAACATTTCTGTTCTGTATATGATGAACATCAGAAATTCCTGACG-----TGGGTCAA 1982
 Db 514 gAsnAsnSerLeuArgThrPheThrProGlnProGlyLeuGlnArgLeuLeuTyrLeuGln 534
 QY 1983 GAAACAGACAGCTTCTTGGAATGTTGAACAATGACATGTCACAACCTGTAGAG-- 2040
 Db 534 uGly-----AsnProTyrAspCysSerCysProLeuVal 546

QY 2041 -----ATGAATACCTCTTACTGATGATTTTAAATATCTTACTCG 2081
 Db 546 aLeuArgAspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCys 566
 QY 2082 T-----TATATGACAGACAAATCATCATGCTGTGCA 2112
 Db 566 sGlnGlyAspAspCysGlnProProValTyrThrTyrAsnAsnIleThrCysAlaSer 585
 RESULT 7
 US-08-190-802A-50
 ; Sequence 50, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: The use of
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Delinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 603 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 ; INDIVIDUAL ISOLATE: pro. complex-ra1, Fig. 33
 ; US-08-190-802A-50
 Alignment Scores:
 Pred. No.: 9 07e-21 Length: 603
 Score: 280.00 Matches: 163
 Percent Similarity: 38.12% Conservative: 81
 Best Local Similarity: 25.47% Mismatches: 221
 Query Match: 5.41% Indels: 176
 DB: 1 Gaps: 26
 US-09-396-985B-46 (1-2951) x US-08-190-802A-50 (1-603)
 QY 322 TGCATGATCAGAAACTCAGCAAGTCCCTGATGACATTCCTTCTTCAACAGAACATA 381
 Db 60 CysSerSerIleAsnLeuThrIleLeuProAspAspIleProValSerThrArgAlaLeu 79
 QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTTATGCTTCTTCAATTTTTCGAA 441
 Db 80 TrpLeuAspGlyAsnLeuLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSer 99
 QY 442 CTTCAGTGGCTGATTTATCCAGGTGGAATTTGAACAATTTGAAGACAAGGATGCAT 501

APPLICATION NUMBER: 08/487,072
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHESES: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-477-346-50

Alignment Scores:
 Pred. No.: 9.07e-21 Length: 603
 Score: 280.00 Matches: 163
 Percent Similarity: 38.12% Conservative: 81
 Best Local Similarity: 25.47% Mismatches: 221
 Query Match: 5.41% Indels: 176
 DB: Gaps: 26

US-09-396-985b-46 (1-2951) x US-08-477-346-50 (1-603)

322 TGCATGATGAGAAAGTCCCTGATGACATCTCTTCTGAACAGACATA 381
 60 Cyssererlysaenleuthrhiseuproasprieprovalseththralaleu 79
 382 GATCTGAGCTTCAACCCCTGAGATCTTAAAGCTATACCTTCTCAATTTTTCAGA 441
 80 Tryleuaspriyandansleuserierleproserialalpheginalseuser 99
 442 CTTCAGTGGCTGATTTATCCAGGTGTAATTAACATTAAGACAGGCTGGCAT 501
 100 LeuaspriheleuandseugllyserTryleuargserleugluproginalleu 119
 502 GGCTTAACCCACCTCTGAACTGATCTGACAGAAACCTATCCAGATTTTCCCA 561
 120 GlyleuandansleuYrTytleuhiseuglularghsnargleuargseuallaleu 139
 562 GGAAGTTCTCTGACTTAACAAGTTTGAACATCTGCTGCTGAGACAAATGGCC 621
 140 GlyleuetherhthsthrProserleuallaserleuserleuserseanleuclly 159
 622 TCTTGAAGAGCTTCCCTATTGACAGCTTAACTTAAAGAACTCAATGTGGCTCAC 681
 160 ArgleuandugllyleuPheglnglyleuserhiseuTrpaspriheleucllyTrp 179
 682 AATTT-----ATCATTCCTGT 699
 180 AsherleuValValleuProasprihValPheglnglyleuGlyasnlhehiseu 199
 700 AAGTTA-----CTGCATATTTTTCATCTGACAGAAC 732
 200 ValleuallaglyleuYrTytleuandansleuProalaleuPheCysgllyleuclly 219
 733 CTAGTACATGATCTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 792
 220 LeuargleuandansleuPheCysgllyleuargseuVallysalasnlValPheVal 239
 793 TTTCTAGTGAAGAAATCCACAGTC---AATCTCTTATGACAGTCTTGAACCATTT 849
 240 Hisleu-----ProargleucllyleuYrTytleuaspriheleu-----Ile 254
 850 GACTTCATTCAGACCAAGCTTTCAGGAGATTAAG---CTGCATGAAGTCACTTAAGA 906

255 ThrzlaValalaproglialapheleuglymetylsalaleuargTrpleuaspriuser 274
 907 GGTAAATTTTATAGTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 966
 275 Hisasn---ArgValalaglyleuemetCylusprThrPheprogllyleucllyleu 293
 967 GTCCATCGTGTGATCTTGGGA-----GAATTTAAAGATGAA 1002
 294 ValleuargleuallahisasnallalealaserleuargProargThrPheleuaspri 313
 1003 AGGATCTGGAATTTTGA-----CCCTTATC 1032
 314 HisPheleuandugllyleuandansleuYrTytleuargleucllyleuargThr 333
 1033 ATGGAAGACTATGAT-----GTACACCTTATGATGATGATGATGATGATGATGAT 1083
 334 PheglnglyleuandansleucllyleuandansleuPheglnglyleucllyleu 353
 1084 AATGATTTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
 354 Arg-----ValGlyalapheserCylleuPheasnValalaleuMetasn 368
 1140 GTCTTGGCAGGTGATCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1199
 369 LeuargleuandansleuargseuPheglnglyleucllyleucllyleucllyleu 383
 1200 ATCTTATCATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1259
 383 ----- 383
 1260 AAAAGTTGACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1319
 384 -----Glyleuasp 386
 1320 AGTCTGATCTATGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1379
 387 Tytleuandansleuandansleuandansleuandansleuandansleuandans 406
 1380 TCTGATTTGGGAACAAACACCTGAGACATCTTAAGCTGATGATGATGATGATGATGAT 424
 407 Ala-----Glyleuandansleuandansleuandansleuandansleuandans 442
 1437 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1496
 425 Ileleuandansleuandansleuandansleuandansleuandansleuandans 441
 1497 TACTTTAAAAAGGTCAAGAAATTC-----TCAGCTTCTTATCCCTGAAAACTACT 1550
 442 -ThrThrAsnargleuandansleuandansleuandansleuandansleuandans 461
 1551 TTACCTTGATCTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1610
 461 Tytleuandansleuandansleuandansleuandansleuandansleuandans 470
 1611 GACAGTCTGAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1670
 470 uThrThrleuser-----Alagl 476
 1671 TGCTTTGAAACAAACAAACTTGAATTCCTGATCTTGAATTAATTAATTAATTAATTA 1730
 476 uValleuandansleuandansleuandansleuandansleuandansleuandans 496
 1731 AATATCTTGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1790
 496 rleuallaglyleuandansleuandansleuandansleuandansleuandans 516
 1791 CAATCTA-----TGTCTTGGATTCATGCCA 1817
 516 nserleuandansleuandansleuandansleuandansleuandansleuandans 536
 1818 TTATTAACAGCTATTCCTCAGACACTTGTATGAGTTGATGATGATGATGATGATGAT 1877
 :::

Db 536 cTrp-----AspCysSer----- 540
 QY 1878 TAAAGAAATCTGACATTTTCA---AAGAGCTAGCCTTCTTCAATCTTACTACAA 1934
 Db 541 -----CysProLeuIyAlaLeuArgpshpheaIaleuGlnaenpr 554
 QY 1935 TTCTGTGCTTGTATATGATGACAAATTCCTGAGTGCTCAAGNA-----CA 1988
 Db 554 ogIyValVal-----ProArgpheaIaGlnThrValCysgluGlyAspAs 569
 QY 1989 GAACGAGCTTCTGTGAATGTGGAACAAATGACATGTGCAACACCTGTAGATGAAT 2046
 Db 569 pCyEglnProValIyThrIyAsnaenIleThrCysAlaGlyProAlaenValSer 588
 RESULT 9
 US-08-473-089-50
 / Sequence 50, Application US/08473089
 / Patent No. 6342368
 / GENERAL INFORMATION:
 / APPLICANT: Mochly-Rosen, Daria
 / APPLICANT: Ron Dorit
 / TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 / TITLE OF INVENTION: Theoreof
 / NUMBER OF SEQUENCES: 265
 / CORRESPONDENCE ADDRESSES:
 / ADDRESSEE: Morison & Foerster
 / STREET: 2000 Pennsylvania Avenue, NW
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20006-1812
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/473,089
 / FILING DATE: 07-JUN-1995
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: MURASHIGE, KATE H.
 / REGISTRATION NUMBER: 29,959
 / REFERENCE/DOCKET NUMBER: 2550-0025.22
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202) 887-1500
 / TELEFAX: (202) 887-0763
 / INFORMATION FOR SEQ ID NO: 50:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 603 amino acids
 / TYPE: amino acid
 / TOPOLOGY: unknown
 / MOLECULE TYPE: protein
 / HYPOTHEetical: NO
 / ANTI-SENSE: NO
 / ORIGINAL SOURCE:
 / INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 / INDIVIDUAL ISOLATE: pro. complex-rac, Fig. 33
 / US-08-473-089-50
 Alignment Scores:
 Pred. No.: 9.07e-21 Length: 603
 Score: 280.00 Matches: 163
 Percent Similarity: 38.12% Conservative: 81
 Best Local Similarity: 25.47% Mismatches: 221
 Query Match: 5.41% Indels: 176
 DB: 3 Gaps: 26
 US-09-396-985B-46 (1-2951) x US-08-473-089-50 (1-603)
 QY 322 TGCATGATCAGAACTCAGCAAGTCCCTGATGATGATCTTCTTCAACCAAGACATA 381
 Db 60 CysSerSerIyAsnIleuThrIleuProAspAspIleProValSerThrArgAlaIeu 79

QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTATAGCTTCTCAATTTTTCAGAA 441
 Db 80 TrpLeuAspIyAsnIleuAsnIleuSerIleProSerIleAlaIaheGlnIleuIleuSer 99
 QY 442 CTTCAGTGGCTGATTTATTCACAGGTGTGAATTTGAACAAATTGAACAGACATGGCAT 501
 Db 100 LeuAspPheLeuIleuIleuGlnIySerTrpLeuArgSerIleuIleuProGlnIleuLeu 119
 QY 502 GCGTTACACACCTTCAAACTTGATACACAGAAACCCATTCAGAGCTTTTCCCA 561
 Db 120 GlyLeuGlnAsnIleuIyTrIyLeuIleuGlnIyAsnIyArgIleuIyAsnIleuAlaVal 139
 QY 562 GGAAGTTTCTCTGAGCTTAACAACTTGAACAACTGTGGCTGTGAGACAAATTTGGCC 621
 Db 140 GlyLeuPheThrIleIsthProSerIleuAlaSerIleuSerIleuSerIleuIleuGly 159
 QY 622 TCTTAGAAGACTTCCCTATTTGACAGCTTATTAACCTTAAAGAACTCAATGTGGCTCAC 681
 Db 160 ArgLeuGlnIyLeuIleuPheGlnIyLeuSerIleuThrAspIleuIleuGlyTrp 179
 QY 682 AATTTT-----ATKATTTCTCT 639
 Db 180 AsnSerIleuValIleuProAspThrValPheGlnIyLeuGlnIyAsnIleuHISgIleu 199
 QY 700 AAGTTA-----CTGCATATTTTTCATCTGACGAC 732
 Db 200 ValIleuAlaGlyAsnIyIleuThrIyTrIyLeuGlnProAlaIleuPheCysglIyLeuGlyIu 219
 QY 733 CTAGTACATGTGATCTTTCTTAACTATATTAACCTTAACTGACAAAGCATTAACAG 792
 Db 220 LeuArgIleuAspIleuSerIleuArgAsnIleuIyAsnIleuValIleuVal 239
 QY 793 TTCTTAGTGAATTAACCAAGTC---AATCTCTTGAACATGTCTTGAACCCAT 849
 Db 240 HisIleu-----ProArgIleuGlnIyIleuIyLeuIyAspIleuIleu-----Ile 254
 QY 850 GACTTCATCAAGACCAAGCCTTTCAGGAAATTAAG---CTCCATGAACCTGACTTAAGA 906
 Db 255 ThrIleValAlaProGlyAlaPheIleuGlnIyMetIyAlaIleuArgTrpIleuAspIleuSer 274
 QY 907 GGTAAATTTTAATAGCTCAAAATATATGAATAAATTCGCTTCAAACTGCTGTTTACAC 966
 Db 275 HisAsn---ArgValAlaGlyLeuMetGluAspThrPheProGlyLeuGlnIyLeuHis 293
 QY 967 GTCCATGGCTTGAATCTTGGCA-----GAATTTAAAGATGAA 1002
 Db 294 ValIleuArgIleuAlaHisAsnAlaIleAlaSerIleuArgProArgThrPheIyAspIleu 313
 QY 1003 AGGAATCTGGAATTTTGA-----CCCTCTATC 1032
 Db 314 HisPheIleuGlnIyLeuGlnIleuGlnIyHisAsnArgIleArgGlnIleuGlyIuArgThr 333
 QY 1033 ATGGAAGACTATGTGAT-----GTGACCATGTGATGATGAGTTTAACATATATA 1083
 Db 334 PheGlnIyLeuGlnIyLeuGlnIyValIleuThrIleuAsnIleuPheGlnIleuThrGlnIyVal 353
 QY 1084 AATGATTTTTCAGATGATATTTGATTTCAATGCTTGGCGAATGTTTCTGC---AAT 1139
 Db 354 Arg-----ValIleuAlaPheSerIyLeuPheAsnValAlaValMetAsn 368
 QY 1140 GTCCTGGCAGGTGATCTATAAATATCTAGAAGATGTTCTTAACATTTCAATGCGCA 1199
 Db 369 LeuSerIyIleuIleuCysIleuAspSerIleuProGlnArg-----ValPheGln----- 383
 QY 1200 ATCTTATCATCATTTAGATGTCAACTAAGACATTTTCAACTGTGATCTAACCTTTCTT 1259
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 QY 1260 AAAAGTTTGACTTTAATATGAACAAAGGCTTATAGTTTAAAAAAAGGCGCTTACCA 1319
 Db 384 -----GlyLeuAsp 386

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QY 1320 AGTCACGCTATCTAGATCTTGAAGAAATGCACTGAGCTTTAGTGCTGCTTTAT 1379
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Db 387 LysLeuH1SerLeuH1LeuGlnH1SerCysLeuGlnH1ValArgLeuH1SerPhe 406
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QY 1380 TGTGATTTGGGACAAACAGCTGGAGACATTGAACCTTCAGCTTAATGCT---GCCATC 1436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 407 Ala-----GlyLeuSerGlyLeuArgLeuPheLeuArgPheSerLeuSer 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1437 ATTATGAGTCGCAATTTGATGAGTGTAGAAAGCTGACAGCACTGATTTTTCAGCACTC 1496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 IleGlnGlnSerLeuAlaGlyLeuSerGlnLeuGlnLeuAsp-----Leu 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1497 TACTTTAAAAAGGCTCAGCAATTC-----TCAGCTTTTATTCCTTGAAGAACTACT 1550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 -ThrThrAsnArgLeuThrH1SerProArgGlnLeuPheGlnGlnGlyLeuGlnH1 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1551 TTACTTGACATCTCTTACTTAACACCAAAATGACTTCAGATGATATTCTTGGCTT 1610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 461 uTyLeuLeuLeuSerTyraGln-----Le 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1611 GACCAAGTCACACATTAATAAATGCTGCAATCTTTCAAGACACACCTTTCAAA 1670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 uThrThrLeuSer-----AlaG1 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1671 TGCTTTGCAAAACACAAACAACTTGACATTCCTGATCTCTTAATGCTAATTGACA 1730
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 uValLeuGlnProLeuGlnArgAlaPheTrpLeuAspIleSerH1AsnH1SerLeuGln 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1731 AATATCTTGGGGGATTTGACACCTTCATAGACTTCAATTAATTAATAGACTACAA 1790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 rLeuAlaGlnGlyLeuPheSerLeuGlyArgValArgTyraLeuSerLeuArgAsnAs 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1791 CAATCTA-----TTGTTTTGATTCATCCCA 1817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 nSerLeuGlnH1rPheSerProGlnProGlyLeuGlnArgLeuTrpLeuAspAlaAsnPr 536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1818 TTATACCACTGATTCCTCAGACACTTGATGCTGATTCATCGCATAGACATC 1877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 536 cTrp-----AspCysSer----- 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1878 TAAAGAAATACGCAACATTTTCCA---AAGAGTCGTACCTTTCTCAATCTTCAACAA 1934
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 -----CysProLeuTyraLeuArgPheAlaLeuGlnAsnPr 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1935 TTCGTGCTGTATATGTGAACATCAGAAATTCCTGACGTGGCTCAAGAA-----CA 1988
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 cGlyValVal-----ProArgPheValGlnThrValCysGlnGlyAsnAs 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1989 GAACAGCTTCTTGATGTGAATGTGAACAAATGACATGTGCAACACCTGTAGAGATGAAT 2046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 569 pCysGlnProValTyraThrTyraAsnAsnIleThrCysAlaGlnProAlaAsnValSer 588
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? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/487,072A
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: MURASHIGE, KATE H.
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 2550-0025.20
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? INFORMATION FOR SEQ ID NO: 50:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 603 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
? INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
? US-08-487-072A-50

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Query Match: 5.41% Indels: 176
DB: 4 Gaps: 26

US-09-396-985b-46 (1-2951) x US-08-487-072A-50 (1-603)

QY 322 TGCATGATCAGAAACTCAGCAAAATGCTGATGACATTCCTTTCAACCAACACATA 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 CysSerSerTyraSerLeuThrH1SerProAspAspIleProValSerThrArgAlaLeu 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 382 GATTCGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTATAGCTTCTCAATTTTGCAG 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 TrpLeuAspIlyAsnAsnLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSer 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 CTCACAGTGGCTGATTTATCCAGGTGGAATTAACATTAAGACAAAGCACTGGCAT 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeu 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 GGGTTACACCACTCTTCAAACTTGATGACAGAAACCTTACAGAGTTTTCCTCCA 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 GlyLeuGlnAsnLeuTyraThrLeuH1SerLeuGlnArgAsnArgLeuArgAsnLeuAlaVal 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 562 GGAAGTTCTCTGAGACTCAACAAGTTTGAACAATCTGGTGGCTGTGAGACAAAATTGGCC 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 GlyLeuPheThrH1SerProSerLeuAlaSerLeuSerLeuSerAsnLeuGly 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 622 TCTCTAGAAAGCTTCCCTATGAGACGCTTATTAACCTTAAGAAACTGATGGCTCAC 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 ArgLeuGlnGlnGlyLeuPheGlnGlyLeuSerHisLeuTrpAspLeuAsnLeuGly 179
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QY 682 AATTTT-----ATACATTCCTGT 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 AsnSerLeuValValLeuProAspThrValPheGlnGlyLeuGlyAsnLeuH1SerLeu 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 700 AAGTTA-----CTGCATATTTTTCATCTGACGAC 732
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 ValLeuAlaGlyAsnAsnLeuThrTyraLeuGlnProAlaLeuPheCysGlyLeuGly 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 733 CTAGTACATGTGATCTTTCTTATTAACCTATTAACAGTATCTGTCAGACGACTTACAG 792
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 LeuArgGlnLeuAspSerArgAsnAlaLeuArgSerValTyraAsnValPheVal 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 793 TTTCTACGTGAAATCCACAAAGTC---AATCTCTTTTGAACATGTCTTGAACCCCAATT 849
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Db 240 HisLeu-----ProArgLeuGlnIleuLeuTyrlleuSerArgLeu-----Ile 254
 QY 850 GACTTCATTCAGAACCAAGCCTTCAGGAATTAG---CTCCATGAACTGACTCTAGACA 906
 Db 255 ThrAlaValAlaProGlyAlaPheLeuGlyMetIleValAlaLeuArgTyrPheLeuAspLeuSer 274
 QY 907 GGTAAATTTTATAGCTCAAAATATATGATAAACTTGCCCTCAAAAACCTGGCTGGTTTACAC 966
 Db 275 HisAsn---ArgValAlaGlyLeuMetGlnAspThrPheProGlyLeuLeuGlyLeuHis 293
 QY 967 GTCCATCGGTGATCTTGGGA-----GAATTTAAAGATGAA 1002
 Db 294 ValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArgProArgTyrPheIleValAspLeu 313
 QY 1003 AGGAATCGGAAATTTTGA-----CCCTCATC 1032
 Db 314 HisPheLeuGlnIleuGlnLeuGlyHisAsnArgIleArgGlnLeuGlyValArgThr 333
 QY 1033 ATGACAGACTATGTGAT-----GTGACCATGATGAGTTCAAGTTAACTATACA 1083
 Db 334 PheGlnIleuLeuGlyGlnLeuGlyValLeuThrLeuAsnSerAsnGlnIleThrGlyVal 353
 QY 1084 AATGATTTTTCAGATGATGTTTAACTTCATTCCTTGGCGAATGTTTCTGC---AAT 1139
 Db 354 Arg-----ValGlyAlaPheSerGlyLeuPheAsnValAlaValMetAsn 368
 QY 1140 GTCTCTGGCAGCTGATCTTAATAATCTAGAAAGATGTTCTTAACATTTCAAAATGGCA 1199
 Db 369 LeuSerGlyAsnCyLeuArgSerLeuProGlyArg-----ValPheGln----- 383
 QY 1200 ATCCTATCAATCATTTAGATGTCAACCTAGACAGTTCCAACTGTGATCACTCTTCTT 1259
 Db 383 ----- 383
 QY 1260 AAAAGTTGACTTAACATGACAAAGGCTTATCATGCTTTAAAAAGGCCCTTACCA 1319
 Db 384 -----GlyLeuAsp 386
 QY 1320 AGTCTCAGTATCTAGATCTTAGAGAAATGCACTGACCTTAGTGCGCTGTCTTAT 1379
 Db 387 LysLeuHisSerLeuHisIleGlnHisSerCysLeuGlyHisValArgLeuHisIleThrPhe 406
 QY 1380 TCTGATTTGGGAAACAAACAGCCTGAGACACTTAGACCTCAAGTGT---GCCACT 1436
 Db 407 Ala-----GlyLeuSerGlyLeuArgArgLeuPheLeuArgAspAsnSerIleSerSer 424
 QY 1437 ATTATGATGCAATTTTCATGGCTTAAAGAGCTGACAGACCTGGAATTTTTCAGACATC 1496
 Db 425 IleGlnIleGlnIleSerLeuAlaGlyLeuSerGlyLeuLeuGlyLeuAsp-----Leu 441
 QY 1497 TACTTTAAAAAGGCTCACAGATTC-----TCAGCGTTCTTATCCCTTGAAAAAGCTACT 1550
 Db 442 -ThrThrAsnArgLeuThrHisIleuProArgGlnLeuPheGlnGlyLeuGlyHisLeuGly 461
 QY 1551 TTACCTTGACATCTTTATCTAACAACCAAAATTCAGTGTATATTCTTGGCTT 1610
 Db 461 uTyrLeuLeuLeuSerTyrAsnGln-----Le 470
 QY 1611 GACCACTGCAACACATTTAAAAATGCTGCAATCTTTCAAGACAAACACCTTTCAAA 1670
 Db 470 uThrThrLeuSer-----AlaGly 476
 QY 1671 TGTCTTTGCAAAACCAAACTTGACATTCCTGGATCCTTCTTAATGTCATTTGAAACA 1730
 Db 476 uValLeuGlyProLeuGlnArgAlaPheTyrPheLeuAspIleSerHisAsnHisLeuGlyThr 496
 QY 1731 AATATCTTGGGGGATTTGACACCCCTCATAGACTCAATTTAATTAATGAGTCAACA 1790
 Db 496 rLeuAlaGlnGlyLeuPheSerSerLeuGlyArgValArgTyrLeuSerLeuArgAsnAs 516
 QY 1791 CAATCTA-----TTGTTTTTGATTCATCCCA 1817
 Db 516 nSerLeuGlnThrPheSerProGlnProGlyLeuGlnArgLeuTyrPheLeuSerPheAlaAsnPr 536

QY 1818 TTATTAACAGCTGATATTCCTCAGACACTCTTATGACAGTTTCAATGCATAGACATC 1877
 Db 536 oTTP-----AspCysSer----- 540
 QY 1878 TAAAGAAATCTGCAACATTTTCCA---AAGACTTACGCTTCTTCAATCTTACTAACA 1934
 Db 541 -----CysProLeuIysAlaLeuArgAspPheAlaLeuGlnAsnPr 554
 QY 1935 TTCTGTCTTGTATATGTGACATCAGAAATTCCTGACGTGGCTCAAGGA-----CA 1988
 Db 554 oGlyVal-----ProArgPheValGlnThrValCysGlnIleIysAspAs 569
 QY 1989 GAACAGTCTCTGTGAATGTGACAAATGTCATGTCGAACCTGTGAGATGAT 2046
 Db 569 pCysGlnProValTyrThrThrAsnAsnIleMetCysAlaGlyProAlaAsnValSer 588
 RESULT 11
 US-09-353-585-2
 ; Sequence 2, Application US/09353585
 ; Patent No. 6287865
 ; GENERAL INFORMATION:
 ; APPLICANT: Dixon, Mark S
 ; Jones, David A
 ; Jones, Jonathan DG
 ; TITLE OF INVENTION: Plant pathogen resistance genes and uses
 ; thereof
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Nixon & Vanderhye PC
 ; STREET: 8th Floor, 1100 No. 6287865th Glebe Road
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: United States of America
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/353,585
 ; FILING DATE: 15-Jul-1999
 ; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
 ; 1/68
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/930,277
 ; FILING DATE: 27-OCT-1997
 ; APPLICATION NUMBER: PCT/GB96/00785
 ; FILING DATE: 01-APR-1996
 ; APPLICATION NUMBER: GB 950658.5
 ; FILING DATE: 31-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ms Mary J Wilson
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 620-69
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4100
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1112 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEetical: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Tomato
 ; STRAIN: Cf2
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-353-585-2

Alignment Scores:

Pred. No.: 3,56e-20 Length: 1112
 Score: 276.00 Matches: 201
 Percent Similarity: 36.05% Conservative: 118
 Best Local Similarity: 22.71% Mismatches: 312
 Query Match: 5.33% Indels: 255
 DB: 3 Gaps: 37

US-09-396-985B-46 (1-2951) x US-09-353-585-2 (1-1112)

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DB 319 SerIuSnmAlaLeuAnSnglySerIleProAlaSerLeuGlyAenLeuYAsnLeuSer 338
QY 78 ----TTGAATATAGTACTTGAGAGGGGACCCACTGGGAGAGAGGACAGTGTCCAG 134
DB 339 ArgLeuAnLeuVal-----AsnAnSnglLeuSerGlySerIleProAlaSerLeu 355
QY 135 GGACTTCGCTGCACCAAGT-----TACAGATGCTATGTTCTCTATGGCTTCACAT 188
DB 356 GlyAnLeuAnLeuAnLeuSerMetLeuYrIeUyRhaAnSnglLeuSerGlySerIle 375
QY 189 GGTTCAGAAAATGCCAGATGATGCTCCCTGCTCCTGCTAGAGACTTGATCATGCGC 248
DB 376 -----ProAlaSerLeuGlyAen-LeuAnAnLeuSerMetLe 388
QY 249 ACTGTTCTCTCCTGCTGCACACAGAGGTTGAATCCCTGATAGAGTATCTCTA 308
DB 388 uYrLeuYrAsnAnSnglLeuSerGlySerIleProAlaSerLeuGlyAenLeuAnAs 408
QY 309 TATTAC-----TACCAATGATGATGATCAAGAACTCAGCAAACTCCCTGATGATCC 362
DB 408 nLeuSerArgLeuYrIeUyRhaAnSnglLeuSerGlySerIleProGluGluIleG 428
QY 363 T-----TCTTCAACCAAGAAATATAGATCTTGAGCTTGAAGATCTTAAAG 416
DB 428 YrIeUyRhaSerLeuThrYrIeUyRhaSerLeuSerArgLeuGlyPheIlePr 448
QY 417 CTATAGTTCTCCCACTTTTTCAGAACTTTCAGTGGCTGATTTATCCAGGTGTAATGA 476
DB 448 AlaSerPheGlyAsnMetSerAnLeuAlaPheLeuPheLeuYrGluAnSnglLeuAl 468
QY 477 AACATTTGAAGACAGCATGTCATGGCTTACACCACTCTCAAACTTGATGATGACAGG 536
DB 468 aSerSerValProGluGluIleGlyYrIeUyRhaSerLeuAnValLeuSerLeuSerG 488
QY 537 AAACCTTACCAAGTTTTCCTCCAGAGAGTTTCTGACCTAAACAAGTTTGAACAATCT 596
DB 488 uAnAlaLeuAnSnglySerIleProAlaSerPheGlyAenLeuAnLeuSerArgLe 508
QY 597 GGTGGCTGTGAGACAAAAATTTGGCTCTCTAGAAAGCTTCCCTATTTGACAGCTTAAAC 656
DB 508 uAnLeuValAsnAnSnglLeuSerGlySerIleProGluGluIleGlyYrIeUyRhaSge 528
QY 657 CTTTAAAGAACTCATGTCATCAATTTTATATACATTCCTGTAAGTTACCTGCATATTT 716
DB 528 rLeuAnValLeuSerLeuSerGluAnAlaLeuAnSngly----SerIleProAlaSerPh 547
QY 717 TTCCAATCTGACAGAACTTATGATGATGATCTTTCTTATATATATATTAACAATTATAC 776
DB 547 eGlyAnLeuAnLeuAnLeuSerArgLeuAnLeuValAsnAnSnglLeuSerGlySerI 567
QY 777 TGTCACGACTTACAGTTTCTAGCTGTAATTCACAAGTCAATCTCTCT----- 825
DB 567 eProGluGluIleGlyYrIeUyRhaSerLeuAnSnglLeuSerGlySerLeuAnAla 587
QY 826 -----TTAGACATG----- 834
DB 587 uAnSnglySerIleProAlaSerLeuGlyAenLeuAnSnglLeuSerMetLeuYrLeuY 607
QY 834 ----- 834
DB 607 rAnAnSnglLeuSerGlySerIleProGluGluIleGlyYrIeUyRhaSerLeuThrY 627

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QY 835 -----TCTTTGAAAC-----CCAATTGACTTCATTTCAAGACA 866
DB 627 rLeuSerLeuGlyAenAnSnglLeuAnSnglLeuIleProAlaSerPheAlaAnMetAr 647
QY 867 AGCTTTTCAAGGAATTAAGTCCATGAACTGACTTAAGAGTTAATTTTAATAGTCA-- 924
DB 647 gAnLeuGluAlaLeuIleLeuAnSnglLeuAnSnglLeuIleGlyGluIleProSerSerVa 667
QY 925 -----AATTAATGA-- 936
DB 667 lCyAnLeuThrSerLeuGluValLeuYrMetProArgAnSnglLeuYrGlyYrVa 687
QY 937 -----ACTTGCTTCAAAACCGGCTGTTTACACGTCATCCGTTGATCTTGAGAAAT 992
DB 687 lProGluCysLeuGlyAenIleSerAnLeuGluValLeuSerMetSerAnSerPh 707
QY 993 TAAAGATGAAAGAAATGTGAAATTTTGAACCTCTATCATGAGAGACTATGTGATGT 1052
DB 707 eSerGlyGluLeu-----ProSerSerIleSerAnLeuThrSerLe 721
QY 1053 GACCATTTGATGATTCAGTTAACAATATACAAATGATTTTCAGATGATTTGTAAGTT 1112
DB 721 uGluIleLeuAnSnglLeu-----ArgAnSnglLeuGluGlyAlaIleProGlu-- 737
QY 1113 CCAATGCTTGGCGAATGTTTCTGCAATGCTCTG----- 1146
DB 738 ----CysPheGlyAenIleSerSerLeuGluValPheAspMetClnAnSnglYsLeuSe 756
QY 1147 -----GCAGGTGATCTATTAATATCTA----- 1170
DB 756 rGlyThrLeuProThrAnSnglLeuIleGlyCysSerLeuIleSerLeuAnLeuHISgl 776
QY 1171 -----GAGATGTTCTTAAACATTTT-----AATGGCAATCTT 1205
DB 776 yAnSnglLeuGluAspGluIleProArgSerLeuAspAnSnglYsLeuGluValLe 796
QY 1206 ATCAATCATTAAGATGATCAATAAGC---AGTTTCCAACCTGAT-----CTACCTT 1255
DB 796 uAspLeuGlyAspAnSnglLeuAnSnglPhePheProMetTrpLeuGlyThrLeuProG 816
QY 1256 TCTTAAAGATTTGACTTAACTATGAAACAA-----GGGTCTATC-----AGTTTAA 1303
DB 816 uLeuArgValLeuArgLeuThrSerAnSnglYsLeuHISglProIleArgSerArGAl 836
QY 1304 AAAAGTGCCCTTCAAGTCTCAAGTATCTAGATCTTATGAAATGACACTGAGCTTAA 1363
DB 836 aGluIleMetPheProAspLeuArgIleIleAspLeuSerArgAnAlaPheSer----- 854
QY 1364 TGTGGCTGTTCTTATTTGATTTGGGAACAAACAGCTGAGACACTTAACCTCAGCTT 1423
DB 855 -----GlnAspLeuProThrSerLeuPheGluHISleu----- 865
QY 1424 CAATGGTCATCATTAATGATGTCACAAATTTCAATGGCTGTAAGAGCTGACGACCTGGA 1483
DB 866 -lYsGlyMetArgThrValAspYrThrMetGluGluProSerTrpGluSerYrYrAs 885
QY 1484 TTTTTCACGACTTACTTAAAGAGGTCACAGAATTTCTGAGGTTCTTATCCCTTGAA 1543
DB 885 pAspSerValValValThrYrGly--LeuGlu-----LeuGluIleValA 901
QY 1544 AGCTACTTATCTTGAATCTCTTATATCTTAACACCAAAATTTGACTTGATGATATTC 1603
DB 901 rGluLeuSerLeu-----YrThr----- 907
QY 1604 TTGGCTTACCAAGTCTCAACATCAATAAATGGCTGCAATTTCTTCAAGACACACACC 1663
DB 908 -----ValIleAspLeuSerSerAnSnglYsPheGluGlyHISle-- 920
QY 1664 TTTCAATGTCTTTGCAACACAAACAAACTTGAATTTCTGATCTTCTTAAATGTCAT 1723
DB 921 -----ProSer----- 922

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537 AAACCTATCCAGAGTTTTCCTCCAGAGAGTTTCTGCACTAACCACTTATGACCAACT 596
 488 uasnalaenleuenglyserileprolaserpheglyasnleuasnleuenserargle 508
 597 GGTGGCTGTGAGACAAATGCGCTCTCTAGAAAAGCTTCCCTATTGACAGCTTATAC 656
 508 uasnleuvalasnleuenglyserileprogluileglytyrleuargse 528
 657 CTTAAGAACTCAATGCGCTCAACATTTTATACATCTGTAAAGTACCTGCAATATT 716
 528 rleuasnvalleuasnleuenserleuasnalaenleuenglyserileprolaserph 547
 717 TTCAATCTGACGAACCTAGTATGATGATCTTTCTTATACATATATCAACTATAC 776
 547 eglyasnleuasnleuenserargleuasnleuvalasnleuenglyserile 567
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 834 ----- 834
 607 rasnleuenglyserileprogluileglytyrleuenserleuthrty 627
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 687 lproglucysleuenglyasnleuenserasnleuenglyvalleuensermetse 707
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 721 ugnleuasnleuasnleuengly-----argasnleuenglyvalleuileproglin-- 737
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 738 ----Cyspheglyasnleuenserleuenglyvalpheasmetclynasnleuengly 756
 1147 -----GCAGGTGATCTTATAAATACTA----- 1170
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 1171 -----GAAGATGTTCTTAAACATTTCT-----AATGGCAATCTT 1205
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836 agluileuetherpheproasnleuarglyleileaspleuenserargasnalaephser----- 854
 1364 TGTGGCTGTCTTATCTGATTTTGGAGACAAACAGCTGAGACCTTATGACCTACACT 1423
 855 -----GlnaspleuProthrSerleuPhegluileu----- 865
 1424 CAATGTCGATCATTTATGAGTGCATTTTCAATGGCTGTAAGAGCTGACACCTGGA 1483
 866 -lysglymetcargthrvalaspleuymetcgluileuileuileuileuileuileuileu 885
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 885 paepservalvalvalthrlysgly-leuileu-----leuileuileuileu 901
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 901 rglyleuenserleu-----tythr----- 907
 1604 TTGGCTTGACCACTGACATCAACATTTAAATGGCTGCAATTTCTTCAAGACACACC 1663
 908 -----Valileaspleuenserasnleuasnleuasnleuasnleuasnleuasnleu 920
 1664 TTTCAAATGCTTTGCAACACAAACAACTTGACATTCCTGATCTTCAATGTCAT 1723
 921 -----Proser----- 922
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 923 -----Valleuenglyasnleuileuileuileuileuileuileuileuileuileu 936
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 956 erleuasnleuenserpheasnleuenser-----glyluileuileuileuileuileuileu 970
 1904 AGAGCTTACCC-----TTCTCAATCTTATCAACATTTCTGTT--G 1942
 970 lngluileuileuileuileuileuileuileuileuileuileuileuileuileuileuileu 990
 1943 CTGTATATGTAACATTCAGAAATTCCTGACAGTG- 1977
 990 lcyserileproglinleuileuileuileuileuileuileuileuileuileuileuileuileu 1010
 1978 -----GTCAAGGACAGA 1990
 1010 spglyleuasnleuileuileuileuileuileuileuileuileuileuileuileuileuileu 1030
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 1030 snlythrvalaseraleuenglyasnleuileuileuileuileuileuileuileuileu 1044
 2051 CTTAGTGTGATTTTAAATTAATTTACCGTTATATGTCAGAGCA-----ATCATCA 2104
 1044 lurbpheasnleuasnleuasnleuasnleuasnleuasnleuasnleuasnleuasnleu 1064
 2105 GTGTGACAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
 1064 lytleuileuileuileuileuileuileuileuileuileuileuileuileuileuileu 1083
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 1083 lreileuenglyleuenglyleuileuileuileuileuileuileuileuileuileuileu 1101
 2210 GAGAAAGCATCTAT 2223
 1101 lylglnargasnlyr 1105

RESULT 13
 US-09-191-647-2


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Db      676 Arglylsarsgllvalthrglyasnproargcysglnlyrsprotyrphleuyluglu 695
Qy      1654 -----GACAC 1659
Db      696 lIleprollleqlnarpvalalalleglnsrphethrcysarbargllysnarpsasn 715
Qy      1660 ACCCTTTCAATGCTCTTGGCAACAACAACCTTGAATCTCGATCTCT----- 1710
Db      716 Serlyserproleuserargcysprothrlucysrthrcysleuabrrthlvalvalrg 735
Qy      1711 ---TCTAATGTCATTTGGAAACAATCTTGGGGGTA----- 1746
Db      736 Cysersasnlysglyleuylvalleuvalprolyslleproargarvalthrglyleu 755
Qy      1747 -----TTGACACCTCCATAGACTT 1767
Db      756 Tytleuabrglyasnlnphethrleuvalprolysglyleuseranlyrlyenileu 775
Qy      1768 CAATTATTAATATGATGACACAAATCTATTTGTTGATTCATCCCATTAATACAG 1827
Db      776 Thrlleuileasrleuserasnandrglleserthleuserannglnserphesasn 795
Qy      1828 CTGTATTCCTTCAGACACTTTGATTCAGTTTCAATGCGATA-----GAG 1872
Db      796 Metthrglnleuethrleuileuserlyasnargleuargcyslleproproarg 815
Qy      1873 ACATCTTAAGGAATATCGCAACATTTCCAAAGCTTAGGCTTTCATCTTACTTAAC 1932
Db      816 Thrphesbrglyleu-----lysersleuargleuuserleuilegly 830
Qy      1933 AATTCTGTGCT----- 1944
Db      831 Asnhsrpleaserlvalproglnglyalrphesasnleuseralaleuserhleu 850
Qy      1945 -----TGTATATGTAACATCGAAATCTTCGACGTGGGTC 1980
Db      851 Alalleglylaasnproleuylrcysarpcysasnmetglntrleuserabrrtrval 870
Qy      1981 AAGGAACAG----- 1989
Db      871 Lysserglnlyrlysglnproglyllealargcyslaaglyproglylmetvalasr 890
Qy      1990 AACCAAGTCTTGCGAAT---GTTGACAAATGATGTCAGACACCTGTAGAGATGAT 2046
Db      891 Lysleuileuethrthrproserlylyserthrcysglnnglyprovalasrvalasn 910
Qy      2047 -----ACC 2049
Db      911 lIleuualalyscysasnprocysleuserasnprocyslysnarbrgllythrcysasn 930
Qy      2050 TCCTTAGTGTGATTTTAATATTTCACTGT---TATATGACAAAGACAT----- 2099
Db      931 Serasrprovalasrphethrcysrthrcysrprolyrlyrphelysglylnarpcys 950
Qy      2100 -----CATCAGTGTGACAGGTGATGATGATGATGATGATGATGATGATGAT 2147
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Qy      2148 TCTGATATACACTTCTATTTTCACTGATATCTTATGCTGGCTGTAAAAAGTACACAG 2207
Db      971 Lysglu-----glyglnglyabrglyrphetr----- 979
Qy      2208 AGAGAAAGCATGTATGATGATTTGT---GATCTACTCGATGACAA 2252
Db      980 -----Cysllecyalaasrlyrphednglyglu 989

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RESULT 14
US-09-540-245A-2
; Sequence 2, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey

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; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; PRIOR APPLICATION NUMBER: 2000-03-31
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PR
; ORGANISM: human
US-09-540-245A-2

Alignment Scores:
Pred. No.: 8 02e-20 Length: 1525
Score: 273.50 Matches: 175
Percent Similarity: 31.63% Conservative: 109
Best Local Similarity: 19.49% Mismatches: 294
Query Match: 5.28% Indels: 321
DB: 3 Gaps: 32

US-09-396-985b-46 (1-2951) x US-09-540-245A-2 (1-1525)
Qy      160 GATCGTCATGTTCTTCATGAGCTCCATCTGTTGCAAAAATGCGAGATATGCTCC 219
Db      214 AspCysHis---LeuAlaTrp-----LeuserAsp 222
Qy      220 TGGCTCTGCTGAGCTGAGCTGATCATGCACTGTTCTTCTGCTGCAACGAGAAC 279
Db      223 Trpleuarglysrproargval---Glyleuylthrglnlysmetglnproserhis 241
Qy      280 TTGAAT----- 285
Db      242 Leuargglyhisasnvalalaglyvalglnlyargluabrglyrphelvalcysserabrglylu 261
Qy      286 -----CCCTGCATAGAG 297
Db      262 Glnglyhisglnserphemetalaoprosercyservalneuiscysproallaacy 281
Qy      298 GTAGTCTTATATTTACCTTCCATGATGATGATGATGATGATGATGATGATGATGAT 357
Db      282 Thrcysersasnasnillevalasrlyserglylyserglyleuylleuylleuylleuyl 301
Qy      358 ATTCTCTTTCACCAACAAGCATGATCTGACCTCAACCCCTTGAGATCTTAAAAAGC 417
Db      302 Leuproglythrthlethrglylleargleuglnghasnhrthleuyllysvalleupro 321
Qy      418 TATAGCTTCTCATATTTTTCAGAACTTCAGATGCTGATGATTTATCCAGTGTGAATTGAA 477
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Qy      478 ACAATGGAAGACAGAGGATGCTTACACCACTTCAACCTTCAACCTTCAACCTTCAAC 537
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Qy      538 AACCTTATCCAGAGTTTTCACAGAGAGTTTCTGAGATTAACAAGTTTATGACAAATCTG 597
Db      362 Asnlyrlethrglyleuvalprolyrlyrlyrlyrlyrlyrlyrlyrlyrlyrlyrlyrly 381
Qy      598 GTGGCTGTGAGACAAAAATGAGCTCTTGAAGAGCTTCCCTATTTGACAGCTTATTAAC 657
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Qy      658 TTAAGAAACTCAATGTGCTGACAAATTTATATATCTCTGTAAGTTACTGATATTTT 717
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QY	778	GTCAACGACTTACAGTTTCTACGTGAAATCCACAGCAATCTCTTTAGACATGCT	837
Db	417	LyseGlythrPheSerProleuArlalleglnthmethSlleu-----Ala	432
QY	838	TTGAACCAATTTGACTTCTATTCAGACCAAGCCTTTCAGGAAATTAAG----	891
Db	433	GlnasnPro-----PheIleCysaspCysHsleuYstrPleuAlaAspTyleuHs	450
QY	892	GAACGACTTAAAGGTAATTTTAATGCTCAATAATTAAGAAACCTGCTTCAAAC	951
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QY	952	CTGGCTGGTTTACACGTCCATCGGTTTGATCTTGGAGAGATTTAAAGTAAGAATCTG	1011
Db	467	LeuAlaasnYrAsnGlle-----GlyGlnIleYrSerYrLys-----	479
QY	1012	GAATTTTGAACCTCTATCATGAGAGAACTAATGTATGTACCAATTAATGACTTCAG	1071
Db	480	-----PheArg	481
QY	1072	TTAACATATACAAATGATTTTTCAGATGATATGTTAAGTTCATGCTTGGCCAAATCT	1131
Db	482	CysSerGlyThrGlnAspTyrArgSerYrLys-----SerGlyAspCysPheAlaAsp	500
QY	1132	TCTGCAATG-----TCTGCGACGGGTGTTCATTAATAATCTA	1170
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QY	1171	GAAGATGTTCTTAAACATTTCAATGAGCAATCTTATCAATCATTAATTAATGATCAAC	1230
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QY	1231	AGTTTCCAACTGTGAT-----CTACCCCTTTCTTAAAGTTGA	1265
Db	540	IupHrThrValleuGlnAlaHrThrGlyIlePheYrYrLeuProGlnleuYrGlySlleA	560
QY	1270	CTTTAATCATGAAACAAGGCTCATCAGTTTAAAAAGTGGCCTTACCAAGTCTCAGCT	1329
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QY	1330	ATCTAGATCTTATGTAAGAAATGCACTGAGCTTTAGTGGTGGCTGTCTTATTTCTGATTTGG	1389
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QY	1380	GAACAACAAGCCTGAGACACTTATGACCTCAGCTCAATGTGTCCATCTATTATGAGTGCCA	1449
Db	586	HrSerAsnArgleuGlnAsn-----ValGlnHsIleYrAsn	597
QY	1450	ATTTCATGGGTGTATAGAGAGCTGACGACCTGTGATTTTTCAGACACTTATTAAGAAAG	1509
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QY	1510	GTCAAGAAATCTCAGCTTTCTTATCCCTTGAAGAACTACTTATTCAGACATCTCTTAT	1568
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QY	1570	ACTTAACACCAAAATTTGACTTGCATGGTATATTTCTTGGCTTGACCAAGTCTCAACATTA	1628
Db	636	AsnGlnIleHrThrValaIaProGlnIaPheAspHrThrLeuHsSerleuSerHrLeu	655
QY	1630	AAAATGGCGTGAATTTCTTTCAA-----	1653
Db	656	AsnleuLeuAlaAsnProPheAsnCYasnCYrYrleuAlaIaTrPleuGlyGlnTrPleu	675
QY	1653	-----	1653
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QY	1654	-----GACAAC	1655

Db	696	ILlerolleGlnAspValAlaIleGlnAspPheThrCysAspAspGlyAspAspAsp	715
QY	1660	ACCCGTTCAAAATGCTTTGGCAACAACAATCTGACATTCCTGGATCCT	1710
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QY	1711	---TCTAAATGTCATTTGGAAACAATATCTGGGGGGTA	1746
Db	736	CysSerAsnLysGlyLeuLysValLeuProLysGlyLLeProArgAspValThrGlyLeu	755
QY	1747	---TTTGAACCCCTCCATAGACTT	1767
Db	756	ThrLeuAspThrLysAsnGlnPheThrLeuValProLysGlyLeuSerAsnThrLysHisLeu	775
QY	1768	CAATTTATTAATATAGATCACAACAATCTATTTGTTGGATTCATCCATTTATACAG	1827
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QY	1828	CTGATATTCCTCAGACACTCTTGATTTGAGATTTCAATGCGATA	1872
Db	796	MetThrGlnLeuThrIleuThrIleLeuSerThrAsnArgGlyLeuCysIleProArg	815
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Db	816	ThrPheAspGlyLeu	830
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Db	871	LysSerGluThrLysGluProGlyIleAlaArgCysAlaGlyProGlyGluMetAlaAsp	890
QY	1990	AAGCAGTCTTGATGTAAT--GTTGAAACAATGACATGTGCAACACCTGTAGAGATGAAT	2046
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QY	2208	AGGAGAAAGCATATATGATGATTTGT---GATCTACTCAGATGAGAA	2252
Db	980	---	989
<p>RESULT 15 US-09-540-153-2 ; Sequence 2, Application US/09540153 ; Patent No. 6270995 ; GENERAL INFORMATION: ; APPLICANT: Goodman, Corey ; APPLICANT: Kid, Thomas ; APPLICANT: Brose, Katja ; APPLICANT: Tessier-Lavigne, Marc ; TITLE OF INVENTION: Modulating Robo: Ligand Interactions</p>			

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; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,153
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/191,647
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: human
US-09-540-153-2

Alignment Scores:
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Score: 273.50 Matches: 175
Percent Similarity: 31.63% Conservative: 109
Best Local Similarity: 19.49% Mismatches: 294
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DB: Gaps: 32

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QY 280 TTGAAT----- 285
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QY 952 CTGGCTGTTTACACCTCCATCGGTTGATCTTGAGAGAAATTTAAAGTGAAGAAATCTG 1011
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Qy	1933	AATCTGTGTGCT-----	1944
Db	831	AsnAspIleSerValValProGluGlyAlaPheAsnAspLeuSerAlaLeuSerHisLeu	850
Qy	1945	-----TGATATGTGAAACATCAGAAATTCCTGACAGTGGCTC	1980
Db	851	AlaIleGlyAlaAsnProLeuTyrCysAsnProCysAsnMetGlnTrpLeuSerAspTrpVal	870
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Qy	2047	-----ACC	2049
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Job time : 79.9256 secs

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Db	90	TyrTrpIleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr	109
QY	535	GGAAACCCCTATCCAGAGTTTTCCCGCAAGAAAGTTTCTCGCATACAACTTATAGACAAAT	594
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QY	895	CTGACTCTAAGAGGTAAATTTTAAATAGCTCAATAATATATGAAAACTTGCCTTCAAAACCTG	954
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Db	227	Leu-----AsnPheGlyGlyThrGlnAsnLeuValIlePheLysGlyLeu	242
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QY	1192	-----AAATGGCAATCCTTATCATATC	1212
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Qy	1563	CTTTTATCTATACACCCAAATTTGACTGCGATATTTCTTGAGCTTGACACAGTCTGAA	1622
Dd	452	uSerLlserLeuLeuAspLlserSerSerGlnGlnLeuPheAspLylLeuProAlaLeuG	472
Qy	1623	CACATTTAAATAGGCTGGCAATTTCTTTCAAGACAAACCCCTT-----TCAAATGCTT	1676
Dd	472	nHlLeuAsnLeuGlnLysAsnHlSpreProLysGlyAsnHlLeuLysThrAsnSerLe	492
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Dd	492	uGlnThrLeuGlyArgLeuGlnLleLeuValLeuSerPheCysAspLeuSerSerLleAs	512
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Qy	1797	ATTGTTTGGAT-----TCATGCCATTAAACACAGCTGATTCCTCCAGACTCT	1847
Dd	532	uThrSerSerSerLleGlnAlaLeuSerHlSleuLysGlyLylLeuYr-----Le	548
Qy	1848	TGATTTGACATTTCAACGATGCATAGACATGCTAAAGAAATCTGCACATTTTCCAAAGAG	1907
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Qy	1908	TCTAGCCTTCTTCAATCTTACTAACAATCTGTTGCTTGATATGATGACATCAAAATTT	1967
Dd	568	nGlnArgThrLleAsnLeuArgLlnAsnProLeuAspCysThrCysSerAsnLlLeuYrH	588
Qy	1968	CTTCAGATGGGTCAAGGACAGAAAGCATCTTGCTGAATCTTGAACAAATGACATGTGC	2027
Dd	588	eLeuGlnLlTrpLylLysGlnAsnMetGlnLysLeuGlnAspThrGlnLyspThrLeuCyG	608
Qy	2028	AACACCTGTAGAGATGAAT-----ACCTCGTAGCTGTGGATTTTAATATATTC	2075
Dd	608	uAsnProProLeuLeuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAl	628
Qy	2076	TACCTGTTATATGTACAAGACAATCATCAGTGTGTCAGTGTCAGTGATGTGTATC	2135
Dd	628	aAlaValGlyLlPhePheLeuLleValPheLeuLeuValPheAlaLleLeuLeuLlPhe	648
Qy	2136	CACGTGTACATTTCTGATATACCACTTCTATTTTCACTG	2175
Dd	648	eAlaValLysTrpPheLeuArgTrpLylYrGlnHlSle	661
RESULT 2			
Toll protein-like receptor DKFPz54710610.1 - human			
CtSpecies: Homo sapiens (man)			
CtDate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004			
CtAccession: T08664			
R.Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wilmann, S.			
submitted to the Protein Sequence Database, May 1999			
A.Reference number: Z16466			
A.Accession: T08664			
A.Molecule type: mRNA			
A.Residues: 1-786 <POU>			
A.Cross-references: UNIPROT:Q15399; EMBL:AL050262			
A.Experimental source: fetal brain; clone DKFPz54710610			
C.Genetics:			
A.Note: DKFPz54710610.1			
Alignment Scores:			
Pred. No.:	4,81e-25	Length:	786
Score:	426.50	Matches:	194
Percent Similarity:	41.32%	Conservative:	144
Best Local Similarity:	23.72%	Mismatches:	324

Query Match:	8-24*	Indels:	157
DB:	2	Gaps:	31
US-09-396-985B-46 (1-2951) x T08664 (1-786)			
QY	GAATTTGAAACATTTGAAACAGGACATGAGCTTACACACACCTTCAAACTTGATG		528
Db	469 GAAATTTGAAACATTTGAAACAGGACATGAGCTTACACACACCTTCAAACTTGATG		528
	24 GAGTGGTGTGCTGGTGGAGACAAATTTGGCTCTTGAAGAGCTTCCATTGTGACAG		648
QY	529 CTGACAGAAACCTTATCCAGATTTTCCCGAGAACTTCTGTGACTACAACTTGA		588
Db	40 -----ProlysAspLeuSerGlnThrIle		49
QY	589 GACATCTGTGGCTGGTGGAGACAAATTTGGCTCTTGAAGAGCTTCCATTGTGACAG		648
Db	50 LeuSniIle-----SerGlnAsnIylIleSerGlnLeuThrIleSerAspIleLeuSer		67
QY	649 CTTATTAACCTTAAAGAACTCAATGTGGCTCAATTTTATATCATCTCTGTAGTACCT		708
Db	68 LeuSerIylLeuAspGlnIleLeuIleIleSerHisAsnIylGlnIylLeuAspIleSer		87
QY	709 GCATATTTTCCCATCTGACGAAACCTTACATGTGATCTTTCTTATATCATATTTGAA		768
Db	88 ValPheIylPheAsn-----GlnGlnIleuGlnIylLeuSerIleSerHisIleuVal		106
QY	769 ACTATTATGTGCACGACTTACAGTTTCTACGTGAATCCAAAGTCAATCTCTC---		825
Db	107 LysIleSerCys-----HisProthValAsnIleuSerHis		118
QY	826 TTAGACATCTCTTGTGAACCCCAATGTACTTTCAAAGCAAGCTTTCAGGGAATTAAG		885
Db	119 LeuAspLeuSerPheAsnAlaPheAspAlaLeuProIleCysIylGlnPheIyl---Asn		137
QY	886 CTCATGACATGTACTTAAAGAGTATTTTAATAGCTCAATATATATGAATAAATTGCTT		945
Db	138 MetSerGlnIleuIylPheIleuGlnIyl---LeuSerThrIleHisIleuGlnIylSerSerVal		156
QY	946 CAAACCGCGCGGTGTACAGTCACATGCG-----TGATCTGGAGGAATTTAAAGAT		999
Db	157 LeuProIleAlaHisLeuAsnIleSerIylValIleuIleValIleuGlnIylThrIyl		176
QY	1000 GAAAGAACTGTGAAATTTTGAACCTCTATCATAGGAAGCATATGTGATGTGACCAT		1058
Db	177 GlnIylSerGln-----AspProIyl-----GlyLeuGlnAspPheAsnThr		189
QY	1060 GATGAGTTCAAGTTATACATAT---ACAATGATTTTTCAGATGATATTGTTAAGTTCCAT		1116
Db	190 GlnSerLeuHisIleIleValPheProThrAsnIyls-----GlnPheHis		203
QY	1117 TGCTTTGGCGAATGTTTTCGCAATGCTCTGCGAGGCTGATATATATAATATCTGAACAT		1176
Db	204 PheIleLeuAspValSerValIylThrValAlaAsnIleuGlnLeuSerAsnIleCys		223
QY	1177 GTTCTTAAACATTTTCAAAATGGCAATCCCTTATCAATCATATAGATGTCAATGACAGTT		1235
Db	224 ValLeuGlnAspSerIylCysSerIylPheLeuSerIleLeuAlaIylLeuGlnIleThrAsn		243
QY	1236 CCAACTCTGTGATCTACCTTTCTTAAAGTTTGACTTAACTATGATAAC-----		1283
Db	244 ProlysLeuSerSerLeuThrLeuAsnAsnIleGlnThrThrIleThrAsnSerPheIleArg		263
QY	1283 -----		1283
Db	264 IleLeuGlnIleuValIleThrIleThrValIleProIylSerSerIleSerAsnValIleu		283
QY	1284 AAGGGTCTATCAGTTTAAAAA-----GTGGCCCTTCAAGTCTCAGC		1328
Db	284 GlnIylGlnIleuAspPheArgAspPheAspIylSerGlnIylThrSerIleuAlaIleuSer		303
QY	1329 TATCTAGATCTTAAGTAAAGAAATGCACTGACCTTATAGTGGCTGTCTTATTTGATTTG		1388
Db	304 IleHisGlnIleValSerAspValPheGlnIylPheProGlnSerIylIleIylGlnIlePhe		323

QY	1389	GGAAACAACACCCGTGAGACAC-----	1409
Db	324	SerAsnMetValIleLysAsnProThrValSerGlyThrArgMetValHisMetLeuCys	343
QY	1410	-----TTAGACCTCAGCTTCAATGGTGCATCATATGATGATGCC	1448
Db	344	ProSerIleValIleSerProPheLeuHisIleuAspPheSerAspAsnIleuLeuThrAspThr	363
QY	1449	AATTTCATGGGT-----CTAGAAAGCTGACACCTGGATTTTTCAGCACTTAC	1499
Db	364	ValPheGluAsnGlySerGlyHisIleuThrGlyLeuGlu-ThrLeuIleLeuGlnMetAsnGln	383
QY	1500	TTTAAAAAGGTCACAGAAATTTCTAGCGTTTCTTATCC-----CTGAAAAGCTACTTTTACT	1556
Db	383	nIleuIleGlyIleuSerIleValIleGlnMetThrGlnMetIleSerLeuGlnIle	403
QY	1557	TGACATCTCTATATCTAACACCAAAATTGAC---TTGATGTGTATTTCTTGGCTTAC	1613
Db	403	uAspIleSerGlnAsnSerValSerTyrAspGlnLysIleValSerLysProCysSerTrpThrLys	423
QY	1614	CAGTCTCAACACATTTAAATAATGGCTGCGACATTTCTTTGAAAGACACACCCCTTGAATGT	1673
Db	423	SerIleuSerIleuSerIleuAsnMetSerSerAsnIleuThrAspThrIlePheArgCysLe	443
QY	1674	CTTTGCAAACACAAACAATTTGACATTCCTTGATTCCTTTCAATATGTCATTTGAAACAAT	1733
Db	443	u-----ProProArgIleLysValIleuAspLeuHisIleSerAsnLysIleLysSerIle	460
QY	1734	ATCTTGAGGGGGTATTATTTGACACCCCTCCATAGACCTTCAATTTATTAATATGATGCACACAA	1793
Db	460	eProLysGlnValVal--LysLeuGlnValIleuGlnIleuAsnValIlePheAsnSe	479
QY	1794	TCATATGTTTGGATTCATCCCATTTATTAACACAGCTGATATCCCTGACAGACTCTTGATTG	1853
Db	479	rIleu-----ThrAspLeuProGlyCysGlySerPheSerSerIleuSerValIleuIleI	497
QY	1854	CAGTTTCATGCATAGACATCTTAAAGAAATCTGCACACATTTCCAAAAGACTTACG	1913
Db	497	eAspHisAsnSerValSerHisProSerAlaAspPhePheGlnSerCysGlnLysMetArg	517
QY	1914	CTTCTTCAAATTTTCAACAATTTCTGTTGCTGTATATATGTAACATCGAATAATTCGCA	1973
Db	517	gSerIleLysAlaGlyAspAsnProPheGlnCysThrCysIleuLeuGlyIleuPheValLys	537
QY	1974	TGGGGTCAGAGAACAGAACAGCTTTGGTGGTAAGTTGACAAATATGACA-----	2022
Db	537	g-----AsnIleAspGlnValSerSerGluValLe	547
QY	2023	-----TGTCAACAACCTGTAGAGATGAATACCTCTTAGT	2057
Db	547	uGluGlyTyrProAspSerTyrLysCysAspTyrProGluSerTyrArgGlyThrLeuLe	567
QY	2058	GTTGGATTTTAAAT-----AATTTCACTGTTATATGTACAAGCAAT	2099
Db	567	uLysAspPheHisMetSerGluLeuSerCysAsnIleThrIleuLeuValIleThrIleVal	587
QY	2100	CATCAGATGTGCATGCTGATGTGATTTGGTATTCACATGTCATGATTTTGTATATACA	2159
Db	587	IAlaThrMetLeuValIleuAlaValIleThrValThrSerLeuCysIleTyrIleuAspLeuPr	607
QY	2160	CTTCTATTTTCACTGATACTTATTTGCTGCTGT-----AAAAAGTACAGACAGG	2210
Db	607	oTrpIleuArgMetVal-----CysGlnIleTrpThrGlnIleThrArgAArgAla	623
QY	2211	AGAAAGATC-----TATATGATCTTTTGAGCTA	2240
Db	623	aArgAsnIleProLeuGlnIleuGlnArgAsnLeuGlnPheHisIlePheIleSerTyr	643
QY	2241	CTTCAGTCAGATAGAGACTGGTGGAGAAATAGACTGTAAAGATTTTAGAA---GAAG	2297
Db	643	rSerGlyHisIleAspSerPheTrpValLysAsnGluIleuLeuProAsnIleuGlyLysGlu	663
QY	2298	AGTCCCGCGCTTTCACCTGTGCTTCACTACAGAGACTTTATTTCTGGTGTAGCCATTGC	2357

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Db      663 yme-----glutleCysleuH1eGluArgAnPheValProGlyLysSerIleVa 680
      ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      2358 TGGCAACATCATCCAGAAAGCGTCCCAAGAGCCGGAAGGTTATTTGTGAGTGTCTAG 2417
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      680 lGluAsnIlele---ThrCysileGlySerTylsSerIlePheValLeuSerP 699
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      2418 ACACCTTATTCAGACCGTGTGTATCTTATCTTGAATATGAGATGCTCAACATGCGAGTT 2477
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      699 oAnPheValGlnSerGlnTyrCysH1sTyrGlnLeuTyrPheAlaH1sAsnLeuPh 719
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      2478 TCTGAGACGCCCTCTGGACATCTTCATTCCTTTCAGAAAGTT--GAGAAAGTCCCT 2534
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      719 eH1eGluGlySerAnSerLeuIleLeuIleLeuGlnProIleProGlnTyrSerI1 739
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      2535 GCTAGACGACAGAGTGAATGTATTCGCTTTCAGCAAGAAACCTTACCTGAGAAAGGA 2594
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      739 eProSerSerTyrH1sLysLeuLysSerLeuMetAlaArgH1sTyrLeuGlnTyrP 759
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      2595 GGACATCTCTGGGAGGACATCTTTCGAGAAAGCTTAAATGACCCCTA 2646
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      759 oLysGlnLysSerLysArgGlyLeuPheTProAlaAsnLeuArgAlaIle 776
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A29943
R/Hashmoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A>Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, at
A/Reference number: A29943; MUID:88135760; PMID:2449285
A/Molecule type: DNA
A/Residues: 1-1097 <HAS>
A/Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:G158640; PIDD:AAA28941.1;
C/Genetics:
A/Gene: FlyBase:TL
A/Cross-references: FlyBase:FBgn0003717
C/Keywords: transmembrane protein
F/1-17/Domain: signal sequence #status predicted <SIG>
F/18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 1,596-22 Length: 1097
Score: 394.50 Matches: 201
Percent Similarity: 38.15% Conservative: 134
Best Local Similarity: 22.89% Mismatches: 296
Query Match: 7.62% Indels: 248
Gaps: 33

US-09-396-985B-46 (1-2951) x A29943 (1-1097)

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Qy      406 ATCTTAAAAAGATATAGCTTCTCCAAATTTTTCAGAACTTCAGTGCCTGATTTATCCAGG 465
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      404 G1Y1LeSerGlyAsp1LePheSerAnLeuGlyAsnLeuValThrLeuValMetSerArg 423
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      466 TGTGAATTTGAACAATTTGAAGCAAGGATGGCATGGCTTACACACCTTCACAACTTG 525
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      424 AsnArgLeuArgH1sLePheSerArgAlaPheValSerThrAnGlyLeuVal 443
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      526 ATATGACAGGAACCCCTATCCAGAGTTTTCGCCAGAAAGTTTCTGTGACATAACAAGT 585
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      444 H1sLeuAspH1sAsnAsp1LeAspLeuGlnPro-----Leu 456
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      586 TTAGACAATCTGTGCTGTGAGACAAATTTGACCTCTTGAAGAACTTCCTATTGGA 645
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      457 LeuAsp-----lLeuLeuGlnThrGlnlAsnSer-----ProPheGly 470
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      646 CAGCTTATTAACCTTAAAGAACTCAATGTGGCTCACAT-----TTTATACATTC 656
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      471 TyrMetH1eGlyLeuLeuThrLeuAnLeuValArgAsnAsnSer1Le1LePheValTyrAsn 490
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      697 TGTAAAGTTACCTGCATATTTTCCAAATCTGACGAACTGATCATGTGATCTTTCTAT 756
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      491 -----AspTyrLysAnThrMetLeuGlnLeuArgGlyLeuAspLeuSerTyr 506
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      757 AACTATATTCAACTATTAATCTGTCAGAACTTACAGTTTCTACGTGAATAATCCACAAGTC 816
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      507 AsnAnlnLeSerSerLeuGlyTyrGlnAspLeuAlaPheLeuSerGlnAn----- 523
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      817 AATCTCTTTAGACATGTCTTTGAACCCAAATGACTTCACT-----CAAGACCAAGCC 870
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      524 ArgLeuH1eValAlaMetCThrH1sAsnLys1LeAlaArgGly1LeAlaLeuProGlnAspVal 543
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      871 TTTCAGGAGATTAAGTCCCACTGAACCTCTGAAGGTAAATTTATAGCTCAAAATATA 930
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      544 H1sLeuGlyGlnGlyTyrAsnAsnAsnLeuValH1sValAspLeuAsnAspProLeu 563
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      931 ATGAAACCTTGC-----CTTCAAAACCTGGCTGCTTTCACAGTCCATCGG 975
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      564 ValCysAspCysH1rIleLeuTyrPheIleGlnLeuValArgGlyValH1sLysProGln 583
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      976 TTGATCTTGGAGATTAATTAAGATGAAGAAAT--CTGAAATTTTGAACCTCTATC 1032
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      584 ---TyrSerArglnPheLysLeuValArgThrAspArgLeuValCysSerGlnProAsnVal 602
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1033 ATGGAAGACATATGTATGTACCATGATGATGATGATGATGATGATGATGATGATGAT 1092
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      603 LeuGlnGlyThrProValArgGlnlLeGlnProGlnThrLeuIleCysProLeuAspPhe 622
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1093 TCAAGATATTTTGTAAATTCATGCTTGGCGAAATGTTTCTGCATATGCTCTGGCAGGT 1152
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      623 SerHsAspProArgGlnArgLysCysProArgGlyCysAsnCys----- 637
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1153 GTATCTATAAATATCTTAAGAAATGTTTCTTAAACATTTCAA--TGGCAATCTTATCA 1209
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      638 -----H1sValArgThrTyrAspLysAlaLeu 646
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1210 ATCATATAGATGTCAATTAAGCATGTTTCCAACTCGATCTTACACCTTTCTTAAAGTTGA 1269
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      647 ValIleAsnCysH1sSerGlyAsnLeu----- 655
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1270 CTTTAACATGACAAAGGCTATCACTTATTAATAAAGTGGCCCTACCAAGTCTCAGCT 1329
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      655 ----- 655
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1330 ATCTAGATCTTAGTAAGAAATGCACTGAGCTTATGTGTGCTGTCTTATTTGATTTGG 1389
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      655 ----- 655
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      1390 GAAACAACAGCTGAGACATTAAGACCTTCAAGCTTCAATGTGTGCATTAATAGAGTGCA 1449
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      656 -----ThrH1sValProArgLeuProAnLeu----- 664
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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OY 1450 ATTTCATGGCTCTAGAGAGCTGACGACCTGGATTCTTTCAGCACTCTACTTAAAG 1509
DB -----HisLeuAsnMetGlnLeu 670
OY 1510 GTACAGAAATTCAGCGCTTCTTATCCCTTGAAAAGCTACTTACTGACATCTCTTAT 1569
DB MetGlu-----LeuHisLeuGlnAsnAsnThrLeuLeuAlaArgLeuProSer 685
OY 1570 ACTAACCAAAATGACTGATGATGATATTTCTTGCTTGACAGCTGCTCAACATTA 1629
DB AlaAsnThrPro-----GlyTyrGlnSerValThrSerLeu 697
OY 1630 AAATGCTGGCAATCTTCTTAAAGACAACACCTTCAATGTCTTTGCAACAACA 1689
DB HisLeuAlaGlyAsnAsnLeu-----ThrSerLeuAspValAspGlnLeuProThr 714
OY 1690 AACTTGACATCTCTGAGATCTCTTAAATGTCAATTTGAAACAATATCTTTGGGGGGTATTT 1749
DB AsnLeuThrHisLeuAsp-----IleSerTrp----- 723
OY 1750 GACACCCCTCAATGATTAATATATAGTGTACACAACATCTATGTTTGTGAT 1809
DB -----AsnHisLeuGlnMetLeuAsn----- 730
OY 1810 TCATCCCATTTATTAACAGCTGTATTCCTCAGCACTGTGATGAGTTGCAATGCAATA 1869
DB -----AlaThrValIleuGlyPheLeuAsnArgThr 740
OY 1870 GAGACATTAAGAATCTGCAACATTTCCAAAGACTTACCTTCTCAATTTACT 1929
DB MetLysTrpArgSerVal-----LysLeuSer 749
OY 1930 AACATTCGTGCTGCTTGTATATGAGACATGCAATTCCTGCACTGGGTCAAGAGACAG 1989
DB GlyAsnProTrpMetCysAspCysThrAlaLysProLeuLeuPheThrGlnAspAsn 769
OY 1990 AAGCAGTCTTGGAATGTTGAACAATGACATGTGCAACAACCTGTGAGATGAAATCC 2049
DB PheGlnArgIleGlyAspArgAsnGlnMetCysValAsn--AlaGlnMetProThr 788
OY 2050 TCCTTAGTGTGATTTTAATATTTCTACCTGTATATGTACAGACATC--ATCAGT 2106
DB ArgMetValGlnLeuSerThrAsnAspIleCysProAlaGlnLysGlyValPheIleAla 808
OY 2107 GGTGAGAGGTC-----AGTGTATGTGTGATTCACCTGTGATTCATTTCTGATATAC 2157
DB LeuAlaValIleAlaLeuThrGlnLeuAlaGlyPheThrAlaAlaLeuTyrTrp 828
OY 2158 CACTTC-----TATTTTCAC--CTGATCTTATTTGCTGGC 2190
DB LysPheGlnThrGlnIleLysIleTrpLeuTyrAlaHisAsnLeuLeuThrPheVal 848
OY 2191 TGTAAAAAGTACAGAGAGAGAAAGCATTTATGATGCAATTTGTGATCTGAGTACAG 2250
DB ThrGlnGlnAspLeuAspLysAspLysPheAspAlaPheIleSerTyrSerHisLys 868
OY 2251 AATGAGACTGGGTAGAAATAGCTGTGTAAGAAATTTGAAGAAGAGTCCCGCTTT 2310
DB AspGlnSerPheIleGlnAspTyrLeuValProGlnLeuGlnHisGlyProGlnLysPhe 888
OY 2311 CACCTGCTGCTCACTACAGACATTTATCTGCTGTAGACCATTTGCTGCCAACAATCTC 2370
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DB Arg---SerValAlaAspSerArgTrpThrIleIleValLeuSerGlnAsnPheIleLys 927
OY 2431 AGCCGTGCTGTATCTTTGAATATAGATTTGCTCAACATGSCATTTTCTAGCAGCCGC 2490
DB SerGlnTrpAlaArgLeuGlnIlePheArgAlaAlaHisArgSerAlaLeuAsnGlnLysArg 947
OY 2491 TCTGCATCATCTTCAATTGTC-----CTTGAAGAAGTTGAGAAATGCC 2532

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DB 948 SerArgIleIleValIleIleTyrSerAspIleGlyAspValGlnLysLeuAspGlu--- 966
OY 2533 CTGCTGAGGACGACGAGGTGATTTGATGGCTTCTTGACGAAGACACTACTGGAATGG 2592
DB -----GlnLeuLysAlaTyrLeuLysMetCysAsnThrTyrLeuLysTrp 980
OY 2593 GAGGACAATCTCTGAGGAGGACACATCTTCTGAGAGAACTTAATAATGCCCCTA 2646
DB -----GlyAspProTrpPheTrpAspLysLeuArgPheAlaLeu 993

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Edison, E.; Kooyer, S.; Develjyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Belien, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking siml.
A:Reference number: Z17796; MUID:95324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <END>
A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA792
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Alignment Scores:
Pred. No.: 5,22e-17 Length: 1389
Score: 324.00 Matches: 235
Percent Similarity: 34.29% Conservative: 146
Best Local Similarity: 21.15% Mismatches: 310
Query Match: 6.26% Indels: 422
DB: 2 Gaps: 47

US-09-396-985b-46 (1-2951) x T13852 (1-1389)
OY 328 GATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTCTTCAACCAAGACATGATCTG 387
DB ----- 411
OY 154 AspAsnAsnIleAspGlnLeuProGlnGlyAlaTyrCysSerMetProSerLeuGlnLeu 173
OY 388 AGCTTCAACCCCTTGAAGATCTTAAAGACATAGCTATGCTTCCCAATTTT----- 435
DB ----- 411
OY 174 LeuAsnLeuThrGlnAsnArgIleArgSerAlaGlnPheLeuGlyPheSerGlnLysLeu 193
OY 436 -----TCAGAATTCAG 447
DB CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValSerGlnLysSerGlnLeuGln 213
OY 448 TGGGTGATTTATCCAGGTGTGAATGAAATTAAGACAAATGACAGCATGCGC--- 504
DB ----- 411
OY 214 ThrLeuAspValSerPheAsnGlnLeuArgSerLeuProAsp---AlaTrpGlyAlaSer 232
OY 505 ---TTACACCACTCTCAAACTTGATATCTGACAGAAACCTATCCAGAGTTTCCCA 561
DB ----- 411
OY 233 ArgLeuArgArgLeuGlnThrLeuSerLeuGlnHisAsnAlaIleSerThrLeuAlaPro 252
OY 562 GGAAGTTCTCTGAGTAAACAAGTTTGAACAATCTGAGTGGCTGTGAGACAAATGCGC 621
DB ----- 411
OY 253 AsnAlaLeuAlaGlyLeuSerSerLeuArgValLeuAsnIleSerTyrAsnHisLeuVal 272
OY 622 TCTTGAAGAC----- 633
DB ----- 411
OY 273 SerLeuProSerGlnAlaPheAlaGlyAsnLysGlnLeuArgGlnLysLeuGlnGly 292
OY 634 -----TTCCTATGACAGCTTATTAACCTTAAGAACTCAATAGT--- 675
DB ----- 411
OY 293 AsnAspLeuTyrGlnLeuProLysGlyLeuLeuHisArgLeuGlnGlnLeuValLeu 312
OY 676 -----GTCACAATTTTATACATTCCTGTAAGTTACTGCA 711

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Db 313 AspleusergluAsnleuThrSerHisValAspAsnSerThr----- 328
 Qy 712 TATTTTCCATCTGAGCAACTGTACATGTGATCTTTTAACTATATCAAACT 771
 Db 329 ---PheIleuArgLeuIleValLeuAsnLeuSerAsnAlaLeuSerThrArg 347
 Qy 772 ATT-----ACTGCAACGACTTACAGTTTCTACGTGAATAATCCAAAGTCATCTC 822
 Db 348 IleGlySerLysThrPheLysGluLeuTyrrPheLeuGln----- 360
 Qy 823 TCTTTAGACATGTCTTTGAACCCAAATTGACTTCAATTCAGAACCAAGCCTTTACAGGAATT 882
 Db 361 IleLeuSerMetArgAsnAsnSerIleGlyHisIleGluGluGlyAlaPheLeuProLeu 380
 Qy 883 ---AAGTCCATGAACTGACTCTTAAGAGGTAAATTTTAATAGCTCAAAATATATGAAAACT 939
 Db 381 TyrAsnLeuHisThrLeu----- 386
 Qy 940 TGCCTTCAAAACCTGGCTGGTTTACAGTCCATCGCTGATCTTGAGAAATTTAAAGAT 999
 Db 387 ---AsnLeuAlaGluAsnArgLeuHisThrLeu-----Asp 397
 Qy 1000 GAAAGATCTGGAATTTTGAACCCCTCTATCATGGAAGACTATGTGATGACCAATT 1059
 Db 398 AsnArg-----IlePheAsnGlyLeuTyrrValLeuThr--- 408
 Qy 1060 GATGAGTTCAAGTTTACATATACAAATGATTTTTCAGATGATTTGTTAGTTCCATTCG 1119
 Db 409 ---LysLeuThrLeuAsnAsnThrPheArgAsnLeuAsnGlnLeuThrGlyLeuArg 424
 Qy 1120 TTGGCAATGTTTTCGAATGCTCTGGCAGGTGATCTATATAAATATCTGAAGATTT 1179
 Db 425 PheArgAsnCySerAspLeuLysGlyLeuAspLeuSerSerAsnGlnLeuThrGlyVal 444
 Qy 1180 CCTAAACATTTCAATGGCAATCCTTATCAATCAATTAGATGT----- 1221
 Db 445 ProGluAlaVal-----GlnAspLeuSerMetLeuLysThrLeuAspLeuGlyGluAsn 462
 Qy 1222 CACTAGACAGTTTCCAACT----- 1241
 Db 463 GlnIleSerGluPheLysAsnAsnThrPheArgAsnLeuAsnGlnLeuThrGlyLeuArg 482
 Qy 1242 -----CTGATCTACCCCTTTCTT 1259
 Db 483 LeuIleAspAsnArgIleGlyAsnIleThrValGlyMetPheGlnAspLeuProArgLeu 502
 Qy 1260 AAAAGTTTGACTTTAACTATGAAACAA--GGGTCTATC-----AGTTTAAAAAA 1307
 Db 503 SerValLeuAsnLeuAlaLysAsnArgIleGlnSerIleGluArgGlyAlaPheAspLys 522
 Qy 1307 ----- 1307
 Db 523 AsnThrGluIleGluAlaIleArgLeuAspLysAsnPheLeuThrAspIleAsnGlyIle 542
 Qy 1308 ---GTGGCCCTACCAAGTCTGAGTATAGATCTTAGTAAAGATGACTGAGCTTTAGT 1364
 Db 543 PheIleThrLeuAlaSerIleLeuThrPheAsnLeuSerGluAsnHisLeuValTrp--- 561
 Qy 1365 GGTGGCTGTTCTTATCTGATTTGGAAACAAACAGCTGAGACACTTGAAGCTCAGCTTC 1424
 Db 562 ---PheAspTyrAlaPheIleProSerAsn---LeuLysTrpLeuAspIleHisGly 578
 Qy 1445 AATGTGTCATCATTAATGAGTCCCAATTTCACTGGGTCTTGAAGAG-----CTGCAAG 1475
 Db 579 Asn---TyrIleGluAlaLeuGlyAsnTyrrLysLeuGlnGluGlnIleArgValAlaThr 597
 Qy 1476 CACCTGGAATTTTTCGACCTCTACTTAAAGAGGTCACAGAAATCTCAGAGCTTTATTC 1535
 Db 598 ThrLeuAspAlaSer-HisAsnArgIleThrGluIleGlyAlaMetSerValProAsnSe 617
 Qy 1536 CTTTGAAGAGCTACTTTTACCTTGACATCTCT-----TATACTAACACC-- 1578
 Db 1578 -----

Db 617 rIleGlu---LeuLeuPheIleAsnAsnAsnIleIleGlyGlnIleGlnAlaAsnThrPh 636
 Qy 1579 -----AAATGACTTCGATGGATATATTTCTGGCTTGACAG 1616
 Db 636 eValAspLysThrArgLeuAlaArgValAspLeuTyrrAlaAsnValLeuSerLysIleSe 656
 Qy 1617 TCTCAACACATTTAAATGAGCT----- 1638
 Db 656 rLeuAsnAlaLeuArgValAlaAlaProValSerAlaGluLysProValProGluPheTyrrLe 676
 Qy 1639 ---GGCAATCTTTCAA----- 1652
 Db 676 uGlyGlyAsnProPheGlnCySerAspCySerMetGluTrpLeuGlnArgIleAsnAsnIle 696
 Qy 1653 ---AGCAACACCCCT-----TTCAATGCTTTGCAACACA 1684
 Db 696 uThrThrArgGlnHisProHisValValaAspLeuGlyAsnIleGluCySerLeuMetProHis 716
 Qy 1685 CAACAAACCTTGACATTCCTGATCCT----- 1710
 Db 716 sSerArg-SerAlaProLeuArgProLeuAlaSerLeuSerAlaSerAspPheValCysL 736
 Qy 1711 -----TCTAAATGTCATTTGG 1726
 Db 736 ySTyrrGluSerHisCySerProThrCySerHisCySerGluTyrrGluGlnCySerGlySerG 756
 Qy 1727 AACAAATATCTTGGGGGGTATTTGACACCCCTCAT----- 1761
 Db 756 IuValIleCySerProGlyAsnCySerCySerPheHisAspAlaThrTrpAlaThrAsnIleV 776
 Qy 1761 ----- 1761
 Db 776 AlaSerCySerGlyArgGlnAspLeuAlaAlaLeuProAsnArgIleProGlnAspValSerA 796
 Qy 1761 ----- 1761
 Db 796 sPLeuTyrrLeuAspGlyAsnAsnMetProGluLeuGluValaGlyHisLysLeuThrGlyArgA 816
 Qy 1762 --AGACTCAATATTAATATATGATGATGACAAACAATCTATGTTTGGATTTCAATCCCAT 1819
 Db 816 rGAsnLeuArgAlaLeuTyrrLeuAsnAlaSerHisLysMetThrLeuGlnAsnGlySerL 836
 Qy 1820 ATAAACAGCTGTATTTCCCTCAGACACTCTTGATTTGCAATTTGCGATGACAGACATCTA 1879
 Db 836 euAlaGlnLeuValAsnLeuArgValLeuHisLysLeuGluAsnValLeuThrAlaLeuG 856
 Qy 1880 AAGGA-----ATAC 1888
 Db 856 IuGlyThrGluPheArgSerLeuGlyLeuLeuArgIuLeuTyrrLeuHisAsnAsnMetL 876
 Qy 1889 TGCACACAT----- 1896
 Db 876 euThrHisLysSerAsnAlaThrPheGluProLeuValaSerLeuGluValaLeuArgLeuA 896
 Qy 1897 -----TTTCCAAAGAGTCTAGCCTTTCTTCA 1921
 Db 896 sPAsnAsnArgLeuSerSerLeuProHisLeuGlnTyrrArgHisLysSerLeuGlnGlyLeuT 916
 Qy 1922 ATCTTACTAACAAATTTCTGTTGCTTGTTATATGTAACAT---CAGAAATTTCTGCAAGTGG 1978
 Db 916 hTrLeuGlyArgAsnAlaTrpSerCySerArgGlnLysLeuArgGluLeuAlaGlnPheV 936
 Qy 1979 TCAAGGAACAGACAGCTGTTCTGTTGTAATGTGAACAAATGACATGT----- 2025
 Db 936 AlSerAspAsnAlaMetValValaArgAspAlaHisAspIleTyrrCySerLeuAspAlaGlyI 956
 Qy 2026 --GCAACACCTGTAGAGATG-----AATACCTCCTTAGTGT 2059
 Db 956 IeLysArgGluLeuGlnLeuIleGlyAsnLeuAlaAsnGlyProAspCySerSerAspLeuL 976
 Qy 2060 TGAATTTTAATTAATCTTACC----- 2079
 Db 976 euAspAlaSerAlaSerAsnLysSerSerGlnAspLeuAlaGlyAlaIleGlyCySerP 996

Oy	2080	---TGTATATGACAGACATTCAGTGTGCTAGTGTGATGTTGGTA-----	2133
Db	996	roCysTTPProAlaValLeuValLeuIlePheLeuValValValLeuIleLeuAlaPheV	1016
Oy	2134	-----TTCACGTGTAGCATTTTGTATATACCACTTCTATTTTCCACGTACTTA	2182
Db	1016	alPheArgGluSerValAlaArgMetCTPLeuPheAlaHleTyrGlyValAlaArgVal-----	1033
Oy	2183	TTGCTGGGCTGTAAA---AAGTACAGACAGAGAGAAAGCATGTATATGTCATTTTGATCT	2239
Db	1034	-----CysGluProAlaArgPheGluAspAlaGlyLysLeuTyrAspAlaIleLeuLeuH	1051
Oy	2240	ACTGAGTCACAAATATGAGCATGTGGTGAGAAATGAGCTGTAAAGATTTAGAGAGAGAG	2299
Db	1051	IeSerGluLysAspTyrGluPheValCysAlaGlnIleAlaAlaGluLeuGluHleGlyA	1071
Oy	2300	TGCCCCGCTTTCACCTGTGCTTCACTACAGAGACTTATTTCTGTGTGACCATTTGCTG	2359
Db	1071	rgPProProPheArgLeuGlyIleGlnGlnAlaArgLeuProPro-----GlnA	1087
Oy	2360	CCAACATATATCCAG-----GAAGGCTTCCACAGAGCGGGAAGTTATTTGTGTAGT	2413
Db	1087	IaSerHleSLeuGluLeuValGluGlyAlaArgAlaSerAlaLysIleLeuValLeuT	1107
Oy	2414	CTAAGACATTTATTCAGAGCCGTTGTTATCTTTGTAATATGAGATTGCTAAACATGCG	2473
Db	1107	hrAlaGlnLeuLeuAlaLeuThrGluTyrPheAlaGlyIleGluPheArgAsnAla-----	1123
Oy	2474	AGTTTCTGACAGACCGCTGTGGCATATC-----TTCATTGTCTTGAGAG-----	2520
Db	1124	--PheHleGluSerLeuAlaGlyLeuAlaGlnLysLeuValIleLeuGluLnuThrSerV	1143
Oy	2521	-----GTTGAGAAGTCCCTGCTGAGGACAGAGGGAATGT	2557
Db	1143	alSerAlaGluAlaGluLysValAlaGluLeuSerProTyrLeuLysSerValProSerA	1163
Oy	2558	ATGCGCTTCTTAGACAGAAACACTTACTGTGAATGGAGAGACATCTCTGGGAGGACACA	2617
Db	1163	snArgLeuLeuThrCysAspArgTyr-----	1171
Oy	2618	TCTTCTGGAGAAAGCTTAAATAATGCCCTA	2646
Db	1172	--PheTyrGluLysLeuAlaTgTyrAlaIle	1180

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RESULT 5
T13887
C|lr protein - fruit fly (Drosophila melanogaster)
C|Species: Drosophila melanogaster
C|Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C|Accession: T13887
R|Chang, C.; Beachy, P.A.
Mach. Dev. 47, 225-239, 1994
A|Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A|Reference number: 217805; MUID:95151581; PMID:7848870
A|Accession: T13887
A|Status: preliminary; translated from GB/EMBL/DBD
A|Molecule type: mRNA
A|Residues: 1-1385 <CHI>
C|Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AA83338
C|Genetics:
A|Cross-references: FlyBase:FBgn004364
A|Note: C|lr

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Alignment Scores:	
Pred. No.:	7,47e-17
Score:	322.00
Percent Similarity:	34.45%
Best local Similarity:	20.76%
Query Match:	6,22%
DB:	2
	Gaps:
	Indels:
	406
	44

US-09-396-985B-46 (1-2951) X T13887 (1-1385)

QY	328	GATGAGAAAC	CTCAGCAAAAGTCCCGATGACATCTCTCTTCAACCAAAACATAGATCTG	387
Db	154	AspAsnAsnIleArgGlnLeuPheGluGlyValTyrCysSerMetProSerLeuGlnIleu		173
QY	388	AGCTTCAACCCCTTGAAGATCTTAAAGAGCTATAGCTTCTGCAATTTT		435
Db	174	LeuAsnIleuThrGlnAsnArgIleArgSerAlaIuIuPheLeuGlyPheSerGluIuIuLeu		193
QY	436	-----	TCAGAACTTCAG	447
Db	194	CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValAlaSerGlyGlySerGluIuGln		213
QY	448	TGGCTGGATTATTCAGAGTGGTAATGAAATGAAACAAATTGAAGCAAGGATGGCATGGC---		504
Db	214	ThrIleuAspValSerPheAsnGluIuLeuArgSerLeuProAsp---	AlaTyrGlyAlaSer	232
QY	505	---TTACACCAACCTCTGAACCTTGAATGTGACAGAAACCTATGSCAGAGTTTTCGCCCA		561
Db	233	ArgLeuArgArgLeuGlnThrLeuSerLeuGlnIleAsnAsnIleSerThrLeuAlaPro		252
QY	562	GGAAGTTTCTCTGGACATTAACAGATTGTAGACAAATCTGGTGGCTGTGAGACAAATGGCC		621
Db	253	AsnAlaLeuAlaGlyLeuSerSerLeuArgValLeuAsnIleSerTyrAsnIleValAl		272
QY	622	TCCTGAAAGACTTCCCTATTTGACAGACTTAATACCTTAAAGAAACCTGAATGGCTGAC		681
Db	273	SerLeuProSerGlnAlaPheAlaGlyValAsnGlyLeuArgGluIuLeuGlnGly		292
QY	682	AATTTTATACCTTCCTGTAAGTTACCT		708
Db	293	AsnAspLeuTyr-----GluLeuProIuArgGlyLeuIuIleArgLeuGlnIuLeu		310
QY	709	-----GCATATTTTCC		720
Db	311	ValLeuAspLeuSerGlyAsnGlnLeuThrAspIleHisValaAspAsnSerThrPheAla		330
QY	721	AATCTGACGAACCTAGTACATGTGGATCTTTCTATTAACCTATATTCAAACTAAT		774
Db	331	GlyLeuIleArgLeuIleValaLeuAsnLeuSerAsnAlaIleuThrArgIleGlySer		350
QY	775	---ACTGTCAACGACTTACAGTTTCTACAGTAAATCCACAAGTCAATCTCTTTACAC		831
Db	351	LysThrPheLeuGluLeuTyrPheLeuGln-----IleAspSer		363
QY	832	ATGTCTTTGAACCAATTGACTTCATTCACAGACCAAGCCTTTACAGGAAAT	---AAGCTC	888
Db	364	MetArgAsnAsnSerIleGlyHisIleLeuGlnIuGlyAlaPheLeuProLeuTyrAsnIleu		383
QY	889	CATGAACCTGACTTGAAGGTAAATTTAATAGTCAATAATATGAAGAACTTGCCTTCAA		948
Db	384	HisPheIleu-----		386
QY	949	AACCTGGCTGGTTTACACGTCCATCGGTGATCTTGGAGAAATTAAAGATGAAGCAAT		1008
Db	387	AsnIleuAlaGluAsnArgLeuHisIleThrLeu-----AspAsnArg-		399
QY	1009	CTGGAATTTTGAACCTCATGACGGAAGGAACTATGTGATGGACCATGATGAGAGTTC		1068
Db	400	-----IlePheAsnGlyLeuTyrValLeuThr-		408
QY	1069	AGGTTAACATATACAAATGATTTTTCAGATGATTTGTTAAGTTCCATTCCTGGCGCAAT		1128
Db	409	LysLeuThrIleuAsnAsnAsnIleVal---SerIleValGluSerGlnAlaPheArgAsn		427
QY	1129	GTTTCTGCATGTCTCTGGCAGCTGTATCTATAAATAATCTAGAAGATGTTCTTAACAT		1188
Db	428	CysSerAspLeuTyrGluLeuAspLeuSerSerAsnGlnLeuThrGluValaProGlu---		446
QY	1189	TTCAAAAGCGAATCCCTATCAATCATATTAAGAT	---CAACTAAGC	1230
Db	447	---AlaAlaGlnAspLeuSerMetLeuIuIuThrLeuAspLeuGlyGluAsnGlnIleSer		465

Db 447 ---AlaAlaGlnAspLeuSerMetLeuysThrLeuAspLeuGlyClnAsnGlnIleSer 465

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QY 1231 AGTTCCAACT----- 1241
DB 466 GluPheYsaAenAthrPheArGAsnLeuAenGlnLeuThrGlyLeuAArgLeuIleAsp 485
QY 1242 -----CTGAGTCAACCTTTCTTAAAGTTTG 1268
DB 486 AsnArgIleGlyAenIleThrValGlyMetPheGlnAerLeuProAArgLeuSerValLeu 505
QY 1269 ACTTAACATAAGACAA--GGGTCTATC-----AGTTTAAAAA----- 1307
DB 506 AsnLeuAlaYsaAenArgIleGlnSerIleGlnAArgGlyAlaPheAerLysAenThrGlu 525
QY 1308 -----GTGACC 1313
DB 526 IleGlnAlaIleAArgLeuAerLysLysPheLeuThrAerIleAenGlyIlePheAlaThr 545
QY 1314 CTACCAAGTCTACGCTATAGATCTTAGAGAAATGCACTGAGCTTTAGTGAGCTGT 1373
DB 546 LeuIleSerLeuLeuThrLeuAenLeuSerGlnAenHisLeuValTrr-----Phe 562
QY 1374 TCTTATTCTGATTTGGAAACAAACAGCTGAGACACTTACCTCAGCTTCAATGGTCC 1433
DB 563 AspTyrAlaPheIleProSerAen--LeuLysTrrLeuAerIleHisGlyAen--Tyr 580
QY 1434 ATCATATTGAGTGCATTTTCATGGGTCTAGAGAG-----CTGCAGACCTGGAT 1484
DB 581 IleGlnAlaLeuGlyAenTrrTrrLysLeuGlnGlnIleAArgValThrThrLeuAer 600
QY 1485 TTTTCAGACCTCTACTTTAAAGGGTGCACAAATTCACGCTTTCTTATCCCTGAAA 1544
DB 601 AlaSer-HisAenArgIleThrGlnIleGlyAlaMetSerValProAenSerIleGlu- 619
QY 1545 GCTCTTACTCTGACATCTCT-----TATACTAACCC----- 1578
DB 620 -LeuLeuPheIleAenAenAenIleIleGlyGlnIleGlnAlaAenThrPheValAerLys 639
QY 1579 -----AAATTTGACTTCGATGTATATTTCTTGCTTGACAGCTCTCAACAC 1625
DB 639 sThrArgLeuAlaArgValAerLeuTrrAlaAenValLeuSerLysIleSerLeuAenAl 659
QY 1626 ATTAAATGCGCT-----GGCA 1643
DB 659 AlaAerGlyAlaProValSerAlaGlnLysProValProGlnPheTrrLeuGlyLys 679
QY 1644 TTTCTTCAA-----AG 1654
DB 679 nProPheGlnCysAerCysSerMetGluTrrLeuGlnAArgIleAenAenLeuThrThr 699
QY 1655 ACAACACCCCT-----TTCAATGTCTTGCAACACAAACAACT 1693
DB 699 gGlnHisProHisValValAerLeuGlyAenIleGlnCysLeuMetProHisSerArg-S 719
QY 1694 TGACATTCCTGGATCT----- 1710
DB 719 eraIaProLeuAArgProLeuAlaSerLeuSerAlaSerAerPheValCysLysTrrGlnS 739
QY 1711 -----TTAAATGTCAATGGAAACAAATAT 1735
DB 739 erHisCysProProThrCysHisCysCysGlyTrrGlnGlnCysGlnValIleC 759
QY 1736 CTGGGGGGGATTTGACACCCCTCCAT----- 1761
DB 759 ysrProGlyAasnCysSerCysPheHisAerAlaThrTrrAlaThrAenIleValAerCysG 779
QY 1761 ----- 1761
DB 779 LysArgGlnAerLeuAlaIleLeuProAenArgIleProGlnAerValSerAerLeuTrrL 799
QY 1762 -----AGACTTC 1768
DB 799 euAerGlyAasnAenMetProGlnLeuGlnValGlyHisLeuThrGlyAArgAerAenLeu 819
QY 1769 AATTATTAAATATGATGACAAACATCTATTGTTTGGATTCATCCCATTAATACAGC 1828
DB 819 rglAleuTrrLysAenAlaSerAenLeuMetThrLeuGlnAenGlySerLeuAlaGlnL 839
QY 1829 TGTATTCCTCCAGACACTCTTGATTTGCAATTCGATACAGACATCTAAAGCA----- 1884
DB 839 euValAenLeuAArgValLeuHisLeuGlnAasnAenLysLeuThrAlaLeuGlnGlyThrG 859
QY 1885 -----ATATGCAACAT- 1896
DB 859 IuPheArgSerLeuGlyLeuLeuAArgLysLeuTrrLeuHisAenAenMetLeuThrHis 879
QY 1896 ----- 1896
DB 879 IeSerAenAlaThrPheGluProLeuValSerLeuGlnValLeuAArgLeuAerAenA 899
QY 1897 -----TTTCCAAAGTCTACGCTTCTTCAATCTTAATA 1930
DB 899 rglLeuSerSerLeuProHisLeuGlnTrrArgHisSerLeuGlnGlyLeuThrLeuGlyA 919
QY 1931 ACAATTCTGTGCTGTATATGTAACAT---CAGAATTCCTGCAGTGGGTCAAGGAC 1987
DB 919 rgaAenAlaTrrPserCysArgCysGlnGlnLeuAArgGlnLeuAlaGlnPheValSerAerA 939
QY 1988 AGAAGCAGTTCTTGTAATGTGAACAAATGACATGT-----GCAACAC 2032
DB 939 enAlaMetValAlaArgAerAlaHisAerLysTrrCysLeuAerAlaGlyIleLysArgG 959
QY 2033 CTGTACAGATG-----AATACCTCTTAAGTGTGGATTTTA 2068
DB 959 IuLeuGlnLeuIleGlyAenLeuAlaAenGlyProAerCysSerAerLeuAerAerAlaS 979
QY 2069 ATATTTCTACCTGTATATG-----TCAAGACATCATCAGTG 2107
DB 979 eraIaSerAenIleSerSerSerGlnAerLeuAlaGlyGlyTrrAArgLeuProLeuA 999
QY 2108 TGTCAAGTGTCAAGTATGTGTATTCACATGACATTTCTGATATACACTTC----- 2163
DB 999 IalAlaValLeuValLeuIlePheLeuAerValValLeuIleIleValPheValPheArgG 1019
QY 2164 -----TATTTTCACTGATCTTATGCTGCTGCTGTAAGAAAGTACA 2203
DB 1019 IuSerValAerMetTrrLeuPheAlaHisTrrGlyAlaAArgValCysGlnProAerPheG 1039
QY 2204 GCAGAGAGAAAGACATGTATGATGATGTGATGTCTACAGTCAAGATGAGAGCTGGG 2263
DB 1039 IuAerAlaGlyLysLeuTrrAerAlaIleLeuHisSerSerGlnLysAerTrrGlnPheV 1059
QY 2264 TGAGAAATGAGCTGTAAAGATTTAGAAAGAGAGTCCCGCTTTCACTGTGCTTC 2323
DB 1059 alCysAerAenIleAlaAlaGlnLeuGlnHisGlyAArgProProPheAArgLeuCysIleG 1079
QY 2324 ACTACAGAGACTTATTCCTGCTGTAGCCATTGTGTCGAACATCATCAG-----GAAG 2377
DB 1079 IuGlnAArgAerLeuProPro-----GlnAlaSerHisLeuGlnIleValAlaGlnG 1095
QY 2378 GCTTCCACAGAGCGGAGGTTATGTGTAGTGTATGATGCTTATTAATCAAGCCGTT 2437
DB 1095 IyAlaAArgAlaSerAerLysIleIleLeuValLeuThrAerAenLeuAerAlaThrGluT 1115
QY 2438 GGTGTATCTTTGAATATGATGTGCTCAACATGCGATTTCTGAGCAGCGCTGTGCA 2497
DB 1115 rpaAenArgIleGlnPheAArgAenAla-----PheHisAerLeuAerGlyL 1131
QY 2498 TCATC-----TTCATGTCTCTTGAGAG-----G 2521
DB 1131 euAlaGlnLysLeuValIleIleGlnGlnLysTrrSerValSerAlaGlnAlaGlnAerValA 1151
QY 2522 TTGAGAGTCCCTGCTGAGCAGCAGGTGAATGTATGCGCTTCTTACGAGAAACCT 2581
DB 1151 IagIuLeuSerProTrrLeuLysSerValProSerAenAArgLeuLeuThrCysAerAerG 1171
QY 2582 ACCTGGAATGGAGAGCAATCTCTGGGAGGACATCTTCTGGAAGAGACTTAAATG 2641

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Db 1171 1Y-----PhetrlgublyseuArqTYra 1179

QY 2642 CCCTA 2646
||:::
Db 1179 latle 1180

RESULT 6

A29944

chaoptin precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: photoreceptor cell-specific membrane protein
C:Species: *Drosophila melanogaster*
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29944; A21123

R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988

A:Title: Chaoptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
A:Reference number: A29944; MUID:88135762; PMID:3124963
A:Accession: A29944

A:Molecule type: DNA

A:Residues: 1-1134 <REI>

A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012

R:Zipursky, S.L.; Venkatesh, T.R.; Teylow, D.B.; Benzer, S.
Cell 36, 15-26, 1984

A:Title: Neuronal development in the *Drosophila* retina: monoclonal antibodies as molecu
A:Reference number: A21123; MUID:84106810; PMID:6420071
A:Accession: A21123

A:Molecule type: protein

A:Residues: 31-43, 'HK', 46-49, 'H' <ZIP>

C:Genetics:

A:Gene: FlyBase:cbp
A:Cross-references: FlyBase:FBgn0000313

A:Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2

C:Superfamily: Chaoptin; leucine-rich alpha-2-glycoprotein repeat homology

C:Keywords: cell adhesion; glycoprotein; membrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-1134/Product: chaoptin #status predicted <MAT>

F:80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR2>

F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:228-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

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F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

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F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

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F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

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F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>

F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR21>

F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR22>

F:626-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR23>

F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR24>

F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR25>

F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR26>

F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR27>

F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR28>

F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR29>

F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR30>

F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR31>

F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR32>

F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR33>

F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR34>

F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR35>

F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR36>

F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR37>

Alignment Scores:	Pred. No.:	1,72e-14	Length:	1134
Score:	291.50	Matches:	177	
Percent Similarity:	36.21%	Conservative:	121	
Best Local Similarity:	21.51%	Mismatches:	278	
Query Match:	5.63%	Indels:	248	
DB:	1	Gaps:	32	

US-09-396-985B-46 (1-2951) x A29944 (1-1134)	
QY 309 TATTACCTTACCAATGATGATCAGAAATCTGACAAATGCTCCGTATGAC-----	357
DB 105 TYRAGLEUPLYSLSERGLYASNHS-LEUTHRIULLEPRODAPARALAPhethecrl	124
QY 358 -----	ATTGCTTC 365
DB 124 YLEUGLARGSERLEUTRGLULEULEUProGLINAsnAPLeuValGLULLEProse	144
QY 366 TTCAAC-----	AAGAACAATAGATCTGACACTTCACCCCTGAA 404
DB 144 ILYSERLEUARGHISLEUGLULYLeuARGHISLeuAspLeuGLUYrASNHSILelh	164
QY 405 GATCTTAAAGACTTATGCTTCCCAATTTTTCAGAA--CTTCAGTGGCTGATTTATC	461
DB 164 RHISLEGLNHSAspSERPHEARGGLYLEUGLAspSERLEUGLINTHRILeuAR	184
QY 462 CAGGTGAAATTGAAACAATTGAAAGACAGGATGGAGCTTACACCACTGTCAA	521
DB 184 GLUAsnCYSLSESERGLINLeuMETSERHISERPhesERGLYLEUleuGLINTH	204
QY 522 CTGTGATATGACAGAAACCCATATCCAGAGTTTTCGCCAGAGTTCC--TTCGACT	578
DB 204 RLEuAspLeuSERGLYAsnLeuLeuPheGLULLeuAspProAsnVALPheVALAspGLYme	224
QY 579 AACAAAGTTTAAACAATCTGATGGCTGTGGAGACAAATTTGGCTCTTGAAGAGCTCCC	638
DB 224 TProARGLeuTHRARGLeuLeuLeuThAspAsnILEuSERGLULLEProTYrAspAL	244
QY 639 TATTGACAGCTTATTAACCTTAAAGAAATCAATGGCTGACAAATTTTATATCATCTCG	698
DB 244 ALLeuGLYProLeuYSERLeuARGThLeuAspRILeSERHISAsnVALIletrPserIle	264
QY 659 TAAGTACCTGCATATTT-----TCCAAATGACGAACCTTACATCATGTGGA	746
DB 264 USErGLYAsnGLINTHrYrGLULLeuYAsLAsERThrLYLeuAsnLeuAspAsnLeuNI	284
QY 747 TCTTTCTATTAACCTATATTAACAACATATTAAGTCAAGCACTTACAGTTTTCACGGA	806
DB 284 SLeuGLINTYrAsnHISILEuVALLeuProAsnSERPHELYSTYrPhe-----	301
QY 807 TCCAAAGTCAATCTCTCTTGAACATGCTCTTGAACCAACCAATGACTTCATTCAGACCA	866
DB 302 ASPThrALAsnARGHThrPhe---PheAspGLYAsnProIleHISThRILeuARGLAs	320
QY 867 AGCTTTCAGGAAATTAACTTCATGAACTGAACTCTAAGA-----	906
DB 320 PALAspHeLYsProALArgLILEArgGLULLeuYMeCARGLYrCYSGLYLeuThAsnIL	340
QY 907 -----GGTAATTTTAATAGCTCAAAATTAATGAAAGAACTGGCTTCA	947
DB 340 ESERProVALAspAspSERLeuVALAsnSERLeuGLINLeuAspLeuSERGLYAs	360
QY 948 AAACCTGGCTGGTTTACACGTCACCGGTTATC-----TTGGG	986
DB 360 nAsnLeuThrLYsLeuHIS---HISLYsLeuPheAsnAsnPheAspVALLeuARGVALIL	379
QY 987 AGAATTTAAGATGAAGAAATCTGGAATTTTGAACCCCTTATCATGAGAGACTATG	1048
DB 379 ESERMeCARAspAsnLYS---ILEuYSLLeuGLYProCHrGLINTHrPheAsnVALAs	398


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QY 1047 TGATGTGACCATGTGATGATTCAGGTTAAACATATACAAATGATTTTCAAGATGATATGTT 1106
Db 398 IHISTYTHIEU-----LeuLYsLeuAAspLeuSerGlyAsp--ArgAsnAspProth 415
QY 1107 TAAGTTCATTCGTTGGGCAATGTTTCTGCAAATG---TCTCTGGCAGGTATGATCTATAAA 1163
Db 415 rAsnLeuGlnThrLeuAArgAsnMetThrArgMetAArgAsnMetAArgSerLeuSerIleSe 435
QY 1164 ATATCTGAGAGATGTT-----CTTAAACATTTCAA-----TGGCA 1199
Db 435 rArgLeuGlySerSerSerValGlyProGluAspPheLeuAspPheGlyValGlyLeuGly 455
QY 1200 ATCTTATTCATCATTTGATGATGCACTAAGACGTTTCCAACTTCGATCTACCCCTT--- 1256
Db 455 uAspLeuGlnIleThrArgAlaSerLeuSerGlyIleGlnSerHisAlaPheLeuHisAla 475
QY 1257 -----CTTAAAGTTTGAATTTTAACTATGAC----- 1283
Db 475 lArgGlyLeuLYsArgLeuAAspPheSerGlyAsnGlyIleSerSerIleGlyAsnAspAl 495
QY 1284 -----AAAGGTCATACGTTTAAAGT 1309
Db 495 aPheHisGlyIleGlyHisSerLeuIleSerLeuLYsMetSerHisGlyTyrSerGlySe 515
QY 1310 GGCCCTACCA-----AGTCTGAGCTATCTAGATCTTAGTAC 1345
Db 515 rAlaLeuProAlaGluProLeuAArgHisAlaLeuThrSerLeuGlnGlyLeuAAspPheSerA 535
QY 1346 AAATGCACTGAGCTTATGTTGGTGGCTGTTCTTATCTGATTTG----- 1388
Db 535 nAsnHisIleSerSerMetSerAspThrSerPheHisPheLeuLYsAsnLeuAArgLeuLe 555
QY 1389 -----GGAACA----- 1394
Db 555 uGlyLeuHisAspAsnArgIleGlyGlnValLeuLYsGlyThrPheGlnGlyAAspIleHis 575
QY 1395 -AACAAGCTGAGACACTGACCTGACGCTCAGCTGATGCTGCATCATTTAGATGGCAAT-- 1451
Db 575 sSerLYsLeuGlnGlyIleSerLeuAArgPheAsnHisAlaLeuThrSerIleSerGlnHisTh 595
QY 1451 ----- 1451
Db 595 rPhePheAspLeuGlyAlaLeuAArgLYsLeuHisAlaLeuAspAsnLYsIleAspLYsIle 615
QY 1452 -----TTCATGGCTTAAAGAGAGCTGCAGCACTG----- 1481
Db 615 eGlyAArgArgAlaPheMetAsnLeuAAspGlyLeuGlnIlyThrLeuSerLeuAArgGlyAAsnLY 635
QY 1481 ----- 1481
Db 635 sIleAsnAsnLeuAlaAspGlySerPheGlnAsnLeuProLYsLeuGlnIleLeuAAspMe 655
QY 1482 -----GATTTTTCAGCACTTACTTAAAGAGCTGCAGCAATTTCT 1522
Db 655 cAlaPheAsnGlnLeuProAsnPheAsnPheAspArgPhe-AspGlnAlaGlyHisLeuS 675
QY 1523 CA-----GCGTTCTTATCCCTTGAAGCTTAACTTAC----- 1554
Db 675 eArgAsnLeuAsnValAsnValSerHisAsnGlnIleArgGlnLeuMetTyrAsnSerSer 695
QY 1555 -----CTTGACACT 1564
Db 695 rPserGlyAArgAsnGlnHisGlyGlyMetTyrHisSerAsnIleLYsIleLeuAspLeuS 715
QY 1565 CTATTAATAACACCAAAATGATCTGATGGATATTTCTT---GCTTGCACAGTCTCA 1621
Db 715 eHisAsnAsnIleSerIleIleHisProGlyTyrPheAArgProAlaGlnIleSerLeuT 735
QY 1622 AACACTTAAATGCTGACATTTCTTCAAGACACACCTTTCAATGCTTTTGCA 1681
Db 735 hrHisLeuHisAlaLeuGlyTyrAsnSerLeuMet---AsnThrThrArgAspValPheGlyA 754

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QY 1682 AACAAACAACTTGACATCTTGATCTGATCTTCTTAAATGCAATTTGAAACAAATGATCTTGGG 1741
Db 754 smMetProHisLeuGlnThrLeuAAspLeuSerTyrAsnThrIleHisGlyLeuAAspPheA 774
QY 1742 GGGTATTTGACACCTCCATGACCTTCAATTTATTAATATGATGCAACAAATCTATGTT 1801
Db 774 sPAlaPheLYsAsnThrLYsGlnLeuGlnLeuValPhePheGlyHisAsnTyrLeuSerA 794
QY 1802 TTTTGATTCATCCCAATTAAACACAGCTGATTCCTCCAGCACTCTTGATTCAGATTTC 1861
Db 794 sPileProGlnAspIlePheLYsArgProValGlnGlyLeuArgIleValAspPheSerHisA 814
QY 1862 AT-----CGCATAGACA 1873
Db 814 smHisLeuAArgGlyLeuProAspAsnLeuPheTyrAsnGlyGlyMetGlyLYsLeuAAspY 834
QY 1874 CATCTAAAGAACTGCAACATTTTCCAAAGCT----- 1908
Db 834 aSerHisAsnMetLeuLYsIleProSerSerLeuSerSerLeuAlaAlaLeuT 854
QY 1909 --CTAGCTTCTTCATCTTATCAATCTGTTGCTGTATATGAA-----C 1957
Db 854 hrLeuCYsGlyLeuHisLeuSerAspAsnPheIleSerThrIleHisSerMetAspLeuS 874
QY 1958 ATCAGAAATTC-----CTGACGTGGGTCAAGACAGAAAGCAATTTCTTGATATGTTG 2011
Db 874 eArgAsnLYsPheAArgSerLeuAArgTyrLeuAAspIleSerTyrAsnTyrGlyLeuAArgIleA 894
QY 2012 AACAAATGACATGTCACACCTGTAGAGATGAATTCCTCTTAGTGTGATTTAATA 2071
Db 894 sPAspAlaValPheAlaThr-----MetProLYsLeuAlaValLeuAAspLeuSerH 911
QY 2072 ATTCT 2076
Db 911 lAsn 912

RESULT 7
T15864
hypothetical protein C56B6.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15864
R/Pulson, L.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C56B6.
A/Reference number: S69019
A/Accession: T15864
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: DNA
A/Residues: 1-1066 <FULL>
A/Cross-references: UNIPROT:Q18902; EMBL:U039996; NID:G1055114; PID:G1055120; PIDN:AAA81
A/Intons: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3;

Alignment Scores:
Pred. No.: 4.58e-14 Length: 1066
Score: 286.00 Matches: 186
Percent Similarity: 35.35% Conservative: 136
Best Local Similarity: 20.42% Mismatches: 234
Query Match: 5.52% Indels: 356
DB: 2 Gaps: 35

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Db 116 LeuAsnAspLeuLYsThrLeuGlnSerIleAspLeuGlnGlyAsn-AsnIleThrHis-- 134
QY 321 ATGATGATGATGAAACTGACGAAAGTCCCTGATGACATTCCTTTCAAACCAAGAAAT 380
Db 135 -----LeuMetAspThrAsnGlnValThrPheGlySerGlyuMetLYsVal 149

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QY	381	AGATGTGAGCTTCAACCCCTTGAACATGATCTTAAAAAGCTATGAGCTTCCATATTTTTCAGA	440
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QY	441	ACTTCAGTGGGTGGATTTATTCAGGTGTGAATTTGAACAATTTGAAGACAAGAGCATGGCA	500
Db	169	al1earglululeuaprl1esertyrAasngh1leolnhrvalgluaipserphg1	189
QY	501	TGCGTTACACACCTTCAAC-----	522
Db	189	uThValGl1sh1smetGlnserleuAaprlseutyraSnargl1eal1atylleuProAr	209
QY	522	-----	522
Db	209	gGl1metleuylvaenphealalyethrleuylstrleuylvleu1agluAasmec11	229
QY	522	-----	522
Db	229	eh1sal1athrProgl1ualaleuAaDgAaprlleuAaDgAsnleuthrh1sleuAenleuAenG1	249
QY	522	-----	522
Db	249	yAsnlyvleuAaSnargl1eAargl1yAaprvallleuylsg1yuthraerThrleuValG1	269
QY	523	-TTGATATGACAGGAACCCCTATTCACAGTTTTCGCCAGAACTTCTCGACTAC	581
Db	269	u1euphe11eal1aasnAen1ytleuGlnh1sl1eProh1sg1yallleuSerG1lymetly	289
QY	582	AAGTTTAGACATCTGTGGGTGTGGAGACAAATTTGGCTCTGTACAA-----	630
Db	289	sg1nleuGln1sleuAaprl1esetyrAasnlysl1leueteerleuylslyrProthrs	309
QY	631	-----AGCTTCCCTATTGGACACTTATTAACCTTAAAGAACTCAATGTGGCTCAAA	683
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QY	684	TTTTATACATTCCTGTAAGTTACCTGGCATTTTTCACATCTGACAAACTTATGACATGT	743
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QY	817	-----AATCTCTTTTACATGTCTTTGAACCAATTTGACTTCATTTCAAGA	863
Db	389	uAaprllyleuAaDg1sh1sleuAenleuAaprn-----Aasn1n1leGlnlysl1eAapAs	407
QY	864	CCAAAGCCTTGAAGGAAT---AAGCTCCAAAGTCACTGACTGAAGGTAAT---	912
Db	407	nPheserleuAlaaprlleuProlysvleGlnh1sleuSerleu1ag1yAasnGlnleuAs	427
QY	913	-----TTTAATAGCTCAAAATATATGAACCTTGACCTTCAAAACCT	953
Db	427	p1le11ethrGluAasnmetPheG1ySerSerSerSerSerleuAenleuysSerleuAenle	447
QY	954	GGCTGGTTTACACGCTCACTGGGTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGGA	1013
Db	447	uAlah1sAasnlysl1eA1sSer11eSerAArgSerPheSerAaprlleuAaprnleuG1	467
QY	1014	AATTTTGAACCCCTATTCATGAAGAAGCTATGTGATGTGACCAATGATGAGTTCAAGTT	1073
Db	467	n-----GlnleuAaDgLe	471
QY	1074	AACATATACAAATGATTTTTCAGATGATTTTAAGTTCCATTTGCTTGGAGAAATGTTTC	1133
Db	471	uSerh1sAasnshn-----11eAaDgThr11eth	480
QY	1134	TGCAATGTCTCTGGCAGGTGA---TCTATAAAAATCTGAAGAATGTTCTCTAAACATTT	1190

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Db      480   :|||::: :::::||||| |||::: :::  
rSerMetThrPheSerLeuAlaGlnLeuArgIleU-----AspLeuSerHisAn-- 498  
  
QY      1191 CAATGGCAATCCATTACATCATTAGATGCATAAG-CAGTTTCCAATCTGTGACT 1249  
::: ::::: ||| |  
Db      499 -----ArgIleLeuSileuProSerAlaLeuTyGlnLeuProAlaLeuAspVa 516  
  
QY      1250 A-----CC 1252  
:  
Db      516 LLeuHileuAAsrHisAnAnleuAnaGluIleAspArgAlaIaPheArgSerPheSe 536  
  
QY      1253 CTTTCCTTAAGAAGTTGACTTAATACATGACAAG----- 1286  
|||:::||||| |||::: ||  
Db      536 rAspLeuGlnSerLeuLysLeuSerHisAsnAlaAPheaArgPheSerCysGluPheLe 556  
  
QY      1287 -GGGCTATATCAGTTTTAAAAAGGCCCTAACCAAGCTCAGCTATATCTAGTAG 1345  
|||:::||||| |||::: |||  
Db      556 uGlySerIleSer-----GlnValHisGlnLeuAspLeuSerSe 569  
  
QY      1346 AAATGCACTGAGC-----TTTAGTGCGGCTGTTCTTATTTCTGATT 1387  
|||:::||||| |||::: |||  
Db      569 rAsnGlnIleAsnGluIleAspIlePheCysIleAlaArgIylIeArgLysLeuSerLe 589  
  
QY      1388 GGGAAACAACAGC-----CTGAG 1405  
|||:::||||| |||  
Db      589 uAlaSerAsnSerValGlulysIleAsnArgLysLeuGlnAspAlaThrGluLeuth 609  
  
QY      1406 ACACCTATGACCTGCATTCATATGGTGCATC---ATTATGAGTGCATATTCAGGGCT 1462  
|||:::||||| |||::: |||  
Db      609 rSerIleAspIleSerHisAsnGlyIleIleAspValAspSerAspAlaPheCysGluCy 629  
  
QY      1463 AGAAGACCTGACGACCTCGATTTTTCAGACCTCTACTTAAA----- 1506  
|||:::||||| |||::: |||  
Db      629 sArgLysLeuSerHisIleLysLeuSer-HisAnTyrlIeArgAsnLeuTrpLysGly 649  
  
QY      1507 -----AGGTCACAGAAATCTCAGCGTTCTTATCC---- 1536  
|||:::||||| |||  
Db      649 hrArgValCysIleProTrpIleSerHisLeuThrTrpPheCysPhePheThrLysGluH 669  
  
QY      1537 --CTTGAAGAAGCTACTTACCCTTGAC----- 1560  
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Db      669 IseuGlnArgThrlIleSerPheSerTyrlIleIleValAspSerSerGlnLeuThrserP 689  
  
QY      1561 -----ATCTTTATATCAACACCAAATATGACTTC-----GATGGTA 1597  
|||:::||||| |||  
Db      689 heglYaenLeuSerIleLeuSerPheAlaAsnAsnLysValAspSerIleGluAspGIya 709  
  
QY      1598 TATTTCTTGGCTGACCAAGTCTCAACCATTTAAAAATGGCTGGCAAT----- 1644  
|||:::||||| |||::: |||  
Db      709 IaPheGluAsnLeuLeuSerIleuLysIleLeuAspLeuSerAsnAsnProValThrsert 729  
  
QY      1645 -----TCCTTCAAAAGAC-----AAACCCCTTCAAAATGTC-----TTTGCAACA 1684  
|||:::||||| |||  
Db      729 rpSerProthrAlaPheArgAspLeuSerHisSerIleSerIleAsnMechAlasnt 749  
  
QY      1685 CA----- 1686  
|||  
Db      749 hrGlyLeuPheSerMetProLysPheSerHisArgSerIleGlnSerLeuAsnIleSerC 769  
  
QY      1687 -----ACAAACTTGACATTCC 1702  
|||::: |||  
Db      769 ysaEnuLysIleTyrgLuleuSerGluLysAspLeuAlaProLeuThrLysValValaLaL 789  
  
QY      1703 TGATTCCTTCAAAATGCAATGGAGCAAAATATCTGGGGGATTTTGACACCCCTCAT 1762  
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Db      789 euAspIleSerHisAsnAsnLeuLysGlnIleSerSerMetAlaPheGluProleuLen 809  
  
QY      1763 GACTTCATATTAATATAGTACACAACAATCTATGTGTTTTGGATTCAATCCATTATA 1822  
|||:::||||| |||::: |||  
Db      809 IsleuLysGlnLeuAsnValSerAlaAsnProIleThrIstleuThraAsnGlnHisIleg 829  
  
QY      1823 ACCACGTGATTCCTC----- 1839  
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Db 829 lnglnleuTyrlYleuTyraSnllleProaSpMeAlaArgProTyGrlnlleserSerI 849
QY 1840 -----AGCACTCTGT 1849
Db 849 leleuSerAaSnleuProProleuHiSthrlYerValaBpIlleYgluSerAlaLeuA 869
QY 1850 ATTGCAGTTTCATCGCATAGACATCTTAAGAAATACAGCAATTTTCCAAAGAGTC 1909
Db 869 sPaYglnPheTy-rThAlaAephThArg-----LeuLeuAghlileu-----ValV 885
QY 1910 TAGCCTTCCTCAATCTTACTTACATCAATCTGTGCTGTGATATGTGAACATCAGAAATTC 1969
Db 885 alAlaAgIaYarYgAsnleuThrlYsIlleGlValglYalAphleAlThrlleArgIlyPhe 904
QY 1970 TGCAGTGGGTCAAGAAACAGAAAGAGTTCTTGTAATGTTGAACAATGACATGTGCA 2029
Db 905 -----ArgV 906
QY 2030 CACCTGAGATGAATACCTCTTAGTGTGATTTTAATTAATCTACCTGTATATGT 2089
Db 906 alArYglleGlulIleHlaaSerSerIlleGlulnleProSerArg-----lleP 923
QY 2090 ACAAGACATCATCATGAGTGTCACTGTGCTGATGTGATTTGCTA----- 2133
Db 923 heaPThrleuThrGlYlleserIlleuSerleuSerleuThraSpAaSnlyleuThrt 943
QY 2134 -----TTCACGTGTAGCA 2145
Db 943 hrPheAaSnProPheGlInSerThrValAla 952

RESULT 8
JC5239
Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: JC5239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Alignment Scores:
Pred. NO.: 4.55e-14 Length: 605
Score: 285.50 Matches: 144
Percent Similarity: 36.06% Conservative: 94
Best Local Similarity: 21.82% Mismatches: 240
Query Match: 5.51% Indels: 183
DB: 2 Gaps: 17

US-09-396-985B-46 (1-2951) x JC5239 (1-605)

QY 301 GTTCTTAATATTACTACCAATGATGATGAGAACTCAGAAAGTCCGTATGACATT 360
Db 53 ValaSnGlInleuSerValPheCySerSerArgAaSnleuThrArgleuProAaBpIlyle 72
QY 361 CCTTCCTCAACCAAGACATAGATCTGAGCTTCAACCCCTTGAAAGATCTTAAGAGCTAT 420
Db 73 ProGlYglYThrGlInAlaLeuThrlYeuAaSerAaSnleuSerIlleProProAla 92
QY 421 AGTTTCTCAATTTTTCAGAACTTCAAGTGTGATTTATCCAGGTGAAATGAAACA 480
Db 93 AlaPheAaSnleuSerSerleuAlaPheleuSnleuGlInglYglInleuGlYser 112
QY 481 ATTGAAGCAAGGATGAGCTTACACACCTCTCAAACTTGAATCTGACAGAAAC 540
Db 113 leuGlInProGlInAlaLeuGlInleuGlInAaSnleuCyShleuHlSleuGlInArgAa 132
QY 541 CCTATCCAGAGTTTTCCTCCAGAAAGTTTCTGTGACATAACAAGTTTGAACATCTGGTG 600

Db 133 GlInleuAaSerleuAlaValglYThrPheAlaTy-rThrProAlaLeuAlaLeuGlY 152
QY 601 GCTGTGAGACAAATTTGGCCTCTCTAGAAAGGTTCCATTGACAGCTTATACCTTA 660
Db 153 leuSerAaSnAaSnIleuSerAaSnleuAaBp----- 163
QY 661 AAGAAATTCATGTGGTCACAATTTTATCATCTCTGTAAGTACCTGCATATTTTCC 720
Db 164 -----GlyleuPheGlIn 167
QY 721 AATTCAGCAACTTACATGAGATCTTTCTTATTAATCTTAATTAATCTTACTGTC 780
Db 168 GlYleuGlYaaSnleuThraPheleuAaSnleuGlYThraAaSerleuAlaVal----- 184
QY 781 AAGCACTTAAGTTTCTAGCTGAAATCCCAAGTCAATCTCTTTAGACATGTCTTG 840
Db 184 ----- 184
QY 841 AACCAATTGACTTATCAAGACCAAGCTTTCAGAGAAAT--AAGCTCAGAACTG 897
Db 185 -----leuProAaBpAlaAlaPheArgIlyleuGlYglYleuAaBpGlInleu 199
QY 898 ACTCTAAGAGTAATTTTAATAGCTCAATATATAGAAACTTGCTTCAAAACCTGGCT 957
Db 200 ValleuAlaGlYaaSn----- 204
QY 958 GGTTTACAGCTCCATGCGTTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGAAT 1017
Db 205 -----ArgleuAlaTyR 208
QY 1018 TTGAACCTCTATCATGAGAGCAATGATGATGACCATGATGAGTTCAAGTTTACA 1077
Db 209 leuGlInProAlaLeuPheSerIlyleuAlaGlInleuAaBp----- 221
QY 1078 TATACAAATGATTTTCAGATGATATTTGTAAGTTCCATGTCTGGGAAATGTTCTGCA 1137
Db 222 -----GlyleuAaBpLeuSerArg 227
QY 1138 ATGTCTGTGGCAGGTGATCTATTAATAATCTGAAGAGTGTCTTAACCTTCAAAATGG 1197
Db 228 AaSnAlaLeuAlaIleYalAaSnValPheAlaGlInleuPro-----Argleu 244
QY 1198 CAATCTTATCAATCATTAATGATGTCATGAAGAGTGTCCAACT-----CTGAT 1247
Db 245 GlInlyleuTyrlYleuAaBpAaBpAaSnleuAlaIleAlaValAlaProGlYAlaPheleuGlY 264
QY 1248 TTACCTTTTCTTAAAGTTTGAATTAATCTATGAACAA-----GGTCTATACGTTT 1301
Db 265 leuYalAlaLeuAaBpAaBpAaSnleuSerAaBpAaBpAaBpAaBpAaBpAaBpAaBp 284
QY 1302 AAAAAAATGGCCCTACCAAGTCTCAAGTATCTGATGTTTGTGAAGATGACAGAGCTT 1361
Db 285 ThrPheProGlYleuGlYleuGlYleuAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBp 304
QY 1362 AGTGTGGCTGTCTTATCTGAT-----TTGGGAACAAC 1397
Db 305 leuAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBp 324
QY 1398 AGCTGAGACATTTAAGCTCAAGCTTCAATGGTGCATGATTAAGTGCACAAATTTGATG 1457
Db 325 ArgIleAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBp 335
QY 1458 GGTTAAGAAAGCTGACAGCACTGTGATTTTACAGACTCTTACTTAAAGAGGTCAAGA 1517
Db 336 GlYleuAlYglInleuGlInValleu-ThrlYeuAaBpAaBpAaBpAaBpAaBpAaBpAaBp 354
QY 1518 ATTCTAGAGCTTATCCCTGAAAGCTACTTATCACTGACATCTTATATCAAC 1577
Db 354 sValGlYAlaPheleuGlYleuThraAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBpAaBp 374
QY 1578 CAATATGACTGATGATATTTCTTGCTTGACCAAGTCTCAACATTAATAATGGC 1637

QY 1327 GCTATCTAGATCTTAGTAGAAGATGACTGAGCTTTAGTGCTGCTTTTATTCTGATT 1386
Db 393 ----- 393
QY 1387 TGGGACAAACAGCGCTGAGACATTAGACCTGAGCTTCATGCTCATTTATGAGTG 1446
Db 393 ----- 393
QY 1447 CCATTTTCATGGCTGAGAGAGCTGAGACCTGATTTTTCAGACCTGACTTTAAA 1506
Db 394 ----- 394
QY 1507 AGGCTACAGAAATCTCAGCGCTTCTTATCCCTGAAAAAGCTATTGACTGAGCTCT 1566
Db 400 ArgTLeuArgLeuHisThr----- 405
QY 1567 TATATCTAACACCAAAATGTAAGCTGATGATATTTCTGGCTTGACCACTGACACA 1626
Db 406 ----- 414
QY 1627 TTTAAATGCTGCGCAATCTTTTCAAGACACCCCTTCAATGTC----- 1674
Db 415 LeuPheLeu-----ArgAspAsnSerIleSerIleGluGluGlnSer 429
QY 1675 TTTCAAAACACAAACAACTTGACATTCCTGATCCTTTAAATGTCATTTGAAACAATA 1734
Db 430 LeuAlaGluLeuSerGluLeuLeuGlnLeuAspLeuThrAlaGlnLeuThrHisLeu 449
QY 1735 TCTTGGGGGCTATTGACACCCCTCCATGACCTTCAATTTAAATATGAGTACACAAAT 1794
Db 450 ProArgGlnLeuPheGlnGlyLeuGlyGlnLeuGlnLeuLeuSerAsnAsnGln 469
QY 1795 CTATGTTTGTGATTCATCCCATTAATACAGCTGATTCCTCAGACCTTGATTC 1854
Db 470 LeuThrLeuSerGluAspValLeuGlyProLeuGlnArgAlaPheTrpLeuAspLeu 489
QY 1855 AGTTTCATGCTCAGTAGAGACA---TCTAAAGAAATGACGAAACATTTCCAAAGAGTCTA 1911
Db 490 SerIleAsnArgLeuGlnThrProAlaGluLeuPheSerLeuGlyArg---Leu 508
QY 1912 GCCTTCTTCATCTTACTTAACAATTCGTGCTGTATATGTAACATCAGAAATTCCTG 1971
Db 509 ArgTyrLeuLeuLeuArgAsnAsnSerLeu-----GlnThrPheVal 522
QY 1972 CAGTGGGTCAAGAACAGACAGATCTTGCTGATGTGAACAATGACATGTCACACA 2031
Db 523 ProGlnProGlyLeuGlnArgLeuTrpLeu---AspAlaAsnProTrpAspCysSerCys 541
QY 2032 CCTGTAGAG-----ATGAATACCTCCTTAGTGTGATTTTAT 2070
Db 542 ProLeuArgAlaLeuArgAspPheAlaLeuGlnAsnProGlyValValProArgPheVal 561
QY 2071 AATTCTACCTGT-----TATATGTAACAAGACATCATCAGT 2106
Db 562 GlnThrValCysGlnGlyAspAspCysGlnProValTyrThrTyrAsnAsnIleThrCys 581
QY 2107 GTGTCAAGTGTCAAGTGTG 2124
Db 582 AlaGlyProAlaAsnVal 587
RESULT 10
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1282
R/Dat: J.; Baker: R.C.
Biochem: Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JC1282; MUID:93038676; PMID:1384485
A/Accession: JC1282
A/Molecule type: mRNA

A/Residue: 1-603 <DAI>
A/Cross-references: UNIPROT:P35859; GB:S46785; MID:g258002; PIDN:AA823770.2; PID:g57059
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F/1-27/Domain: signal sequence #status predicted <Sig>
F/28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F/267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
Alignment Scores:
Pred. No.: 1 22e-13 Length: 603
Score: 280.00 Matches: 163
Percent Similarity: 38.12% Conservative: 81
Best Local Similarity: 25.47% Mismatches: 221
Query Match: 5.41% Indels: 176
DB: 2 Gaps: 26
US-09-396-985b-46 (1-2951) x JC1282 (1-603)
QY 322 TGCATGATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTTCACCAAGAACATA 381
Db 60 CysSerSerIleAsnLeuThrHisLeuProAspAspIleProValSerThrArgAlaLeu 79
QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTATAGCTTTCCTCAATTTTTCAGAA 441
Db 80 TrpLeuAspGlyAsnAsnLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSerSer 99
QY 442 CTTCAGTGGCTGATTTATCCAGGTGTGAATTTGAACAAATTTGAAGACAGAGCGCAT 501
Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeu 119
QY 502 GGGTTACACACCTTCAAACTTGATAGTACGACGAAACCTTATCCAGAGTTTTCCTCA 561
Db 120 GlyLeuGlnAsnLeuTyrTyrLeuHisLeuGlnAlaArgAsnArgLeuArgAsnLeuAlaVal 139
QY 562 GGAAGTTCTCTGCTGACTTAACAAGTTTGAACAATCTGTGCTGTGAGACAAATTTGCC 621
Db 140 GlyLeuPheThrHisThrProSerLeuAlaSerLeuSerLeuSerAsnLeuGly 159
QY 622 TCTCTGAAGACCTTCCCTATGAGACCTTATTAACCTTAAAGAACTCATGTGGCTCAC 681
Db 160 ArgLeuGlnGluGlyLeuPheGlnGlyLeuSerHisLeuTrpAspLeuAsnLeuGlyTyr 179
QY 682 AATTTT-----ATACATTCCTGT 699
Db 180 AsnSerLeuValValLeuProAspThrValPheGlnGlyLeuGlyAsnLeuHisLeuLeu 199
QY 700 AAGTTA-----CTGCATATTTTTCATTCGACGAC 732
Db 200 ValLeuAlaGlyAsnGlyLeuThrTyrLeuGlnProAlaLeuPheCysGlyLeuGlyGlu 219
QY 732 CTAGTACATGATGATCTTCTTAACTATATTAATTAATTAATTAATTAATTAATTAATTA 792
Db 220 LeuArgGluLeuAspLeuSerArgAsnAlaLeuArgSerValIleAsnValPheVal 239
QY 793 TTTCTACGTAAGAAATCACAAGTC---AATCTCTTTTGAAGATGTTGAACCCCAAT 849
Db 240 HisLeu-----ProArgLeuGlnGlyLeuTyrLeuSerArgAsnLeu-----Ile 254
QY 850 GACTTCAATTCAGACCAAGCCTTTCAGGGAATTAAG---CTCCATGAATGACTCTTAA 906
Db 255 ThrAlaValAlaProGlyAlaPheLeuGlyMetLeuAlaLeuArgTrpLeuAspLeuSer 274
QY 907 GGTAATTTTAATGCTCAAAATATATATGAAACCTTGCAAAAACCTGGCTGGTTTACAC 966
Db 275 HisAsn---ArgValAlaGlyLeuMetGlnAspThrPheProGlyLeuGlyLeuHis 293
QY 967 GTCCATGCGTGTGATCTTTGGA-----GAATTTAAAGATGAA 1002
Db 294 ValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArgProArgThrPheIleArgAspLeu 313
QY 1003 AGGAATCTGAAATTTTGA-----CCCTCATC 1032
Db 314 HisPheLeuGlnGluLeuGlnLeuGlyHisAsnArgIleArgGlnLeuGlyGluArgThr 333

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OY 1033 ATGAGAGACTATGTGAT-----GTACCATTGATGAGTTCAGTTAACAATATACA 1083
    |||||
DB 334 PheGluGluLeuGluGlnLeuGluValLeuThrLeuAsnAspAsnGlnIleThrGluVal 353
OY 1084 AATGATTTTTCAGATGATTTGTTAAGTTCATTCCTGGCGCAATGTTCTGC---AAT 1139
    |||||
DB 354 Arg-----ValGluAlaPheSerGlyLeuPheAsnValAlaValMetAsn 368
OY 1140 GTCTCTGGAGGTGATCTATATAAATATCTAGAAGATGTTCTTAACATTGCAATGGCA 1199
    |||||
DB 369 LeuSerGlyAsnCysLeuArgSerLeuProGluArg-----ValPheGln----- 383
OY 1200 ATCTTATCAATCATTAAGATGTCACACTAAGACAGTTTCCAACTCGATCTACCTTCTT 1259
    |||||
DB 383 ----- 383
OY 1260 AAAAGTTGACTTTAATGAAACAAGGCTCTATCAGTTTAAAAAGTCCCTACCA 1319
    |||||
DB 384 -----GlyLeuAsp 386
OY 1320 AGCTCAGCTATCTGATCTTATGTAAGAAATGCATGAGCTTATGTTGGCTGTTTAT 1379
    |||||
DB 387 LysLeuHisSerLeuHisLeuGlnHisSerCysLeuGlnHisValArgLeuHisThrPhe 406
OY 1380 TCTGATTTGGGAAACAAGCCTGAGACACTGAGCTTCAATGCT---GCCATC 1436
    |||||
DB 407 Ala-----GlyLeuSerGlyLeuArgLeuPheLeuArgAspHisSerIleSer 424
OY 1437 ATTATAGAGTCCCAATTTTCATGGGCTGAGAGAGCTGACACCTGATTTTTCACAGCTC 1496
    |||||
DB 425 IleGluGlnGlnSerLeuAlaGlyLeuSerGlnLeuLeuGlnLeuAsp-----Leu 441
OY 1497 TACTTAAAAAGGCTCACGAATTC-----TCAGCTTCTTATCCCTTGAAGACTACT 1550
    |||||
DB 442 -ThrThrAsnArgLeuThrHisLeuProArgGlnLeuPheGlnGlyLeuGlnIleGln 461
OY 1551 TTACCTGACATCTCTTATTAACAACCAAAATGACTTCATGATGATATTTCTGGGCTT 1610
    |||||
DB 461 uTyrLeuLeuLeuSerTyrAsnGln-----Le 470
OY 1611 GACCAAGTTCACACATTTAAATGAGCTGGCAATTCCTTCAAAACAACCCCTTCAA 1670
    |||||
DB 470 uThrThrLeuSer-----AlaGln 476
OY 1671 TGTCTTTGCAACAACAACAACTTACATCTCTGATCTTAAATGTCATTGGAACA 1730
    |||||
DB 476 uValLeuGlyProLeuGlnArgAlaPheThrLeuAspIleSerHisAsnHisLeuGlnIle 496
OY 1731 AATATCTGGGGGATTTGACACCTCCATAGACTTCATTAATTAATGAGTACACA 1790
    |||||
DB 496 PheuAlaGluGlyLeuPheSerSerLeuGlyArgValArgTyrLeuSerLeuArgAspHis 516
OY 1791 CAATCTA-----TTGTTTGGATTCAATCCCA 1817
    |||||
DB 516 nSerLeuGlnThrPheSerProGlnProGlyLeuGlnArgLeuThrPheLeuAspAlaAsnPr 536
OY 1818 TTATACACAGCTGATTTCCCTCAGACACTTGTGATTGACAGTTCAATCCGATAGACATC 1877
    |||||
DB 536 cTTP-----AspCysSer----- 540
OY 1878 TAAAGAAATACGCAACATTTTCCA---AAGAGCTAGAGCTTCTCAATCTTACTAACA 1934
    |||||
DB 541 -----CysProLeuValAlaLeuArgAspPheAlaLeuGlnAsnPr 554
OY 1935 TTCTCTTGCTGTATATGTAACATCAGAAATTCCTGAGAGTGTCAAGAA-----CA 1988
    |||||
DB 554 cGlyValVal-----ProArgPheValGlnThrCysGluGlyAspAs 569
OY 1989 GAAGCATTTCTTGATGATGTTGAACAACAATGACATGTGACACACTGTAGAGATGAAT 2046
    |||||
DB 569 pCysGlnProValTyrThrTyrAsnAsnIleThrCysAlaGlyProAlaAsnValSer 588

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RESULT 11
T10504
disease resistance protein Cf-2.1 - currant tomato
C.Species: Lycopersicon pimpinellifolium (currant tomato)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C.Accession: T10504; T10515
R.Dixon, M.S.; Jones, D.A.; Keddle, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A.Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoded
A.Reference number: Z17062; MUID:96190812; PMID:8608599
A.Accession: T10504
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-1112 <DIX>
A.Cross-references: UNIPROT:Q41397; EMBL:U42444; NID:g1184074; PIDN:AACT5779.1; PID:g111
A.Experimental source: cultivar Cf 2
A.Accession: T10515
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-1066, 'I', 1068-1085, 'E', 1087-1110, 'R', 1112 <DIX>
A.Cross-references: EMBL:U42445; NID:g1184076; PIDN:AACT5780.1; PID:g1184077
A.Experimental source: cultivar Cf 2

Alignment Scores:
Pred. No.: 4.76e-13 Length: 1112
Score: 273.00 Matches: 201
Percent Similarity: 36.05% Conservative: 118
Best Local Similarity: 22.71% Mismatches: 312
Query Match: 5.27% Indels: 255
DB: 2 Gaps: 37

US-09-396-985b-46 (1-2951) x T10504 (1-1112)
OY 42 AGTGAATGCTTAAGTTGGACTCTCACTTCTCT----- 77
    |||||
DB 319 SerGlnAsnAlaLeuAsnGlySerIleProAlaSerLeuGlnGlyAsnLeuYAsnLeuSer 338
OY 78 ---TTGATATAGTACTTGACAGAGGGGACCCAGGGAGGAGGAGGAGGAGGAGGAGGAGG 134
    |||||
DB 339 ArgLeuAsnLeuVal-----AsnAsnGlnLeuSerGlySerIleProAlaSerLeu 355
OY 135 GAGCTCGCGCTGCACCAAGT-----TACAGATGTCATGATTTCTCATGAGCTCCACT 188
    |||||
DB 356 GlyAsnLeuAsnLeuSerMetLeuTyrTrpAsnGlnLeuSerGlySerIle 375
OY 189 GGTTCGAGAAATGCCAGATGATGCTCCTCGCTCCTGCTGAGCTTGCATCATGCGC 248
    |||||
DB 376 -----ProAlaSerLeuGlyAsn-LeuAsnAsnLeuSerMetLe 388
OY 249 ACTGTTCTTCCTCGCTGCACACAGAGAGGTTGAATCCCTGCATAGAGTATCTTAA 308
    |||||
DB 388 uTyrLeuTyrAsnAsnGlnLeuSerGlySerIleProAlaSerLeuGlyAsnLeuAsnAs 408
OY 309 TATTACC-----TACCAATCATGATCAGAAACTCAGAAAGTCCCTGATGACATTC 362
    |||||
DB 408 nLeuSerArgLeuTyrTrpAsnGlnLeuSerGlySerIleProGluGlnIleGln 428
OY 363 T-----TCTTCAACAAGAACATGATCTGAGCTTCAACCCCTTGAAGATCTTAAAG 416
    |||||
DB 428 YTyrLeuSerSerLeuThrTyrLeuAspLeuSerAsnAsnSerIleAsnGlyPheIlePr 448
OY 417 CTATAGCTTCCTCCATTTTTCAGAACTTCAGTGGCTGATTTATCCAGGTGTGAATTA 476
    |||||
DB 448 cAlaSerPheGlyAsnMetSerAsnLeuAlaPheLeuPheLeuTyrGluAsnGlnLeuAl 468
OY 477 AACATTTAAGAACAGAGCATGAGCTTACACACCTTCAACTGATGATGACAGAG 536
    |||||
DB 468 aSerSerValProGluGluIleGlyTyrLeuArgSerLeuAsnValLeuAspLeuSerGln 488
OY 537 AAACCTTATCCAGAGTTTTCCTCCAGAGAGTTTCTCGAGATTAACAATTGACAACTCT 596
    |||||
DB 488 uAsnAlaLeuAsnGlySerIleProAlaSerPheGlyAsnLeuAsnAsnLeuSerArgLe 508

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Qy	597	GGTGGCTGTGAGACAAAAATTTGGGCTCTCTAGAAAGCTTCCCTATTGGACAGCTTAAAC	656
Db	508	uAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIleGlyIleuArgSe	528
Qy	657	CTTAAAGAACTCAATGAGCTCTCACAATTTATACATTTCTCTGTAAAGTTACCTGCATATT	716
Db	528	rLeuAsnValLeuAsnProLeuSerGluAsnAlaLeuAsnGly---SerIleProAlaSerPh	547
Qy	717	TTCCAACTGACGAACCTAGTACATGTGGATCTTTCTTATATACATATATTCGAACATATAC	776
Db	547	eGlyAsnLeuAsnAsnLeuSerArgLeuAsnLeuValAsnAsnGlnLeuSerGlySerIle	567
Qy	777	TGTCAAGACCTTACAGTTTCTACCTGGAAGAAATCCACAGTCAATCTCTC-----	825
Db	567	eProGluGluIleGlyIleuArgSerLeuAsnAspLeuGlnLeuSerGlnAsnAlaLe	587
Qy	826	-----TTAGACATG-----	834
Db	587	uAsnGlySerIleProAlaSerLeuGlyAsnLeuAsnAsnLeuSerMetLeuIleuTy	607
Qy	834	-----	834
Db	607	rAsnAsnGlnLeuSerGlySerIleProGluGluIleGlyIleuSerSerLeuThrTy	627
Qy	835	-----TCTTGAAC-----CCAACTGACCTTCATTCGAAGCCA	866
Db	627	rLeuSerLeuGlyAsnAsnSerLeuAsnGlnGlyLeuIleProAlaSerPheGlyAsnMetAr	647
Qy	867	AGCCTTACAGGAATTAAGCTCCCAATGAACTGACTCTAAGAGTAAATTTAAATAGCTCA--	924
Db	647	gAsnLeuGlnAlaLeuIleLeuAsnAspAsnAsnLeuIleGlyIleuIleProSerSerVa	667
Qy	925	-----AATATATGAAA-----	936
Db	667	lCyAsnLeuThrSerLeuGluValLeuTyMetProArgAsnAsnLeuIleuGlyIleVa	687
Qy	937	----ACTTGCCCTCAAAAACCTGGCTGTTTACAGTCCATCGGTTGATCTTTGGAGAAAT	992
Db	687	lProGlnGlyLeuGlnYanIleSerAsnLeuGlnValLeuSerMetSerSerAsnSerPh	707
Qy	993	TAAAGATGAAGAAGAACTCGAAATTTTGAACCCCTCATCATGGAAGACATATGTATGT	1052
Db	707	eSerGlyIleuLeu-----ProSerSerIleSerAsnLeuThrSerIle	721
Qy	1053	GACCAATGATGAGTTCAGGTTAACAATATACAATGATTTTTCAGATGATATTTGAAGTT	1112
Db	721	uGlnIleLeuAsnProPheGly-----ArgAsnAsnLeuGluGlyAlaIleProGln--	737
Qy	1113	CCATTGCTTGGGGAATGTTTCTGCATATCTCTG-----	1146
Db	738	---CysPheGlyAsnIleSerSerLeuGlnValPheAspMetGlnAsnAsnIleuLeuSe	756
Qy	1147	-----GAGGGGTATCTATAAATATCA-----	1170
Db	756	rGlyIleuProThrAsnProIleSerIleGlyCysSerLeuIleSerLeuAsnLeuHiSGI	776
Qy	1171	-----GAGATGTTTCTTAAACATTTTC-----AAATGGCAATCCTT	1205
Db	776	yAsnGlnLeuGlnuAspGluIleProArgSerLeuAspAsnGlyIleGlyIleGlnValLe	796
Qy	1206	ATCAATCATCTAGATGCTCAACTAGC--AGTTTCCACTCTGGAT-----CTACCCCT	1255
Db	796	uAspLeuGlyAspAsnGlnLeuAsnAspThrPheProMetThrPheuGlyThrLeuProGI	816
Qy	1256	TCTTAAAGTTGACTTAACTTAACATGAAAGAA-----GGGCTATATC-----AATTATTA	1303
Db	816	uLeuArgValLeuArgLeuThrSerAsnIleuHiSGIlyProIleArgSerSerArgAl	836
Qy	1304	AAAATGGCCCCCAACAGTCTCAGCTATCATGATCTTTAGTGAATATGACATGACCTTTAG	1363
Db	836	acGluIleMetPheProAspLeuArgIleIleIleAspLeuSerArgAsnAlaPheSer-----	854
Qy	1364	TGTGGCTGTGTTCTTATCTGATTTGGGAAACAAACAGCTGAGACCTTAGACCTTACGCTT	1423

Db	855	-----				-----	855	
Qy	1424	CAATGGTC	CAATTA	TGAGTGC	CAATTTT	CATGGGCT	TGAAGAAGCTGCAGCACTGGA 1483	
Db	866	-LysGly	MetArg	ThrVal	AspIys	ThrMet	GluGluProSer	TyrGluSerTyrTrpAs 885
Qy	1484	TTTTTCAG	CACTCACT	TTTAAAA	AGGTCAC	AGAAATTC	GTGAGGCTTCTTATCCCTGAAA 1543	
Db	885	PaapSer	ValVal	ValVal	ThrLys	GlyL- LeuGlu	----- LeuGluLeuValA 901	
Qy	1544	AGCACTT	CACTTCA	CTCTTA	TACTTA	CAACAAAT	TGACTTGATGTATATTTTC 1603	
Db	901	rglieLeu	SerLeu	-----	TyrThr	-----	----- 907	
Qy	1604	TTGGCTTG	ACACGT	TCACACAT	TAAAAA	TGGCTGG	CAATTTCTTCAAAAGACAAACCC 1663	
Db	908	-----	-----	Valile	AspLeu	SerSer	AsnLysPheGluGlyHisIle- 920	
Qy	1664	TTTCAAA	TGTCCTT	TGCACAA	CACAAACAA	CTTGACAT	TCTCGATCTTCTTAAATGTCAAT 1723	
Db	921	-----	-----	-----	-----	ProSer	----- 922	
Qy	1724	TGAAACAA	ATATCT	TGGGGGG	TATTTG	ACACCC	TACAGCTCAATTTATATATGA 1783	
Db	923	-----	-----	Valleu	GlyAsp	LeuIle	AlaIleArgIleLeuAsnValS 936	
Qy	1784	GTCAACA	CAATCTA	TGTTT	TGGATTC	ATCCCAT	TATTAACAGAGCTATTTCCCTCAGCA 1843	
Db	936	erHis	AsnAla	IleGln	GlyLys	ProSer	SerLeuGlySerLeuSerIleLeuGluS 956	
Qy	1844	CTCTTG	ATGCA	GTTTCA	TTCGCA	TAGACAT	CTTAAGACAAATCTGCAACATTTTCCA 1903	
Db	956	erLeu	AspLeu	SerPhe	AsnGln	LeuSer	----- GlyGluIleProG 970	
Qy	1904	AGAGT	CTAGGC	-----	-----	TTCTTCA	TCTTACTTAACAAATTCGTGTT---G 1942	
Db	970	Inglu	AsnAla	SerLeu	ThrPhe	LeuGlu	PheLeuAsnLeuSerHisAsnTyrLeuGlnG 990	
Qy	1943	CTTGAT	ATATG	GCACAT	CAAGAAAT	TCTG	CAGTGG----- 1977	
Db	990	Lys	ValIle	ProGln	GlyLys	ProGln	PheArgThrPheGluSerAsnSerTyrGluGlyAsnA 1010	
Qy	1978	-----	-----	-----	-----	GTCAAGA	ACACGA 1980	
Db	1010	spg	LysLeu	ArgGlyLys	ProVal	SerLys	GlyLysValAspProValSerLysIlyAsA 1030	
Qy	1991	AGCAG	TCTTG	TGGTAA	TGTTG	GAACAAAT	GACATGTGCACACCTGTAGAGTAGTAATCCT 2050	
Db	1030	snTyr	ThrVal	SerAla	LeuGln	IlyAspGln	----- GluSerAsnSerG 1044	
Qy	2051	CCTTAG	TGTTG	ATTTAA	TATTAAT	CTCACTG	TATATGACACAGACATCACTCAGTGT 2110	
Db	1044	Iuphe	PheAsn	AspPhe	ThrLys	AlaAla	IleMetGlyTyrGlyGlySerGlyLeuGlySileG 1064	
Qy	2111	CAGT	GGTCA	GTGTG	-----	ATGTG	GTGATTCACCT-----GTACCATTTCTGA 2152	
Db	1064	Lylle	SerMet	IleTyrIle	LeuLeu	SerThrGly	AsnLeuArgTrpLeuAlaArgIleI 1084	
Qy	2153	TATAC	CACTT	GTATTT	CACTG	TACTTAT	TCTGCTGCTGTAAAAAGTACAGCAGAGSAG 2212	
Db	1084	leg	LysLys	ValLeu	GlnHis	IleVal	IleIleMetGlnArg-----ArgLysLysGlnArgGlyG 1102	
Qy	2213	AAAG	CACT	TAT 2223	-----	-----	-----	
Db	1102	Iln	Arg	AsnTyr 1105	-----	-----	-----	

C:Accession: T42218
 R:Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Accession: T42218
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1531 <NA>
 A:Cross-references: UNIPROT:088279; EMBL:AB011530; NID:93449289; PIDN:BA32460.1; PID:93
 A:Experimental source: strain Sprague-Dawley; brain
 C:Gene: MEGF4
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Alignment Scores:

Pred. No.:	5.5e-13	Length:	1531
Score:	272.50	Matches:	169
Percent Similarity:	33.58%	Conservative:	98
Best Local Similarity:	21.26%	Mismatches:	260
Query Match:	2	Indels:	268
DB:		Gaps:	28

US-09-396-985B-46 (1-2951) x T42218 (1-1531)

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QY 160 GATCGTCATGTCCTCATGCGCTCCACTGTTGCAGAAATGCGAGATGATGCTCC 219
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DB 220 AspCysHisLeuAlaTrp-----LeuSerGln 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 220 TGGCTCTGGCTAGAGACTCTGATCATGCGACTGTTCTCTCGCTGACACAGAAAC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 229 TrpLeuArgGlnArgProThrIle---GlyLeuPheThrGlnCysSerGlyProAlaSer 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 280 TTGAAT----- 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 248 LeuArgGlyLeuAsnValAlaGlnValGlnYserGlnPheSerCysSerGlyGlnGly 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 286 -----CCCTGCATAGAGTA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 GlnAlaAlaGlnValProAlaCysThrLeuSerSerGlySerCysProAlaMetCysSer 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 301 GTTCTCAATATTACTTACCATGATGATGACAAATCAGCAAAATGCTGATGACATT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 288 CysSerAsnGlyIleValAspCysArgGlyGlySerGlyLeuThrAlaIleProAlaAsnLeu 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 361 CCTTTTCAACCAAGAACTAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTAT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 308 ProGlnThrMetThrGlnIleArgLeuGlnLeuAsnGlyIleYserIleProGly 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 421 AGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCCAGGTGGAATTGAACA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 328 AlaPheSerProArgIleArgGlyLeuArgGlyIleAspLeuSerAsnAsnGlnIleAlaGln 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 481 ATTGAAGCAAGGCGATGCGATGCTTACACCACTCTCAAACTTGATGACAGAAAC 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 348 IleAlaProAspAlaPheGlnGlyLeuArgSerLeuAsnSerLeuValLeuTyrcylAsn 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 541 CCTATCCAGAGTTTTCCTCCAGAAAGTTTCTGAGACTPAACAGTTTGAACATCTGATG 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 368 LysIleThrAspLeuProArgGlyValPheGlyGlyLeuTyThrLeuGlnLeuLeu--- 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 601 GCTGTGAGAGCAAAATTTGGCTCTCTAGAAAGCTTCCTATTTGACACTTATAACCTTA 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 387 -----LeuLeuAsnAla 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 661 AAGAACTCAATGCTGCTCACAATTTTATACATCTCTGTAAGTACCTGCAATTTTCC 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 AsnLysIleAsn-----CysIleArgProAspAlaPheGln 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 721 AATTCAGGAACCTTGTACATGTGATCTTTCTTATTAACATAATTAACAATATTATCTGTC 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 AspLeuGlnAsnLeuSerLeuSerLeuTyTrpAspAsnLysIleGlnSerLeuAlaLys 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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QY 781 AAGCACTTACAGTTTCTACGTGAAATTCACAAAGTCAATCTCTTACAGATGCTTTG 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 GlyThrPheThrSerLeuArg-----AlaIleGlnThrLeuHisLeuAlaGln 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 841 AACCAATGACCTTCATTCACAGACCAACCCCTTACAGGAATTAAGCTCCAGTCACTG 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 AsnPro-----PheIleCysAsp-----CysAsnLeuLys 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 901 CTAAAGGTAATTTTAATAGCTCAAAATATATGAAACT-----TGCCTT--- 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 TrpLeuAlaAspPheLeuArgThrAsnProIleGlnThrGlnGlyAlaArgCysAlaSer 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 946 ---CAAACTGCTGCTGTTTACACGTCCATGCGTGGTATCTTGGAGAAATTAAGATGAA 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 469 ProArgArgLeuAlaAsnLysArgIleGlyGlnIleLysSerLysLysPheArgCysSer 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1003 AGGAATTCGAAATTTTGAACCTCTATCATGGAAGACTATGTGATGATGACATGAT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 489 AlaLysGlnGlnTyThrPheIleProGly-----ThrGln 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1063 GAGTTCAGGTAACTATACAAATGATTTTCAAGATGATTTGTT-----AAGTTC 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 AspTyThrIleLeu-----AsnSerGlnCysThrSerAspValAlaCysProHisLysCys 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1114 CATTCCTGGGGAATGTTTCTGCAATGCTCTGCGAGGCTGATCTATAAATATCTAGAA 1173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 ArgCysGlnAlaSerVal-ValGlnCys-SerGlyLeuLysSerLysIleProGln 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1174 GATGTTCTTAATAATTTCAAAATGCGCAATCTTATCATGATGATGATCAATGACAGT 1233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 537 rgIlePro-----GlnSerThrThrGln- 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1234 TTCCAACCTCGATCTACCTTTCTTAAAGTTGACTTATACATGTAACAAAGGCTCTA 1293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 -----LeuArgLeuAsnAsnAsnGlnI 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1294 TCAGT-----TTTAAAAAAGTGCCCTCCAGAGCTCAGCTATC 1332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 IeSerIleLeuGlnAlaThrGlyLeuPheLysLys-----LeuSerHisLeuLysLysI 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1333 TAGATCTTAGTAGAATGCACTGAGC-----TTTAGTGCTGCTGTT 1374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 LeuAsnLeuSerAsnAsnLysValSerGlnIleGlnAspGlyThrPheGlnGlyAlaThrS 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1375 CTATATCTGAT-----TTGGAAACAAACAGCCTGAGACACTTGAACCTCAGCTTCAATG 1428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 590 eValSerGlnLeuHisLeuThrAlaAsnGlnLeuGlnSer----- 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1429 GTGCCATCATATAGAGTCCCAATTTCAATGGGCTTAGAAGAGCTGACGACCTGATTTT 1488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 -----ValArgSerGlyMetPheArgGlyLeuAspGlyLeuArg-ThrLeuMetLeu 620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1489 CAGCACTCTACTTAAAAAAGGCTACAGAAATTCACAGGTCCTTATCCCTTGAAGAGCTA 1548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 621 ArgAsnAsnAsnArgIleSerCysIleHisAsn---AspSerPheThrGlnLeuArgAsnVal 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1549 CTTTACCTTGACATCTCTTATATACACCAAAATTGACTTGATGATATTTCTTGGC 1608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 640 ArgLeuLeuSerLeuTyTrpAspAsnHisIleThrThrIleSerProGlyAlaPheAspThr 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1609 TTGACAGGCTCCACACATTTTAAATAGGCTGGCAATCTTCAAGAACAC----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 660 LeuGlnAlaLeuSerThrLeuAsnLeuLeuAlaAsnProPheAsnCysAsnCysGlnLeu 679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 680 AlaThrLeuGlnAspThrLeuArgLysLysIleValThrGlyAsnProArgCysGln 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 700 AsnProAspPheLeuArgGlnIleProLeuGlnAspValAlaPheProAspPheArgCys 719
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Db 720 GluInluGluIngluValGlyCysLeuProArProGInGysProGIngluCysAla 739
 1660 -----ACCTTTCAAT-----GTC 1674
 Qy 740 CysLeuArThrValValArgCysSerAsnLysHsIleuGlnAlaIleuProLysGlyIle 759
 Db 1675 TTTCGAACACCAAACTTGACATTCCTCGATCTCTAAATGTCATTTGGAACAATA 1734
 Qy 760 ProLysAsnValThrGluLeu---TyrLeuAspLysGlnPheThrLeuValPro--- 777
 Db 1735 TCTTGGGGGTATTTGACACCCCTGCATAGACTTCAATTTATTAATGAGTCACAAACAT 1794
 778 -----GlyGlnLeuSerThrPheLysTyrIleuGlnLeuValAspLeuSerAsnLys 795
 Qy 1795 STATTGTTTGGATTCATCCCATTTATPACAGCTGATTTCCCTCAGACCTTTGATTC 1854
 796 IleSerLeuSerLeuSerSerPheThrAsnMetSerGlnLeuThrThrIleLeu 815
 Db 1855 AGTTTCATGCGATAGACATCTTAAGGAATGACATTTCCAAAGCTAGCC 1914
 816 SerTyrAsnAlaLeuGlnCysIleProProLeuAlaPheGlnGlyLeuArgSerLeuArg 835
 Qy 1915 TTCTTCATCTTACTTAACAATTCGTGCT----- 1944
 Db 836 LeuLeuSerLeuHsIleGlyAsnAspValSerThrLeuGlnGluGlyIlePheAlaAspVal 855
 Qy 1945 -----TGTATTTGTGAACATCAG 1962
 Db 856 ThrSerLeuSerHsIleValAlaIleGlyAlaAsnProLeuTyrCysAspCysHsIleAsnArg 875
 Qy 1963 AAATTCCTGCAGTGGGTCAAGAAACAGAGAGCTTCTTGATGATTTGGAACAATGACA 2022
 Db 876 TrpLeuSerSerThrValLysThrGlyTyrLys-----GluProGlyIleAlaArg 892
 Qy 2023 TGTGCAACACCTGTAGAGATGAATACCTCTTAGTGTG 2061
 Db 893 CysAlaGlyProProGlnMetGluGlyLysLeuLeuLeu 905
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 A41915
 Insulin-like growth factor-binding complex acid-labile chain precursor - human
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 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A41915
 R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
 Mol. Endocrinol. 6, 870-876, 1992
 A:Title: Structure and functional expression of the acid-labile subunit of the insulin-1
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 A:Status: preliminary
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 A:Residues: 1-605 <LBO>
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 A:Experimental source: liver
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 60 CysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
 Db 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTCCAAATTTTTCAGA 441
 80 TrpLeuAspLysAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
 Qy 442 CTTCAGTGGCTGATTTATTCAGGTGTAATGAAATGAAATGAAATGAAATGAAATGAAATG 501
 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGluProGlnAlaLeuLeu 119
 Qy 502 GGCCTTACACCAACCTTCAACCTGATGATGACAGAAACCTTACAGAGTTTTCGCCA 561
 120 GlyLeuGluAsnLeuCysHsIleHsIleValGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
 Db 562 GAAATTTCTCTGACTTAACAAGTTTGAACATCTGCTGCTGCTGAGACAAATTTGACC 621
 140 GlyThrPheAlaHsIleThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
 Qy 622 TCTCTAGAAAGCTTCCCTATGACACGCTTATTAACCTTAAGAAACCTCAATGTGGCTCAC 681
 160 ArgLeuGluAsp----- 163
 Db 682 AATTTTATACATTCCTGATGATTAACGATATTTTTCATGCTGACGAACCTAGTACAT 741
 164 -----GlyLeuPheGluGlyLeuGlySerLeuTrpAsp 174
 Qy 742 GTGATCTTCTTATATCTATATTAATCAACATTAATGATCAACGATTCAGTTTCTACGT 801
 175 LeuAsnLeuGlyTrpAsnSerLeuAlaVal----- 184
 Db 802 GAAATTCACAGATCAATCTCTCTTATGACATGCTTGAACCCATTAATGATTCATTCAC 861
 185 -----LeuPro 186
 Qy 862 GACCAAGCTTTCAGGGAATT---AGCTCCATGAACTGACTPAGAGGTAATTTTAAT 918
 187 AspAlaAlaPheArgGlyLeuGlySerLeuArgGluLeuValLeuAlaGlyAsn----- 204
 Db 919 AGCTCAATATATGAAAACTGCTCAAAACCTGCTGCTGTTACGATCGATCGGTG 978
 204 ----- 204
 Qy 979 ATCTGGAGAAATTAAGATGAAAGAAATCTGAAATTTTGAACCTCTATCATGAA 1038
 205 -----ArgLeuAlaTyrLeuGlnProAlaLeuPheSer 215
 Db 1039 GGAATATGATGATGACATTTGATGATTCAGTTACATATACATTAATGATTTTTCGAT 1098
 216 GlyLeuAlaGluLeuArg-----GluLeuAspLeuSerArg 227
 Qy 1099 GATATGTTGATGATGATGCTGGAGATGTTCTGCAATGCTCTGAGAGGTATCT 1158
 228 Asn-AlaLeuArgAlaIleLysAlaAsnValPheValGln-----Le 241
 Db 1159 ATAAATATCTAGAAAGATGTTCTTAAACATTTCAATGCAATCTTATCATCATTTAGA 1218
 241 UPProArgLeuGlnLysLeuTyrLeu-----AspArgAsn-LeuIle-----A 255

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OY 1219 TGTCACTAAGCAGGTTTCCAACTTGATCTACCCCTTTCTTAAAGTTGACTTTAAGTA 1278
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Db 1255 TAAATValAlaProGlyAlaPheLeuGlyLeuLysAlaLeuArgTrpLeuAspLeuSerH 275
OY 1279 TGAACAAA-----GGGTCTACGATTTTAAAAAGTGGCCCTTACCAAGTCTCAGCTATC 1332
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Db 275 TAspArgValAlaLysLeuLeuGlyAspTrpPheProGlyLeuLeuGlyLeuArgValL 295
OY 1333 TAGATCTTAGTGAAGAAGTACCTTTAGTGGTGGCTTATCTATCTGAT----- 1385
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Db 295 euArgLeuSerHisAsnAlaLeuAspLeuArgProArgTrpPheLysAspLeuHisP 315
OY 1386 -----TTGGACAAACACAGCTTACCACTTACCTCAGCTTCAATG 1428
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Db 315 heLeuGlyLeuLeuLeuLeuGlyHisAsnArgLysArgLysLeu----- 329
OY 1429 GTGCCATCATTTATGATGTCGCAATTTTCATGGCTTGAAGAAGCTGACAGCTGATTTT 1488
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Db 330 -----AlaGluArgSerPheGlyGlyLeuGlyGlnLeuGlyValLeu-ThrLeu 345
OY 1489 CAGCACTGACTTTTAAAAAGGTCACAGAAATTCAGGGTCTTATCCCTTGAAGAAAGTA 1548
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Db 346 AspHisAsnGlnLeuGlyGlnLysVal--LysAlaGlyAlaPheLeuGlyLeuThrAsnVal 364
OY 1549 CTTTACCTTACATCTTATATCTAATACACCAAAATTTGACCTTGATATATTTCTTGGC 1608
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Db 365 AlaValMetAsnLeuSerGlyAsnGlyLeuArgAsnLeuProGlyGlnValPheArgGly 384
OY 1609 TTGACAGCTCTTCACACATATAAAATGGCTGGCAATTT----- 1647
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Db 385 LeuGlyLysLeuHisSerLeuHisLeuGlyGlySerCysLeuGlyArgLysProHis 404
OY 1648 -----TTCAAGACACACACCTTTCAAT 1671
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Db 405 ThrPheTrpGlyLeuSerGlyLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGly 424
OY 1672 GTCTTTGCAACACAC-----ACAAACTGACATTCCTTGATCTTCTTAAAGT 1719
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Db 425 IleGlyGlnGlnSerLeuTrpGlyLeuAlaGlnLeuLeuGlnLeuAspLeuThrSerAsn 444
OY 1720 CAATTGGAACAATAATCTTGGGGGGTATTTGACACCCCTTCATAGACTTCAATTATTAAT 1779
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Db 445 GlnLeuTrpHisLeuProHisArgLeuPheGlnGlyLeuGlyLysLeuGlyLysLeuLeu 464
OY 1780 ATGATGTCACACATCTATTTGTTTGGATTCATCCCATTTTAAACACCTGATATTCCTC 1839
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Db 465 LeuSerArgAsnArgLeuAlaGlnLeuProAlaAspAlaLeuGlyProLeuGlnArgAla 484
OY 1840 AGCACTTTGATTTGAGATTTCAATGCAATAGACATATAAGAAATCTGCACATTTT 1899
    ||||| ||||| ||||| ||||| |||||
Db 485 PheTrpLeuAspValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeuAlaPro 504
OY 1900 CCAAGAAGCTAGCCCTTCTTCAATCTTACTAACAATTTCTTGCTTGATATGTGAACAT 1959
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Db 505 LeuGlyArgLeuArgGlyLeuSerSerLeuArgAsnSerLeuArgTrpPheThrProGln 524
OY 1960 CAGAAATTCCTGCAG-----TTGGTCAAGAAACAGAAAGCATTCTTGTAATGTTGAA 2013
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Db 525 ProProGlyLeuGlnArgLeuTrpLeuGlnGly-----Asn 536
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Db 537 ProTrpAspCysGlyCysProLeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSer 556
OY 2053 TTAGTGTGATTTTATATATCTTCACTGT-----TAT 2085
    ||||| ||||| ||||| ||||| |||||
Db 557 AlaValAlaProArgPheValGlnAlaLysCysGlyGlyAspAspCysGlnProAlaLys 576
OY 2086 ATGTCACAGACATATCATGATGTGTGCTGCTGCTGCTGATTT 2127
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Db 577 ThrTyraAsnAsnIleThrCysAlaSerProProGlyValVal 590

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RESULT 14
B36665
silt protein 2 precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C:Accession: B36665
R:Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A:Title: silt: an extracellular protein necessary for development of midline glia and c
A:Reference number: A36665; MUID:91099665; PMID:2176636
A:Accession: B36665
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1469 <ROT>
A:Cross-references: GB:X53959
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A:Gene: FlyBase:silt
A:Cross-references: FlyBase:FBgn0003425
A:Superfamily: fruit fly silt protein; EGF homology; leucine-rich alpha-2-glycoprotein
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F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
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F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
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F:465-537/Domain: proteoglycan amino-terminal homology <PAH3>
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F:791-861/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:862-1061/Domain: EGF homology <EGF>
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Pred. No.: 5.64e-12 Length: 1469
Score: 259.50 Matches: 183
Percent Similarity: 32.05% Conservative: 91
Best Local Similarity: 21.40% Mismatches: 273
Query Match: 5.01% Indels: 309
DB: 2 Gaps: 33

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Db 220 GlyArgLeuArgAlaLeuArgLeuSerAspAsnProPheAlaCysAspCysHis--Leu 238
OY 175 TCAATGGCTTCACCTGCTTGACGAAATGCCAGATATGCTCTGCTGCTGCTGCTGCTAGG 234
    ||||| ||||| ||||| ||||| |||||
Db 239 SerTrpLeuSerArgPheLeuArgSerAlaThrArgLeuAlaPro----- 253
OY 235 ACTCTGATCATGGACACTGTTCTTCTCTGCTGCTGACACAGAAAGCTTG----- 282
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Db 254 -----TyrThrArgCysGlnSerProSerGlnLeuLysGlyGlnAsn 267
OY 282 ----- 282
Db 268 ValAlaAspLeuHisAspGlnGlyPheLysCysSerGlyLeuThrGlnHisAlaProMet 287

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QY 283 -----AATCCGTGATAGAGTAGTTCCTAATATTACC 315
 Db GluCyeglValaglAuaenseCyProHisProcys---ArgCybAlaAspGlyLeval 306
 QY 316 TACCAATGCATGCATCAGAAATCAGCAAAAGTCCCTGATGCATTCCTTTCCACCAAG 375
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 QY 307 ---AspCybAspGluYbSerLeuThrSerValProValThrLeuProAspPthThr 325
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 QY 376 AACATAGATCTGCATTCACCCCTTGAAAGCTTTAAAAAGCTATAGCTTTCCAAATTT 435
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 QY 465 AspYrLeuHisYbAsnPro-----IleGlnThrSer-GlyAlaArgCy 479
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 QY 479 AsgLeuSerProLysArgMetHisArgArgArgIleGlnSerLeuArg----- 494
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 QY 910 AATTTAATAGCTCAAAATATATAGAAACTTGCCCTCAAAACCTGGGTGTTACAGGTC 969
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 QY 495 -----GlnGlnYbPheYbCyS--- 500
 Db -----
 QY 970 CATCGTTGATCTTGAGAGAAATTAAAGATGAAGAAATCTGAATTTTGAACCTCT 1029
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 QY 508 ----- 508
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 QY 616 LeuGlyLeuHisGlnLeuYbThrLeuAsnLeuYrAspAsnGlnIleSerCybValMet 635
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 QY 1888 -----CTGCAACATTTTCCA----- 1902
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 CDate: 30-Apr-1991 #sequence revision 30-Apr-1991 #text change 02-Aug-2002
 CAccession: A36665; A31640; S13523
 R.Robberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A>Title: Blot: an extracellular protein necessary for development of midline glia and co
 A.Reference number: A36665; MUID:9109665; PMID:2176636
 A.Accession: A36665
 A>Status: preliminary
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 A.Residues: 1-1480 <ROT>
 A.Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98615
 R.Robberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
 Cell 55, 1047-1059, 1988
 A>Title: Blot: An EGF-homologous locus of D. melanogaster involved in the development of
 A.Reference number: A31640; MUID:89077533; PMID:3144436
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 Pred. No.: 5.64e-12 Length: 1480
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 Percent Similarity: 32.05% Conservative: 91

Beet Local Similarity: 21.40% Mismatches: 273
 Query Match: 5.01% Indels: 309
 DB: 2 Gaps: 33
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 QY 175 TCATGCGCTCCAGCTGGTTGCAGAAAATCCAGATGATGCTCCCTGGCTCTGGCTAGG 234
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 QY 235 ACTGATGATCAGGAGCTGTCTTCTCCGCTGACACAGAGAGTTG----- 282
 Db 254 -----TyrThrArgCysGlnSerProSerGlnLeuLysGlnAsn 267
 QY 282 ----- 282
 Db 268 ValAlaSerLeuHisAspGlnGlnPheLysCysSerGlyLeuThrGlnHisAlaProMet 287
 QY 283 -----AATCCCTGCATAGAGGATGTTCTTAATATTAC 315
 Db 288 GluCysGlyAlaGlnAsnSerCysProHisProCys--ArgCysAlaAspGlyLeuAl 306
 QY 316 TACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
 Db 307 --AspCysArgGlnLysSerLeuThrSerValProValThrLeuProAspAspThrThr 325
 QY 376 AACATAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
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 QY 556 TCCCAAGAGATTTCTCTGAGCTAACAGAGTTTACACATCTGGTGGTGGAGCAAA 615
 Db 386 ProSerGlyValPheLysGlyLeuGlySerLeuArgLeuLeuLeuLeuAlaAsnGln 405
 QY 616 TTGACCTCTCAGAAACCTCTCTATTGAGCAGCTTATTAACCTTAAAGAACTCAATGTG 675
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 QY 676 GCTCACAATTTTATACATTCCTGTGAAGTACCTGATATTTTCCATCTGACAGAACTTA 735
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 QY 736 GTACATGATGATCTTTCTTTTAAAC--TATATTCAAACTATTACTGACAGAACTTA--- 789
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 QY 910 AATTTTAATAGCTCAATATATATATGAAATCTGCTTCAAAACCTGGCTGTTACAGTTC 969
 Db 495 -----GluGlyLysPheLysCys----- 500
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 QY 1131 -----TTTCGAATGCTCTGGCAGGATATCTATAAATATCTAGAAGATGTTCCATAA 1185
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 Db 543 spIlePro---LeuNHISThrThrGluLeuLeuAsnAspAsnGluLeuGluYArgIles 562
 QY 1297 GTTTTAAAAAGTG-----GCCCTACCAAGTCTCAGGTATCTAGATCTTAGTGAATG 1350
 Db 562 eISerAspGlyLeuPheGlyValArgLeuProHISLeuValLysLeuGluLeuLysArgAsnG 582
 QY 1351 CACTGAGCTTTAGTGGTGGCTGTTCTTATTCGTGATTTGGGAACAACAGCTGAGACACT 1410
 Db 582 InLeu-----ThrGlyIleGluProAsnAla----- 590
 QY 1411 TAGACCTCAGCTCAATGGTGCATCATTTATGATGCCAATTTCAAGGCTGAGAGAGAC 1470
 Db 591 -----PheGluGlyAlaSerHIS 597
 QY 1471 TGCAACACCTGGATTTTTCAGCACTCTAATTAAAGGTCACAGAAATTCACGCTTC 1530
 Db 597 IeGluGluLeuGluLeuGly-GluAsnLysIleLysGluIleSerAsn--LysMetPhe 615
 QY 1531 TTATCCCTTGAAGAGCTACTTACCTTGACATCTCTTATACTAACACCAAAATTCGACTTC 1590
 Db 616 LeuGlyLeuNHISGluLeuYThrLeuAsnLeuYThrAspAsnGluIleSerCysValMet 635
 QY 1591 GATGGTATATTTCTGGCTTGACCAAGTCTCAACACATTTAAATAGCTGGCAATTCCTTTC 1650
 Db 636 ProGlySerPheGluNHISLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPhe 655
 QY 1651 AAAACAAACACCTTCAATGTCTTGCAACAACACAAACTTGACATTCCTGGAT--- 1707
 Db 656 AsnCysAsnCysNHISLeuAlaTrpPheAlaGluCysValArgLysLysSerLeuAsnGly 675
 QY 1708 -----CCTTCTPAAA----- 1716
 Db 676 GlyAlaAlaArgCysGlyAlaProSerLysValArgAspValGluIleLysAspLeuPro 695
 QY 1716 ----- 1716
 Db 696 HISserGluPheLysCysSerSerGluAsnSerGluGlyCysLeuGlyAspGlyTrpCys 715
 QY 1717 -----TGT----- 1719
 Db 716 ProProSerCysThrCysThrGlyThrValValaLacCysSerArgAsnGluLeuLysGlu 735
 QY 1720 -----CAATGGGA 1728
 Db 736 IleProArgGlyIleProAlaGluThrSerGluLeuYThrLeuGluSerAsnGluIleGlu 755
 QY 1729 CAAATATCTTGGGGGATTTTGACACCTCCATAGACTTCAATATTATTAATATGATGAC 1788
 Db 756 GluNHISThrGlyArgGluArgNHISLeuArgSerLeuThrArgLeuAspLeuSerAsn 775
 QY 1789 AACATCATTTGTTTGGATTCATCCATATATTAACAGCTGTATTCCTTCAGACATCTTT 1848
 Db 776 AsnGluNHISThrIleLeuSerAsnLysThrPheAlaAsnLeuThrLysLeuSerThrLeu 795

QY 1849 GATTGACGTTTCAATGCGATTAAG-----ACATCTAAAGGAATA----- 1887
 Db 796 IleIleSerTrpAsnLysLeuGluGlnCysLeuGluAlaArgNHISAlaLeuSerGlyLeuAsnAsn 815
 QY 1888 -----CTGCAACATTTTCCA----- 1902
 Db 816 LeuArgValaLserLeuNHISGluAsnArgIleSerMetLeuProGluGlySerPheGlu 835
 QY 1903 -----AAGAGTCAAGCTTCTTCAATCTTACTAACATCTGTGCTGTATATGTA 1956
 Db 836 AspLeuLysSerLeuThrNHISIleAlaLeuGlySerAsnProLeuYTrpCysAspCysGly 855
 QY 1957 CATCAGAAATTCCTGCAAGTGGTCAAGGAACAGAACAGATTCTTGTAATGTTGAACAA 2016
 Db 856 LeuLysThrPheSerAspTrpIleLys-----LeuAspTrpValGluPro 870
 QY 2017 -----ATGACATGTGCACACCTGTGAGAGATGAATACCTCTTCAAGTTGATTTAAT 2070
 Db 871 GlyIleAlaArgCysAlaGluProGluGluMetLysAspLysLeuIleLeuSerThrPro 890
 QY 2071 AATTCTTAC----- 2079
 Db 891 SerSerSerPheValCysArgGlyArgValaLysAsnAspIleLeuAlaLysCysAsnAla 910
 QY 2080 TGTATAT-----GTACAAACAATCATCACTGTGTCACT-----GGT 2117
 Db 911 CysPheGluGluProCysGluAsnGluAlaGluCysValaLleuProGluArgGluTrp 930
 QY 2118 CAGTGTGATTTGT-----GGTATCCACTGT 2141
 Db 931 GlnCysLeuCysGluProGluYTrpNHISGlyLysHISCys 943

Search completed: March 29, 2005, 17:35:41
 Job time : 89.7375 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 159.482 Seconds

(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-46

Perfect score: 5177
Sequence: 1 cctcctgcgaagcagacat.....ccttaatcgaagagaag 2951

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+np2.model -DEV=xlh
-Q=/cgn2.1/USPTO/spool/US09396985/runat_28032005.155743.21146/app.query.fasta.1.85098
-DB=UniProt_03 -QFMT=fastran -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CGN 1.1 5213 @runat.28032005.155743.21146 -NCPu=6 -ICPU=3
-NO.MMAP -LARGQUEERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4283	82.7	835	TLR4_MOUSE	Q9guk6 mus musculu
2	4264	82.4	835	Q8K2T5	Q8K2T5 mus musculu
3	3683	71.1	835	TLR4_RAT	Q9guk6 mus musculu
4	3371.5	65.1	838	TLR4_CRIGR	Q9guk6 mus musculu
5	2792	53.9	839	TLR4_HUMAN	Q9guk6 mus musculu
6	2792	53.9	839	TLR4_HUMAN	Q9guk6 mus musculu
7	2791	53.9	843	TLR4_HORSE	Q9guk6 mus musculu
8	2783	53.8	826	TLR4_PAPAN	Q9guk6 mus musculu
9	2762.5	53.4	833	TLR4_FELCA	Q9guk6 mus musculu
10	2753	53.2	837	Q8SPB8	Q8SPB8 gorilla gor
11	2751	53.1	828	TLR4_PONPY	Q8SPB8 pongo pygma
12	2737	52.9	841	TLR4_POVIN	Q9guk6 mus musculu
13	2734	52.8	841	Q8SQ55	Q8SQ55 bos taurus
14	2732	52.8	841	Q6WCDS	Q6WCDS bos taurus
15	2730	52.7	841	Q6WCDS	Q6WCDS bos taurus
16	2656	51.3	841	TLR4_PIG	Q6gys6 sus scrofa

17	2573.5	49.7	839	2	Q8MIQ2	Q8miq2 oryctolagus
18	1902.5	36.7	636	2	Q8SOH3	Q8soh3 canis famli
19	1705.5	32.9	843	2	Q7ZTG5	Q7ztg5 gallus galli
20	1183	22.9	819	2	Q6TSA1	Q6tsa1 brachydanio
21	1163	22.5	817	2	Q6NV08	Q6nv08 brachydanio
22	743	14.4	258	2	Q70EX4	Q70ex4 sus scrofa
23	681	13.2	991	2	Q6R5N8	Q6r5n8 mus musculu
24	664.5	12.8	940	2	Q8T753	Q8t753 branchiosto
25	631	12.2	945	2	Q8O1P9	Q8o1p9 carassius a
26	611.5	11.8	973	2	Q6KCC7	Q6kcc7 oncorhynch
27	607.5	11.7	961	2	Q76CT9	Q76ct9 paralichthy
28	598.5	11.6	961	2	Q76CT7	Q76ct7 paralichthy
29	579.5	11.2	661	1	C180_HUMAN	Q99467 homo sapien
30	569.5	11.0	661	2	Q8C251	Q8c251 mus musculu
31	567.5	11.0	661	2	C180_MOUSE	Q62192 mus musculu
32	559	10.8	1032	1	TLR8_MOUSE	P56682 mus musculu
33	541	10.5	1041	2	Q6UX16	Q6ux16 homo sapien
34	539	10.4	1041	1	TLR8_HUMAN	Q9ntr97 homo sapien
35	531	10.3	1028	2	Q865R7	Q865r7 sus scrofa
36	530.5	10.2	661	2	Q7YRL4	Q7yrl4 sus scrofa
37	519.5	10.0	784	2	Q6YGU2	Q6ygu2 rattus norv
38	514	9.9	785	2	Q6TN21	Q6tn21 sus scrofa
39	514	9.9	785	2	Q76L24	Q76l24 sus scrofa
40	513.5	9.9	784	1	TLR2_MOUSE	Q9gun7 mus musculu
41	513	9.9	1050	1	TLR7_MOUSE	P58681 mus musculu
42	512	9.9	104	2	Q7YSE1	Q7yse1 sus scrofa
43	510.5	9.9	784	2	Q8KID9	Q8kid9 mus musculu
44	506.5	9.8	784	2	Q8LIT5	Q8lit5 mus musculu
45	506	9.8	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien

ALIGNMENTS

RESULT 1
ID TLR4_MOUSE STANDARD; Q92203; PRT; 835 AA.
AC Q9OUK6; Q9D691; Q9Q2F5; Q9Z203;
AD Q9OUK6; Q9D691; Q9Q2F5; Q9Z203;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4; Synonyms=Lps;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RC MEDLINE=99187984; PubMed=10087992; DOI=10.1006/bcmd.1998.0201;
RX Poltorak A., Smirnova I., He X., Liu M.-Y., Van Huffel C., Chan E.K.L.,
RA Birdwell D., Alejos E., Silva M., Du X., Thompson P., Chan E.K.L.,
RA Ledesma J., Roe B., Clifton S., Vogel S.N., Beutler B.,
RT "Genetic and physical mapping of the Lps locus: identification of the
RT Toll-4 receptor as a candidate gene in the critical region."
RL Blood Cells Mol. Dis. 24:340-355(1998).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C3H/HeJ;
RC MEDLINE=99069627; PubMed=9851930; DOI=10.1126/science.282.5396.2085;
RX Poltorak A., He X., Smirnova I., Liu M.-Y., Van Huffel C., Du X.,
RA Birdwell D., Alejos E., Silva M., Galanos C., Freudenberg M.,
RA Ricciardi-Castagnoli P., Layton B., Beutler B.,
RT "Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: mutations
RT in Tlr4 gene."
RL Science 282:2085-2088(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C57BL/6J;
RC MEDLINE=99145502; PubMed=9989976;
RX Qureshi S.T., Lattiviere L., Leveque G., Clermont S., Moore K.J.,
RA Gros P., Malo D.,
RT "Endotoxin-tolerant mice have mutations in Toll-like receptor 4

RT (TIR4).";

RL J. Exp. Med. 189:615-625 (1999).

RL [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Macrophage;

RX MEDLINE=20014145; PubMed=10548109; DOI=10.1038/44605;

RA Underhill D.M., Ozinsky A., Hajjar A.M., Stevens A., Wilson C.B.,

RA Baerentzen M., Ademar A.;

RT "The Toll-like receptor 2 is recruited to macrophage phagosomes and

RT discriminates between pathogens.";

RL Nature 401:811-815 (1999).

RL [5]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-94; ILE-209; GLY-219; ILE-254;

RP ILE-423; SER-477; ALA-516; ASP-593; ILE-600; VAL-607; ILE-637; HIS-761

RP AND IYS-811.

RC STRAIN=Various strains;

RX MEDLINE=20558910; PubMed=11104518;

RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4

RT locus (TLR4).";

RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).

RL [6]

RP SEQUENCE OF 1-154 FROM N.A.

RX STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nishida I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Baldairell R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirral L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Busic J., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,

RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.W., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lehnardt B., Lyons P.A.,

RA Majlout D.R., Maltais L., Marchionni L., McKenzie L., Mili H.,

RA Nageshima T., Numata K., Okido T., Pavan W.J., Pettea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrincci P., Hayatsu N.,

RA Hironaka-Kishikawa T., Komuro H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda S.,

RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yamunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

RL [7]

RP FUNCTION.

RX MEDLINE=20507837; PubMed=10952994; DOI=10.1074/jbc.M007386200;

RT "Murine Toll-like receptor 4 confers lipopolysaccharide responsiveness

RT as determined by activation of NF kappa B and expression of the

RT inducible cyclooxygenase.";

RL J. Biol. Chem. 275:34035-34040 (2000).

RL [8]

RP FUNCTION: Cooperates with LY96 and CD14 to mediate the innate

RP immune response to bacterial lipopolysaccharide (LPS). Acts via

RP MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine

RP secretion and the inflammatory response (By similarity).

CC -1 SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a

CC multi-protein complex containing at least CD14, LY96 and TIRAP.

CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via

CC their respective TIR domains.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1 TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and

CC muscle. Lower levels are found in liver and kidney.

CC -1 POLYMORPHISM: Interstrain analysis reveals that TLR4 is a

CC polymorphic protein and that the extracellular domain is far more

CC variable than the cytoplasmic domain, which is variable at the C-

CC terminal.

CC -1 DISEASE: The protein is encoded by the Lps locus, an important

CC susceptibility locus, influencing the propensity to develop a

CC disseminated Gram-negative infection.

CC -1 SIMILARITY: Belongs to the Toll-like receptor family.

CC -1 SIMILARITY: Contains 19 leucine-rich (LRR) repeats.

CC -1 SIMILARITY: Contains 1 TIR domain.

CC -----

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CC or send an email to license@1sb-sib.ch).

CC -----

DR EMBL; AF095353; AAC9411.1; -;

DR EMBL; AF185285; AAF04278.1; -;

DR EMBL; AF110133; AAD29272.1; -;

DR EMBL; AF177767; AAF05317.1; -;

DR EMBL; AK014533; -; NOT_ANNOTATED_CDS.

DR HSSP; Q15399; 1FVV.

DR MGP; MGI.96824; TLR4.

DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.

DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO; GO:0004888; F:transmembrane receptor activity; ISS.

DR GO; GO:0007250; P:activation of NF-kappa-B-inducing kinase; NAS.

DR GO; GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:mast cell activation; NAS.

DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.

DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; NAS.

DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.

DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; NAS.

DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; NAS.

DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR_Cterm.

DR InterPro; IPR00157; TIR.

DR Pfam; PF00560; LRR; 10.

DR Pfam; PF01582; TIR; 1.

DR PRINTS; PR00019; LEURICRPT.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00285; TIR; 1.

DR PROSITE; PS50104; TIR; 1.

KW Disease mutation; Glycoprotein; Immune response;

KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;

KW Repeat; Signal; Transmembrane.

FT SIGNAL 1 25 Potential.

FT CHAIN 26 835 Toll-like receptor 4.

FT DOMAIN 26 638 Extracellular (Potential).

FT TRANSMEM 639 659 Potential.

FT DOMAIN 660 835 Cytoplasmic (Potential).

FT REPEAT 29 52 LRR 1.

FT REPEAT 53 75 LRR 2.

FT REPEAT 76 99 LRR 3.

FT REPEAT 100 123 LRR 4.

FT REPEAT 127 148 LRR 5.

FT REPEAT 149 172 LRR 6.

FT REPEAT 173 196 LRR 7.

FT REPEAT 201 224 LRR 8.

FT REPEAT 227 251 LRR 9.

FT REPEAT 305 330 LRR 10.

FT REPEAT 348 370 LRR 11.

FT REPEAT 371 393 LRR 12.

FT REPEAT 396 419 LRR 13.

FT REPEAT 420 443 LRR 14.

FT REPEAT 468 492 LRR 15.

FT REPEAT 494 516 LRR 16.

FT REPEAT 517 540 LRR 17.
 FT REPEAT 542 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 75 75 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 204 204 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 237 237 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 492 492 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 613 613 N-linked (GlcNAc . . .) (Potential).

 Alignment Scores:
 Pred. No.: 0 Length: 835
 Score: 4283.00 Matches: 831
 Percent Similarity: 99.52% Conservative: 1
 Best Local Similarity: 99.40% Mismatches: 3
 Query Match: 82.73% Indels: 2
 DB: 1 Gaps: 0

 US-09-396-985b-46 (1-2951) x TLR4_MOUSE (1-835)

Db 221 AlaPheGlnGlyIleuLeuHISGluLeuThrLeuArgIleAsnPheAsnSerSerAsn 240
 Qy 928 ATATAGAAAGCTGCGCTTCAAAACCTGGCGGTTCACGTCGATCGGTTGATTTGGGA 987
 241 ILeuLeuThrCysLeuGlnAsnLeuValGlyLeuHISValHisArgLeuIleLeuGly 260
 Qy 988 GAATTTAAAGATGAAGGAATCTGGAATTTTGAACCCCTCATCATGGAAGACATATGT 1047
 261 GluPheLeuSerGluAsnLeuGluIlePheGluProSerIleMetGluGlyLeuCys 280
 Qy 1048 GATGTGACCATGATGAGTTCAAGTTAACAATATACAAATGATTTTCAATGATATGTT 1107
 281 AspValThrIleAspGluPheArgLeuThrTyrThrAsnAspPheSerAspIleVal 300
 Qy 1108 AAGTTCATGCTTGGGGAATGTTTTCGCAATGCTTCGGCAGGTGATCTATAAATAT 1167
 301 LysPheHisCysLeuAlaAsnValSerAlaMetSerLeuValGlyValSerIleLeuTyr 320
 Qy 1168 CTAGAAGATGTTCTTAAACATTTCAAAATGGCAATCCTTATCAATCATTTAGATGCACT- 1226
 321 LeuGluAspValAlaProLysHisPheLeuTyrGlnSerLeuSerIleIleArgCysGlnLeu 340
 Qy 1227 AAGCAGTTTCAACTGTGATCTAACCTTTCTTAAAGTTGACTTTAACTATGACAA 1286
 341 LysGlnPheProThrLeuAspLeuProPheLeuLeuSerLeuThrLeuThrMetAsnLys 360
 Qy 1287 GGGCTATACGTTTAAAGAGGCGCCTTCAAGTCTCAGCTATCTAGATCTTAGAGA 1346
 361 GlySerIleSerPheLeuValValAlaLeuProSerLeuSerLeuValLeuAspLeuSerArg 380
 Qy 1347 AATGCACTGAGCTTATGATGCTGCTGTTCTTATTTGATTTGGGAACAACAGCCTAGA 1406
 381 AsnAlaLeuSerPheSerArgCysCysSerTyrSerAspLeuGlyThrAsnSerLeuArg 400
 Qy 1407 CACTTAGACCTCAGCTTCAATGGTGCCATTAATAGAGCCAAATTTGATGGCTAGAA 1466
 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGlu 420
 Qy 1467 GAGCTGACGACCTGATTTTTCAGCACTTACTTTAAAGGGTCACAGAAATTTCTAGC 1526
 421 GluLeuGlnHisLeuAsp-PheGlnHisSerThrLeuLysArgValThrGluPheSerAla 440
 Qy 1527 GTCTTATCCCTTGAAGGCTACTTAACTTGAATCTTATTAACAACCAAAATTTGA 1586
 440 AsnLeuSerLeuGluLeuLeuLeuTyrLeuAspIleSerTyrThrAsnThrLysIleAs 460
 Qy 1587 CTTCAGTGTATATTTCTGGCTTGACCACTCTCAACACATTAATAATGGCTGGCAATTC 1646
 460 PheAspGlyIlePheLeuGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSer 480
 Qy 1647 TTTCAAAGACACACCCCTTCAAAATGCTTTTGCAAAACACAAACTTGACATTCCTGGA 1706
 480 rPheLysAspAsnThrLeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAs 500
 Qy 1707 TCCTTCAAAATGTCATTTGGAACAATATCTTGAGGGGGATTTTGACACCCCTGCATAGCT 1766
 500 PheLeuSerCysGlnLeuGluGlnIleSerTrpGlyValaPheAspThrLeuHisArgLe 520
 Qy 1767 TCAATTAATAATATAGTACACAAACATCATTTGTTTGGATTCATCCCATTAATACCA 1826
 520 uGlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisArgAsnGln 540
 Qy 1827 GCTGTATTCCTTCAAGCACTTGTATGACGTTTCAATGCGATAGACATCTAAGGAAT 1886
 540 LeuTyrSerLeuSerThrLeuAspCysSerPheAsnArgIleGluThrSerLysGlyIle 560
 Qy 1887 ACTGCAACATTTTCCAAAGAGCTAGCCTTCTTCAATCTTAACCAAAATCTGTGCTGG 1946
 560 GluGlnHisPheProLysSerLeuValaPhePheAsnLeuThrAsnAsnSerValaLac 580
 Qy 1947 TATATGTGAACATCAGAAATTTCTGCAAGTGGTCAAGGAACAGAACTGTTGGTGA 2006
 580 sIleCysGlnHisGlnLysPheLeuGlnTrpValLysGluGlnLysGlnPheLeuVala 600

QY 2007 TGTGAACAAATGACATGTGCAACACCTGTAGAGATGATTAACCTCTTAGTGTTGATTT 2066
 DB 600 nvalglgimcthrncysalathrprovalglmeasnthserleuvalleuapn 620
 QY 2067 TAAATATCTACCTGTATATATGACAGAACATCATGCTGTGTCACTGTGTAT 2126
 DB 620 eaanaanserthrcyserymetrlystrhrillelleserValserValserVal 640
 QY 2127 TGTGTATCCACTGTAGACATTTCTGATATACACCTTTATTTTCACTGTATCTTATTC 2186
 DB 640 evalValserThValAlahleuileuileuRhIspherlyPhehIsleuileuileu 660
 QY 2187 TGGCTGAAAAAGATGACAGAGAGAGAGAGAGATTAATGATGATTTGTGTACTGTAG 2246
 DB 660 aglyCyshysylserThserThglYgluserllyThasplahenehilleuYserse 680
 QY 2247 TCAGAAATGAGACTGTGTGAGAAATGAGCTGTAAAGATTTAGAGAGAGAGAGAGAT 2306
 DB 680 rglaasngluasprlprValarnganslualeuVallyasleugluuigluYalproar 700
 QY 2307 CTTTCACTCTGCTTCTACTACACAGACTTTATTCCTGTGTGTAGCCATTGCTGCAACAT 2366
 DB 700 gphehIsleuCyshysleuThsThyThrgaasprheleleProglYValAlaAlaAlaenil 720
 QY 2367 CATCCAGAGAGGCTTCACAGAGAGAGAGAGGTTATTTGTGTGTGTGTGTGTGTGTGTAT 2426
 DB 720 ellleugluuigluYphehIslyserThasplahenehilleuYalValserThsThsThs 740
 QY 2427 TCAGAGCCGTGTGTGTATCTTTGATATGAGATTTGCTCAAAATGAGAGAGAGAGAGAT 2486
 DB 740 eglaserArgThrcyslelehegluYrgluillealgluThThrplnheleuIsers 760
 QY 2487 CCGCTCTGACATCATCTTCACTTGTCTTGTGAGAGAGTTGAGAGAGTTGCTGTGAGAGAG 2546
 DB 760 rAsyserglyllelehehelleuValleuGuYValgluYserleuIsleuThrglngl 780
 QY 2547 GGTGGAATGTATGAGCTTCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2606
 DB 780 nvalgluileuThThrgleuIsleuSerThsThsThsThsThsThsThsThsThsThs 800
 QY 2607 GGGAGGACACATCTTCTGAG 2666
 DB 800 uglYArgHIslelehehThrprargleuYasAlaleuIsleuIsleuIsleuIsleuIsleu 820
 QY 2667 TCTGTAG 2712
 DB 820 nProgluInThThrAlagluInguInguInguInguInThThrThrThr 835
 RESULT 2
 OS 08K2T5 PRELIMINARY; PRT; 835 AA.
 AC 08K2T5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3ECH II; TISSUE=Mammary tumor;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinisa K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skaleka U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3ECH II; TISSUE=Mammary tumor;
 RA Strausberg R.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029856; AAH29856.1; -.
 DR HSSP; 060603; 1077.
 DR MGD; MGI:96824; Tlr4.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; P:receptor activity; IDA.
 DR GO; GO:0007249; P:1-kappaB kinase/NF-kappaB cascade; IDA.
 DR GO; GO:0008063; P:Toll signaling pathway; IDA.
 DR InterPro; IPR000887; Aldise_KDpg_KHG.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 10.
 DR Pfam; PF01582; TIR_1.
 DR PRINTS; PRO0019; LRRICHRPT.
 DR SMART; SM00082; LRRCT_1.
 DR SMART; SM00255; TIR_1.
 DR PROSITE; PS00159; ALDOLASE_KDpg_KHG_1; UNKNOWN_1.
 DR PROSITE; PS50104; TIR_1.
 DR KX Receptor.
 SQ SEQUENCE 835 AA; 95488 MW; A103C3997A59CF5B CRC64;
 Alignment Scores:
 Pred. No.: 0 Length: 835
 Score: 4264.00 Matches: 826
 Percent Similarity: 99.40% Conservative: 5
 Best Local Similarity: 98.80% Mismatches: 4
 Query Match: 82.36% Indels: 2
 DB: 2 Gaps: 0
 US-09-396-985b-46 (1-2951) x 08K2T5 (1-835)
 QY 208 ATGATGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 267
 DB 1 MetMetProProThrIleuLeuAlaArgThrIleuIleuMetAlaLeuHehPheSerCyshleu 20
 QY 268 ACAACGAGAGAGCTTGAATCCCTGCATAGAGTAGTTCCTAAATTAATCTACCAATGATG 327
 DB 21 ThrProglYserleuIsleuIsleuProCysIleleuValAlaProAsnIleThrYrGlnCysmet 40
 QY 328 GATGAGAACTGAGAAAGTCCCTGATGACATCTCTTCTTCAACAGAAACATGATGCTG 387
 DB 41 AspglnlyleuIsleuSerlyValProAspApilProSerSerThrlyAsnIleAspleu 60
 QY 388 AGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTCCAAATTTTCAAGACTTCA 447
 DB 61 SerPheAsnProleuIsleuIsleuYserlySerPheSerAsnHehSerGluLeuGln 80
 QY 448 TGTGTGATTTATCCAGGTGTGAAATTTGAAACATGAGAGAGAGAGAGAGAGAGAGAGAG 507
 DB 81 TrpleuAspPheSerThrcysgluileuInThIleGlnAspysAlatrphIsleu 100
 QY 508 CACCACTCTCAAACTTGAATGATGACAGAGAAACCTTATCCAGAGTTTTCGCCAGAGAGT 567
 DB 101 HshIsleuSerAsnleuIleuThrgluYanProIleGlnSerPheSerProglYser 120

QY 568 TTCTGTGACATAACAGTTTGTAGACATCTGGTGGCTGAGACAAATTTGGCCCTCTTA 627
 Db 121 PheSerGlyLeuThrSerLeuGlnSerValAlaValGlnThrIleuAlaSerIeu 140
 QY 628 GAAAGCTTCCCTTATTTGACAGCTTATTAACCTTAAAGAAATCTGATGGCTCACAATTTT 687
 Db 141 GluSerPheProIleGlyGlnLeuIleThrLeuIleuValAlaHisAsnIle 160
 QY 688 ATACATTCCTGTAGTTACCTGACATATTTTCCATCTGACGAACCTTGTATCATGTGAT 747
 Db 161 IleHisSerCysIleuProAlaIlePheSerAsnLeuThrAsnLeuValHisValAsp 180
 QY 748 CTTTCTTATTAATCTATATCAACTATTAAGTCTCAACGACTTACAGTTTCTACGTGAAT 807
 Db 181 LeuSerIleuAsnIleGlnThrIleThrValAsnAspLeuGlnPheLeuAlaArgIleuAsn 200
 QY 808 CCACAGTCAATCTCTCTTATAGACATGTCTTTGAAACCAATTTGATTCATTCAGAACCA 867
 Db 201 ProGlnValAsnLeuSerLeuAspIleSerLeuAsnProIleAspPheIleGlnAspIle 220
 QY 868 GCCTTTGAGGAATTAAGTCTCAATGAATGACTCTAAGAGGTAATTTTAATAGTCAAT 927
 Db 221 AlaPheGlnGlyIleuIleuValGlnLeuThrLeuArgIleuAsnPheAsnSerSerAsn 240
 QY 928 ATATGAAAACTTGCTTCAAAACCTGGCTGTTTACAGCTCCATCGGTGATCTGGGA 987
 Db 241 IleLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260
 QY 988 GAATTTAAAGATGAAGGAATCTGAAATTTTGTGAACCTCTATCATGGAAGACTATGT 1047
 Db 261 GluPheIleuAspGluArgAsnLeuGlnIlePheGluProSerIleMetGluGlyLeuCys 280
 QY 1048 GATGTGACATTTGATGAGTTTCAAGTTTAAATATGATTTTTCAGATGATTTGTT 1107
 Db 281 AspValThrIleAspGluPheArgLeuThrIleThrAsnAspPheSerAspIleVal 300
 QY 1108 AAGTTCATCTGCTGGGGAATGTCTTGTGCAATGTCTGCGAGGGTATCTATTAATAT 1167
 Db 301 LysPheHisCysLeuAlaAsnValSerAlaMetSerLeuAlaGlyValSerIleuIleuIleu 320
 QY 1168 CTAGAAGATGTTCTTAAACATTTCAATGCAATCTTATCATGATAGTCAACT- 1226
 Db 321 LeuGlnAspValProLysHisPheIleuThrPheGlnSerLeuSerIleIleArgCysGlnLeu 340
 QY 1227 AAGCAGTTTCCAACTCTGAGATCTACCTTTCTTAAAGTTTGAATTTTACTATGACAA 1286
 Db 341 LysGlnPheProIleuAspLeuProPheLeuIleuIleuIleuIleuIleuIleuIleuIleu 360
 QY 1287 GGGCTATCAAGTTTAAAGAGGAGGCTTACCAAGTCTCAGCTTATAGATCTAGTGA 1346
 Db 361 GlySerIleSerPheIleuValAlaLeuProSerLeuSerIleuIleuAspLeuSerIleu 380
 QY 1347 AATCAGCTGAGCTTATGAGTGTGAGCTGTCTTATTTCTGATTTGGGAAACAAACAGCTGGA 1406
 Db 381 AsnIleuLeuSerPheSerGlyCysCysSerIleuIleuIleuIleuIleuIleuIleuIleu 400
 QY 1407 CACTTAAGCTCAGCTTCAATGATGTGCAATCTATTAAGTGCATTTTATGAGTCTAGAA 1466
 Db 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGln 420
 QY 1467 GAGGTGAGAGCCTCGATTTTTCAGCACTCTACTTTTAAAGGGTCAAGAAATTTCTCAGC 1526
 Db 421 GlnLeuGlnHisLeuAsp-PheGlnHisSerThrLeuIleuValArgValThrGluPheSerAl 440
 QY 1527 GTTCTTATCCCTTAAAAAGTACTTTTACTTGAATCTTATTAATAACCAAAATTTGA 1586
 Db 440 AspLeuSerLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 460
 QY 1587 CTTGATGATGATATTTCTTGCTGACCAAGTCTCAACATTAATAATGCTGCAATTC 1646
 Db 460 pPheAspGlyIlePheLeuGlyLeuThrSerLeuAsnThrIleuIleuMetAlaGlyAsn 480

QY 1647 TTTCAAGACACACCCCTTTCAAATGTCTTTGCAACACAAACAACTTGACATTCCTGGA 1706
 Db 480 rPheIleAspAsnThrIleuSerAsnValPheAlaAsnThrIleuIleuIleuIleuIleuIleu 500
 QY 1707 TCTTCTTAATGTCAATTTGAAACAAATATCTTGGGGGGTATTTGACACCTTCATAGCT 1766
 Db 500 pLeuSerIleCysGlnLeuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 520
 QY 1767 TCAATTTAATATGAGTCAACAAATCTATGTTTTTGGATTCATCCCATTTAACA 1826
 Db 520 uGlnLeuIleuAsnMetSerHisAsnAsnLeuLeuPheIleuAspSerHisIleuIleuIleu 540
 QY 1827 GCTGTATTCCTCAGCACTCTTGAATTCAGTTTCAATCGATAGACATCTAAAGAAAT 1886
 Db 540 nLeuIleuSerLeuSerThrIleuAspCysSerPheAsnArgIleGlnThrSerIleuIleuIleu 560
 QY 1887 ACTGCAACATTTTCAAAAGCTTACGCTTCTTCAATCTTATCTAACAATTTGTGTGCTTG 1946
 Db 560 eLeuGlnHisPheProLysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
 QY 1947 TATATGTGAACATGAGAAATTCCTGAGTGGGTCAAGAACGAGAAAGCTTGTGGA 2006
 Db 580 sIleCysGlnHisGlnIleuPheLeuGlnIleuValLysAspGlnIleuGlnPheLeuValAs 600
 QY 2007 TGTGAACAAATGACATGTGCAACACCTGTAGAGATGAATPACTCTTATGTTGATTT 2066
 Db 600 nValGlnGlnMetThrCysAlaIleThrProValGlnMetAsnThrSerLeuValIleuAspPh 620
 QY 2067 TAATTAATCTAACCTGTATATGTACAAAGACATCATGATGTGTCAAGTGTGAT 2126
 Db 620 eAsnAsnSerThrCysIleuMetIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 640
 QY 2127 TGTGTATCCACTGATGACATTTTGAATATACACTTCTATTTTCACTGATCTTATTC 2186
 Db 640 eValValSerThrValAlaPheLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 660
 QY 2187 TGGCTGTAAAAAGTACAGCAGAGAGAGAGATCTAAGATGCAATTTGATGATCTGAG 2246
 Db 660 aGlyCysIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 680
 QY 2247 TCAGAAATGAGACTGGGTGAGAAATGAGCTGTGAAGAAATTTAGAAAGAGAGTCCCG 2306
 Db 680 rGlnAsnGlnAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 700
 QY 2307 CTTTCACTCTGCTTCACTTACAGAGACTTTATCTCTGGGTGATGATGATGATGATGAT 2366
 Db 700 gPheHisLeuCysLeuHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 720
 QY 2367 CATCCAGAAAGGCTTCCACAAGAGCCGGAAGGTAATGTGTGATGTCTAGACACTTAT 2426
 Db 720 eIleGlnGlnGlyPheHisIleuSerArgIleuValIleuValValSerArgHisPheIleu 740
 QY 2427 TCAGAGCCGTGTGTATCTTTGATATGAGATTTGCTCAAAACATGAGAGTTTCTGACAG 2486
 Db 740 eGlnSerArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 760
 QY 2487 CCGCTCTGCAATCATCTTCAATGTCTTGAAGAGTTGAGAAAGTCCCTGCTGAGGCAACA 2546
 Db 760 rArgSerGlyIleIlePheIleuValLeuGlnIleuValGlnIleuSerLeuIleuArgGlnI 780
 QY 2547 GGTGGAATGTATCGCTTCTTGAAGAAACACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2606
 Db 780 nValGlnLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 800
 QY 2607 GGGAGGACATCTTCTGAGAAAGTAAATAATGACCTTATGATGAGAAAGCTGCAAA 2666
 Db 800 uGlnArgHisIleIlePheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 820
 QY 2667 TCTGAGCAACACGACAGAGAAAGAAACAAAGAACGCACTTGGACC 2712
 Db 820 nProGlnGlnThrAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 835

RESULT 3

TLR4_RAT
ID TLR4_RAT STANDARD; PRT; 835 AA.
AC O90X05;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TOLL-like receptor 4 precursor (TOLL4).
GN Name=TLR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN=Sprague-Dawley; TISSUE=Heart;
RX MEDLINE=99352487; Pubmed=10430608;
RA Franz S., Kobzik L., Kim Y.-D., Fukazawa R., Medzhitov R., Lee R.T.,
RA Kelly R.A.;
RT "TOLL4 (TLR4) expression in cardiac myocytes in normal and failing
myocardium";
RT J. Clin. Invest. 104:271-280(1999).
RL J. Clin. Invest. 104:271-280(1999).
CC -!- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
immune response to bacterial lipopolysaccharide (LPS). Acts via
MyD88, TIRAP and IRAKs, leading to NF-kappa-B activation, cytokine
secretion and the inflammatory response (By similarity).
CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the TOLL-like receptor family.
CC -!- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.

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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
or send an email to license@ebi.ac.uk).

CC
DR EMBL; AF057025; AAC1313.1; -.
DR HSSP; Q15399; 1FV.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 10.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 835 TOLL-like receptor 4.
FT DOMAIN 26 638 Extracellular (Potential).
FT TRANSMEM 639 659 Potential.
FT DOMAIN 660 835 Cytoplasmic (Potential).
FT REPEAT 32 52 LRR 1.
FT REPEAT 53 75 LRR 2.
FT REPEAT 76 99 LRR 3.
FT REPEAT 100 123 LRR 4.
FT REPEAT 148 172 LRR 5.
FT REPEAT 173 196 LRR 6.
FT REPEAT 201 224 LRR 7.
FT REPEAT 227 251 LRR 8.
FT REPEAT 305 330 LRR 9.
FT REPEAT 370 393 LRR 10.
FT REPEAT 396 419 LRR 11.
FT REPEAT 420 443 LRR 12.
FT REPEAT 468 492 LRR 13.

FT REPEAT 493 516 LRR 14.
FT REPEAT 518 540 LRR 15.
FT REPEAT 542 563 LRR 16.
FT REPEAT 565 589 LRR 17.
FT DOMAIN 670 816 TIR.
FT CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 237 237 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 281 281 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 835 AA; 96071 MW; DF5E16A30851B3A0 CRC64;

Alignment Scores:
Pred. No.: 4.31e-279 Length: 835
Score: 3683.00 Matches: 711
Percent Similarity: 91.27% Conservative: 52
Best Local Similarity: 85.05% Mismatches: 72
Query Match: 71.14% Indels: 2
DB: 1 Gaps: 0

US-09-396-985b-46 (1-2951) x TLR4_RAT (1-835)

QY 208 ATGATGCTCCCTGAGCTGCTGAGACTGTGATGCACTGTTCTTCTGCTG 267
Dd 1 MetMetProteinLeuHsiLeuAlaGlyThrLeuIleMetAlaLeuPheLeuSerCysLeu 20
QY 268 ACACCGAAGAGCTTGAATCCCTGCATRAGAGTGCTTCAATTTACCTCAAGATGATG 327
Dd 21 ArgProGlySerLeuSerProCysIleGluValLeuProAsnIleThrYrGlnCysMet 40
QY 328 GATCGAAGAACTGACGAAGAGCTGATGACATTCCTTCTTCAACGAAGATAGATCTG 387
Dd 41 AspGlnAsnLeuSerYsIleProH1bAspIleProYrSerThrYsAsnLeuAspLeu 60
QY 388 AGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTTCAATTTTTCAGAACTTCA 447
Dd 61 SerPheAsnProLeuYsIleLeuArgSerYsSerPheThrAsnPheSerGlnLeuGln 80
QY 448 TGGCTGATTTATCCAGGTGTGAATTTGAACATTTAGAGACAAAGCATGGCTTGA 507
Dd 81 TrpLeuSerPheLeuSerArgCysGlnIleGluThrIleGluAspYsAlaIlePheIleGlu 100
QY 508 CACCACCTCTCAACACTGATGATGACAGGAACCTTACAGAGTTTTCCTCCAGGAAGT 567
Dd 101 AsnGlnLeuSerThrLeuValIleThrGlyAsnProIleYsSerPheSerProGlySer 120
QY 568 TTCTTGAAGCTTAAAGATTTAGACAATCTGTGGTGTGTGAGACAAATTTGGCTCTCTA 627
Dd 121 PheSerGlyLeuThrAsnLeuGluAsnLeuValAlaValIleThrYrYsMetThrSerLeu 140
QY 628 GAAAGCTTCCCTATTTGACAGCTTATTAACCTTAAAGAACTCAATGTGGCTCACAAATTT 687
Dd 141 GlnGlyPheHsiIleGlyGlnLeuIleSerLeuYsIleAsnValAlaHsiAsnLeu 160
QY 688 ATATATCCGTGAAGTATGATGATTTTTCACAACTGAGCAACCTAGTACATGGAGAT 747
Dd 161 IleHsiSerPheYsLeuProGlyYrPheSerAsnLeuThrAsnLeuGluHsiValAsp 180
QY 748 CTTTCTTATATATATTCAAACTATTAAGTCAACAGCAAGTTTCTTCAAGTGAAT 807
Dd 181 LeuSerYrAsnYrIleGlnThrIleSerValYsAspLeuGlnPheLeuAspGluAsn 200
QY 808 CCACAACTCAATCTCTTGAACATGCTTTGAACCAATTTGACTTCAATTCAGAACCA 867

Db 201 ProGlnValAsnLeuSerLeuAspLeuSerProIleAspSerIleGlnAlaIn 220
 Qy 868 GCCTTTGAGGAATTAAGCTCATGAATGACTTAAGAGGTAATTTAATAGCCAAAT 927
 Db 221 AlphegInGlyIleArgLeuHISGlnLeuThrLeuAspGlnSerAspAspSerSerAsn 240
 Qy 928 ATAAAGAAAATTGCTTCAAAACCTGGCTGGTTTACAGCTCAATCGGTGATCTTGGA 987
 Db 241 ValLeuSerMetCysLeuGlnAsnMetThrGlyLeuHISValHISArgLeuIleLeuGly 260
 Qy 988 GAATTTAAAGATGAAGAATCTGGAATTTTGAACCTTATCATGGAAGAACTATGT 1047
 Db 261 GluPheLeuAsnGluArgAsnLeuGlnSerPheAspArgSerValMetGluGlyLeuGly 280
 Qy 1048 GATGAGCACTTGAAGTGAAGTTACATATACAAATGATTTTTCAGATGATTTGTT 1107
 Db 281 AsnValSerIleAspGlnPheArgLeuThrTyrlleAsnHISpHeSerAspAspIleTyx 300
 Qy 1108 AAGTTCATGCTTGGCGAATGTTTCTGCAATGCTCTGCGAGGTGATCTATAAATAT 1167
 Db 301 AsnLeuAsnCysLeuAlaAsnHISerAlaMetSerPheThrGlyValHISileGlyHIS 320
 Qy 1168 CTAGAAGATGTTCTTAAACATTTTGAATGCAATCTTATCATGATTAATGATGCACT- 1226
 Db 321 IleAlaAspValProArgHISpHeLeuSerGlnSerLeuSerIleIleArgCysHISLeu 340
 Qy 1227 AAGAGATTTTCACTGCACTGCACTACCTCTTAAAGTTTGAAGTTTACATGACAA 1286
 Db 341 LysProPheProLysLeuSerLeuProPheLeuLysSerTyrlleThrThrAsnArg 360
 Qy 1287 GGGCTCATAGTTTAAAAAAGTGCGCCCTTACCAAGTCTGCACTTATGATCTTATG 1346
 Db 361 GluAspIleSerPheGlyGlnLeuAlaLeuProSerLeuArgTyrlleAspLeuSerArg 380
 Qy 1347 AATGCACTGAGCTTTTATGCTGCTGCTGCTTATTTCTGATTTTGAAGCAACAGCTG 1406
 Db 381 AsnAlaMetSerPheArgGlyCysCysSerTyrlleAspPheGlyThrAsnAsnLeuGly 400
 Qy 1407 CACTTAAGCTTCACTTCAATGATGCTCATTTATGATGCTCAATTTTCAATGCTTGA 1466
 Db 401 TyrlleAspLeuSerPheAsnGlyValIleLeuMetSerIleAlaAsnPheMetGlyLeuGln 420
 Qy 1467 GAGCTGAGCAGCTGATTTTTCAGCACTTACTTAAAGAGGTCACAGAAATCTGAGC 1526
 Db 421 GluLeuGlnTyrlleAspPheGlnHISerThrLeuLysGlyValThrGlnPheSerVal 440
 Qy 1527 GTTCTTATCCCTTGAAGAACTTACTTATGATGATCTTATTAATTAACCAAAATTTGA 1586
 Db 440 LpHeLeuSerLeuGlnLysLeuLeuTyrlleAspIleSerTyrlleThrAsnThrLysIleAs 460
 Qy 1587 CTTGATGATGATTTTCTGCTGCTGACCAAGTCTCAACATTAATAATGCTGCGCAATTC 1646
 Db 460 PheAspGlyIlePheLeuGlnLeuIleSerLeuAsnThrLeuLysMetAlaGlyAsnSe 480
 Qy 1647 TTTCAGAGACACACCTTTCAAATGCTTTCAGAAACACAAATTTGACATTCCTGGA 1706
 Db 480 rPheLysAspAsnThrLeuSerAsnValPheThrAsnThrThrAsnLeuThrPheLeuAs 500
 Qy 1707 TCCTTTAAATGTCATTTGAAACAATATCTTGGGGGGTATTTGACACCTTCATAGACT 1766
 Db 500 PheSerLysCysGlnLeuGlnIleSerArgGlyValPheAspThrLeuTyrlleArgLe 520
 Qy 1767 TCATTTATTAATTAATGAGTCACAAACATCTATGTTTGGATTCATCCCTTTAAACCA 1826
 Db 520 uGlnLeuLeuAsnMetSerHISAsnAsnLeuLeuPheLeuAspProSerHISTyrlleSGI 540
 Qy 1827 GCTGATTTCCCTGAGCACTCTTGAATGCAATTTCAATGCAATGCAATGCAATTAAGGAT 1886
 Db 540 nLeuTyrlleSerLeuArgThrLeuAspCysSerPheAsnHISGlyIleGlnThrSerLysGlyI 560
 Qy 1887 ACTGCAACATTTTCCAAAGAGTCTGAGCTTCTTCAATCTTACTAACAATTCGTGCTG 1946

Db 560 eLeuGlnHISpHeProLysSerLeuAlaValPheAsnLeuThrAsnAsnSerValAlaCys 580
 Qy 1947 TATATGACATCAGAAATTCCTGAGTGGGTCAAGGACAGAAAGCAAGTCTTGATGAA 2006
 Db 580 sIleCysGlnTyrlleAsnPheLeuGlnThrPheValIleAspGlnLysMetPheLeuValAs 600
 Qy 2007 TGTGAAACAAATGACATGTGCAACACCTGTAGAGANTGAATTCCTTATGTTGATTT 2066
 Db 600 nValGlnGlnMetLysCysAlaSerProIleAspMetLysAlaSerLeuValLeuAspPh 620
 Qy 2067 TAAATATTTCACTGTTATATGTCACAAACATATCATGCTGTGTCAGTGTGATGAT 2126
 Db 620 eThrAsnSerThrCysTyrlleTyrlleTyrlleIleSerValSerValIleValIle 640
 Qy 2127 TGCGTATTCACCTGATGATTTTGAATATTCATATTCATTTTTCAGTATGATTTGCT 2186
 Db 640 uValValAlaThrValAlaPheLeuIleTyrlleHISpHeLeuThrHISLeuIleLeuIleAl 660
 Qy 2187 TGCGTATTAAGATGACAGACAGAGGAAAGCATATGATGATGATGATGATGATGAT 2246
 Db 660 aGlyCysLysLysTyrlleSerArgGlyGlnSerIleTyrlleAspAlaPheValIleTyrlleSer 680
 Qy 2247 TCAGATGAGGATCTGGGTGAGAAATGAGCTGCTGTAAGATTTAAGAGAGAGTCCCG 2306
 Db 680 rGlnAsnGlnAspTyrlleValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyValProAr 700
 Qy 2307 CTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2366
 Db 700 gPheGlnLeuCysLeuHISTyrlleArgAspPheIleProGlyValAlaIleAlaAlaAsnIle 720
 Qy 2367 CATCCAGAAAGGCTTCCACAAAGCCGGAAGTATTTGCTGATGCTGATGATGATGAT 2426
 Db 720 eIleGlnGlnGlyPheHISLysSerArgLysValIleValValValSerArgHISpHeIle 740
 Qy 2427 TCAGAGCCGTGCTGATCTTTGAATATGAGATTTCTCAACATGCGAGATTTCTGAGCAG 2486
 Db 740 eGlnSerArgTyrllePheGlyTyrlleGlyIleAlaGlnThrTyrllePheLeuSerSe 760
 Qy 2487 CCGCTGAGGATCATCTTCATGCTGCTGAGAGGTTGAGAGAGTCCCTGCGAGAGCA 2546
 Db 760 rArgSerGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeuLeuArgGlnI 780
 Qy 2547 GGTGAAATTTATGCTTCTTATGACAGAAACACCTGATGATGAGAGAGCAATCTCT 2606
 Db 780 nValGlnLeuTyrlleArgLeuLeuSerArgAsnThrTyrlleGlnTyrlleGlnAspAlaIle 800
 Qy 2607 GGGAGGACACATCTTCTGAGAGAGCTTAAATAATGCTTATGATGAGAGAGCTTCGAA 2666
 Db 800 uGlyArgHISIlePheThrArgLeuLysValAlaLeuLeuAspGlyLysAlaLeuAs 820
 Qy 2667 TCTGAGCAACACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2712
 Db 820 nProAspGlnThrSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 835

RESULT 4
 ID TLR4_CRIGR STANDARD; PRT; 838 AA.
 AC Q9WV82;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Cricetusulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetusulus.
 OC NCBI_TaxID=10029;
 RX NCBI_TaxID=10029;
 RP SEQUENCE FROM N. A.
 RC TISSUE=Macrophage;
 RX MEDLINE=20148868; PubMed=10683379;
 RA Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,

RA Panton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,
 RA Ingalls R.R., Golenbock D.T.,
 RT "Toll-like receptor 4 imparts ligand-specific recognition of bacterial
 RT lipopolysaccharide.",
 RL J. Clin. Invest. 105:497-504(2000).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (by similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
 CC their respective TIR domains.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
 CC hamster ovary fibroblast cell line.
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 DR EMBL, AF153676, AAD41891.1, -.
 DR HSSP, Q15399, 1FVY.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Lyp.
 DR InterPro: IPR001577; TIR.
 DR Pfam, PF00560; LRR; 8.
 DR Pfam, PF01582; TIR; 1.
 DR PRINTS, PRO0019, LEU1CHRPT.
 DR SMART, SM00082; LRCT; 1.
 DR SMART, SM00369; LRR_TYP; 1.
 DR SMART, SM00255; TIR; 1.
 DR PROSITE, PS0104, TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 838
 FT DOMAIN 26 629
 FT TRANSMEM 630 650
 FT DOMAIN 651 838
 FT REPEAT 31 52
 FT REPEAT 53 75
 FT REPEAT 76 99
 FT REPEAT 100 123
 FT REPEAT 127 148
 FT REPEAT 149 172
 FT REPEAT 173 196
 FT REPEAT 200 224
 FT REPEAT 227 251
 FT REPEAT 305 330
 FT REPEAT 351 370
 FT REPEAT 371 393
 FT REPEAT 396 419
 FT REPEAT 420 443
 FT REPEAT 468 492
 FT REPEAT 494 516
 FT REPEAT 517 538
 FT REPEAT 541 563
 FT REPEAT 565 589
 FT DOMAIN 670 816
 FT CARBOHYD 34 34
 FT CARBOHYD 115 115
 FT CARBOHYD 172 172
 FT CARBOHYD 204 204
 FT CARBOHYD 237 237

FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 838 AA; 96277 MW; 129B33596B908B48 CRC64;
 Alignment Scores:
 Pred. No.: 9 99e-255 Length: 838
 Score: 3371.50 Matches: 652
 Percent Similarity: 86.50% Conservative: 72
 Best Local Similarity: 77.90% Mismatches: 109
 Query Match: 65.12% Indels: 5
 DB: 1 Gaps: 1
 US-09-396-985b-46 (1-2951) x TLR4_CRIGR (1-838)
 QY 208 ATGATGCTCCCTGGCTCTGGCTGAGACTGTGATGACATGACATGCTTCTCTGCTG 267
 Db 1 MetMetProSerPheCysLeuAlaGlyThrLeuMetMetValLeuPheLeuSerLeu 20
 QY 268 AACACGAGAACTTGAATCCCTGCATGAGAGTGTCCTTAATTTACCTACATGATGATG 327
 Db 21 ArgProGluSerLeuSerProCysValGluValAspSerAsnThrSerTyrglnCysMet 40
 QY 328 GATCAGAACTCAGCAAGGCCCTGATGACATTCCTTCTTCAACCAAGACATGATGATCTG 387
 Db 41 AspArgAsnLeuAsnLysIleProAspAsnIleProSerSerValLysHisLeuAspLeu 60
 QY 388 AGCTTCACCCCTTGAAGATCTTAAAGATATATAGCTTCTCAATTTTTCAGAACTTCAG 447
 Db 61 SerPheAsnProLeuLysThrLeuGlySerHisSerPheAsnProGluLeuLys 80
 QY 448 TGCGTGATTTATTCAGGTGTAAATTTGAAACATTTGAGAGACAAAGCATGCGATGCTTA 507
 Db 81 LeuLeuAspLeuSerLeuArgCysGluIleGluThrIleGluAspLysAlaTyrglnGlyLeu 100
 QY 508 CACCACTCTCAAACTTGAATGATGACAGCAAGCACTTCAAGGTTTTCACCAAGAGT 567
 Db 101 HisGlnLeuThrThrLeuIleLeuThrGlyAspProIleGlnAsnLeuSerLysGlyThr 120
 QY 568 TTCTGAGACTTAACTTGAATGATGATGCTGCTGTGAGACAAATTTGGCCTCTCTA 627
 Db 121 PheSerGlyLeuAlaAsnLeuGlnAlaLeuValAlaValGluIleLysLeuAlaSerLeu 140
 QY 628 GAAAGCTTCCCTTATGAGACGCTTATTAACCTTAAAGAACTCAATGTGGCTCACAAATTT 687
 Db 141 AspSerLeuProIleGlyHisLeuValThrLeuLysLeuAsnValAlaHisAsnLeu 160
 QY 688 ATACATTCCTGTAGTACTGATGATTTTTCATCTGACGAACCTAGTACATGTGGAT 747
 Db 161 IleHisSerPheLysLeuProGluTyrrPheSerAsnLeuThrAsnLeuGluHisLeuAsp 180
 QY 748 CTTTCTTAACTATATTTCAACTATTACTGCAACGACTTAAAGTTTCTTACGTGAAT 807
 Db 181 LeuSerAsnAsnTyrrIleGlnThrIleTyrrThrAspLeuGlnThrLeuAlaGluAsn 200
 QY 808 CCAACAGTCAATCTCTTTAGACATGCTTTTGAACCAATTAAGTCACTTCAAGACCA 867
 Db 201 ProGlnLeuAsnLeuSerLeuGluLeuSerLeuAsnProIleAspPheIleGlnProGly 220
 QY 868 GCCTTCAGGGAATTAAGCTCCATGAACTGATCTTAAGAGTAATTTTATAGTCAAT 927
 Db 221 AlaPheGlnGlyIleAlaGluHisGluLeuThrLeuLysSerAsnProAsnSerThrAsn 240
 QY 928 ATAATGAACCTGCTTCAAAACCTGGCTGTGTTACAGCTCATGCGTGTGATCTTGGGA 987
 Db 241 ValMetLysThrCysIleHisAsnLeuAspGlyLeuGlnValHisAspGluIleLeuGly 260
 QY 988 GAATTTAAAGATGAAGAACTGGAATTTTGAACCCCTCTATCATGAGAGACTATGT 1047
 Db 261 GluPheLysAsnGluArgAsnValGluArgPheAspArgTyrrValIleGluGlyLeuCys 280

OY	1048	GATGGACCATGATGAGGATTCAGGGTTAAACAATCAAAATGATTTTCAGACATATGTT	1107
Db	281	LysValThrIleGlnGluPheArgPheThrItyrAlaAsnGluPheSerGluAspIleThr	300
OY	1108	AAGTTCATGCTGGCGCAATGTTTCTGCATATGCTCTCGGACGGGTATCTATAAAATAT	1167
Db	301	AspPheArgCysLeuAlaAsnValSerAlaMetSerLeuAlaAsnValTyrLeuValArg	320
OY	1168	CTAGAAAGATGTTCCCTTAAACATTTCAAAATGGCAATCCTTATCATCATTTAGATGCACT-	1228
Db	321	LeuGluAspIleProTyrSerTyrPheTyrTrpGlnThrLeuAlaValIleArgCysGluLeu	340
OY	1227	AAGCAGTTTCCAACTCTGATCTACCTCTTCTTAAAGTTTGACTTTAACTATGAACAA	1286
Db	341	LysGlnPheProProLeuGluLeuProPheLeuValArgLeuIlePheIleThrAsnLys	360
OY	1287	GGGTCTATCAGTTTAAAAAAGTGCGCCCTTACCAATCTCAGCTATCTATGATCTTAGTGA	1346
Db	361	GlyAlaThrSerPheProGluValAsnLeuProSerLeuThrPheLeuAspLeuSerGly	380
OY	1347	AATGCATGACGTTTATGATGGCGCTGTTCTTATTTCTGATTTTGGGAAACAACGCTGAGA	1406
Db	381	AsnGlyMetSerPheArgGlyCysCysSerTyrThrAspLeuGlyAlaArgSerLeuLys	400
OY	1407	CACTTAGACCTTCAGCTTCAATATGGTGCCTACATATATGATGGCAATTTATATGGGTCTAGA	1466
Db	401	HisLeuAspLeuSerPheAsnGlyValIleSerMetSerGluAsnPheMetGlyLeuGlu	420
OY	1467	GAGCTGCGACACCTGATTTTTCAGCAGCTCTACTTATAAAAGGGTCACAGAATCTCGAC	1526
Db	421	GlnLeuGlnTyrLeuAsp-PheGlnHisSerThrLeuLysValAlaTrpGluPheSerMet	440
OY	1527	GTTCTTATCCCTTGA AAAAGCTACTTACCTTGACATCTCTTATATCTAACACCAAAATTGA	1586
Db	440	C-PheLeuProLeuGluLysLeuLeuTyrLeuAspIleSerTyrThrAsnThrLysIleAs	460
OY	1587	CTTGATGATGATATTTCTTGCGGTGACCAAGTCTCAACACATTA AAAATGCGCTGGCAATTC	1646
Db	460	PheAsnLysIlePhePheGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSer	480
OY	1647	TTTCAAAACAGCAACCCCTTCAAAATGCTTTGCAAAACAACAACCTTGACATTCCTGGGA	1706
Db	480	C-PheLysAspAsnIleLeuSerAsnValAPheThrAsnThrLysAsnLeuThrPheLeuAs	500
OY	1707	TCCTTCTTAAAGTCATATGGAACAATATCTTGGGGGTATTTTGGACACCTCCATAGACT	1766
Db	500	PileSerLysCysGlnLeuGlnGlnValSerTyrGlyAlaPheAspThrLeuHisArgLeu	520
OY	1767	TCAAATTATTAATATAGTCAACAACAATCTATGTTTGGATTCATCCCATTTAAACA	1826
Db	520	GluLeuLeuAsnMetSerHisAsnAsnLeuLeuLeuAspLeuPheHisTyrLysGly	540
OY	1827	GCTGATTTCCCTCAGACACTCTTGATTTGAGATTTCAATGCGATAGACATCTTAAAGAAAT	1886
Db	540	NLeuHisSerLeuLysThrLeuAspCysSerPheAsnHisIleGlnThrSerLysGlyIle	560
OY	1887	ACTGCAACATTTTCCAAAGAGCTAGACCTTCTGCATTTTACTTAAACAATCTGTGGCTG	1946
Db	560	MetGlnHisPheProLysSerLeuAlaPheLeuAsnLeuThrLysAsnProPheAlaCys	580
OY	1947	TATATGTGAACATGAGAAATCTCGAGTGGGTGAGGAACAAGACAGCAAGTCTTGATGA	2006
Db	580	SileCysGlnHisGlnAsnPheLeuGlnTrpValLysAspGlnArgLeuPheLeuValLys	600
OY	2007	TGTTGAACAATGACATGTGCAACACTGTAGAGATGAATACCTTCCTTAGTGTGAATTT	2066
Db	600	StrGlnGlnMetThrCysAlaThrProValGlnMetLysAspSerLeuValLeuAspPh	620
OY	2067	TAATPAACTCAACCTGTTATATGTACAACAACAATATCATGTCGTGTCAGGTGATGGAT	2126
Db	620	ArgAsnAlaThrCysTyrValGlnLysThrIleLeuSerValSerValIleSerValLeu	640

Oy		2127	TGAGTATCCACTGTACCTATTTCGAATATCACTTTGATTTTGACCTGAACTTATATGC	2186
Dd		640	vvaIvalSerThrIleAlaPheLeuValTYrLysPheTYrPheHisLeuIleuIleAl	660
Oy		2187	TGGCTGTAAAAAGTAGACAGCAGAGAGAAGCATCTATGATGACTTTGTGATCTACTCGAG	2246
Dd		660	aGIcYelyelyletyrtyserarnglyluserlleTyAspAlaPheValilleTyrserse	680
Oy		2247	TCGAATAGAGAGCTGGGTGAGAAATGAGCTGGTAAAGATTTTGAAGAAGAGAGTCCCCG	2306
Dd		680	rGlnAspGlnAspTrpValArgasnGluValLyAsnLeuGlUglUgylValProPr	700
Oy		2307	CTTTCACCTTCGCCCTTCACTACACAGAGACTTATTCCTGGTGAAGCCATTGGTGGCAACAT	2366
Dd		700	opneGlnLeuCysLeuHisTYrArgAspPheIleproGlyValAlaIleAlaIleamtl	720
Oy		2367	CATCCAGAAAGCCTTCACAAGAACCAGAAAGTTATTTGTGTAGTGTCTAACACTTAT	2426
Dd		720	eIIeGInGUgLYPheHIslysserArGlybValIleValValSerArghIsPheIl	740
Oy		2427	TCAGAGCCCTTGGTGTATCTTTGAATATGAGATTGCTCAACATGCGACTTCTGACAG	2486
Dd		740	egInsErArGrTpCYsIlePheGluTYrGuIlleAlaGlnThrTrpGlnPheLeuSere	760
Oy		2487	CCGCTCGGAGATATCTTCATTTGCCCTTGAAGAGCTTGAAAGTCCCTGCGTAGAGCAGCA	2546
Dd		760	rHIsErgdlYIlellePheIleValLeuGluLyValGlnLysSerleuLeuYsgIngl	780
Oy		2547	GGTGAATTTTATTCGCTCTTTCAGCAAACACCTACCTGGAATGGAGAGACAATCCTCT	2606
Dd		780	nvaIGlnLeuTYrArgLeuLeuSerArGaantHTYrLeuGlnUTRpLysAspnaIale	800
Oy		2607	GCGAGGCGACATCTTCTGAGAAAGACTTAATAAATGCCCTATTTGATGAGAAAAGCTTCGAA	2666
Dd		800	ugLYArGHIsIlePheTrpArgArgLeuSLysAlaLeuLeuAspLIyArgAlaTrpas	820
Oy		2667	TCCGAGCAACACAGCAGAGAGA-----CAAGAAACGGCAACT	2706
Dd		820	nProGlnGUgLYAlaThrGlnValaGlnAsnAngInGlnGUthrThrThr	836
RESULT 5				
TLR4_HUMAN				
ID	_TLR4_HUMAN	STANDARD;	PRT;	839 AA.
AC	000206; Q9UK78; Q9DMS7;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, last sequence update)			
DE	25-JAN-2005 (Rel. 46, last annotation update)			
DR	Toll-like receptor 4 precursor (htoll).			
GN	Name=TLR4;			
OS	Homo sapiens (human) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=97379437; PubMed=9237759; DOI=10.1038/44131;			
RA	Medzhitov R., Preston-Hurlburt P., Janeway C.A. Jr.;			
RT	"A human homologue of the Drosophila Toll protein signals activation			
RT	of adaptive immunity.";			
RL	Nature 368:394-397(1997).			
RN	[2]			
RP	SEQUENCE OF 41-839 FROM N.A.			
RC	TISSUE=Petal liver, Lung, and Placenta;			
RX	MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.589;			
RA	Rock F.L., Hardman G., Timans J.C., Kastelein R.A., Bazan J.F.;			
RT	"A family of human receptors structurally related to Drosophila			
RT	Toll.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND VARIANTS GLY-299 AND ILE-399.			
RX	MEDLINE=20558910; PubMed=11104518;			
RA	Smlirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;			

FT CARBOHYD 526 526 N-linked (GlcNAc . . .)
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .)
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .)
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 FT VARIANT 188 188 O -> R.
 FT VARIANT 246 246 /FtId=VAR_018729.
 FT VARIANT 299 299 C -> S.
 FT VARIANT 299 299 /FtId=VAR_018730.
 FT VARIANT 329 329 D -> G (in allele TUR4*B; reduced LPS-
 FT VARIANT 399 399 response; dbSNP:4986790).
 FT VARIANT 399 399 /FtId=VAR_012739.
 FT VARIANT 443 443 N -> S.
 FT VARIANT 443 443 /FtId=VAR_018731.
 FT VARIANT 474 474 T -> I (in allele TUR4*B; reduced LPS-
 FT VARIANT 510 510 response; dbSNP:4986791).
 FT VARIANT 694 694 /FtId=VAR_012740.
 FT VARIANT 694 694 F -> L.
 FT VARIANT 694 694 /FtId=VAR_018732.
 FT VARIANT 694 694 E -> K.
 FT VARIANT 694 694 /FtId=VAR_018733.
 FT VARIANT 694 694 O -> H.
 FT VARIANT 694 694 /FtId=VAR_018734.
 FT VARIANT 694 694 K -> R.

Alignment Scores:

Pred. No.: 2,12e-209 Length: 839
 Score: 2792.00 Matches: 557
 Percent Similarity: 79.35% Conservative: 100
 Best Local Similarity: 67.27% Mismatches: 166
 Query Match: 53.93% Indels: 6
 DB: 1 Gaps: 4

US-09-396-985b-46 (1-2951) x TUR4_HUMAN (1-839)

QY 208 ATGATGCTCCCTGGCTCCGCTGAGACTGTGATGACGACTG---TTCTTCTCTGCG 264
 Db 1 MetMetSer1aSeratgLeu1aG1YThrLeu1lePro1aMet1aPheLeuSerCys 20
 QY 265 CTGACACGAGAGCTTGAATCCCTGCATGAGGTAGTTCCTATATTACCTCAATGCG 324
 Db 21 ValArgProGluSerTrpGluProCysValGluValProAsn1leThrTYrGlnCys 40
 QY 325 ATGAGACGAAACTCAGCAAAAGTCCCTGATGACATTCCTCTTCAACCAAGACATGAT 384
 Db 41 MetGluLeuAsnPheTYr1leProAsnLeuProPheSerThr1yAsnLeuAsp 60
 QY 385 CTGAGCTTCAACCCCTTGAAGATTTAAAGATTAAGCTTCTCCAAATTTTCAAGACT 444
 Db 61 LeuSerPheAsnProLeuArg1aLeuG1ySerTYrSerPhePheSerPheProGluLeu 80
 QY 445 CAGGCGGTGATTTATCCAGGTGTAATGAATGAACATTTGAAGACAGGATGGCATGCG 504
 Db 81 GluValLeuAsnProLeuSerArgGlu1leGlnThr1leGluAspG1yAlaTYrGlnSer 100
 QY 505 TTACACCACTCTCAACCTTGAATGATGACAGAAACCTATCCAGAGTTTTCCTCCAGA 564
 Db 101 LeuSerThr1leuSerThr1leuThr1leuThr1leuThr1leuThr1leuThr1leu 120
 QY 565 AGTTTCTCTGACTTAACAAGTTTGAACATCTGGTGGCTGTGAGACAAAATTTGGCTCT 624
 Db 121 AlPheSerG1yLeuSerSerLeuGln1yLeuVal1aVal1GluThr1aAsnLeu1aSer 140
 QY 625 CTGAAAGCTTCCCTATGAGAGCTTATACTTAAGAACTCAATGTGGCTCAAT 684
 Db 141 LeuGluAsnPhePro1leG1y1a1leu1ySerThr1leu1ySerThr1leu1aAsn 160
 QY 685 TTATACACTCTGTAAGTTACCTGATATTTTTCATCTGACGAACCTAGTACATGTG 744
 Db 161 Leu1leGlnSerPhe1y1leuProGluTYrPheSer1aAsn1leuThr1aAsn1leu 180
 QY 745 GATCTTTCTTATATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
 Db 181 AspLeuSerSer1aAsn1y1leGlnSer1leTYrCysThr1aPhe1aVal1leu1aGln 200

QY 805 AATCCACAGATCAATCTCTCTTTAGACATGCTTTGAACCCAAATGACTTCATTCAGAAC 864
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPhe1leGlnPro 220
 QY 865 CAAGCTTTCAAGGAAATTAAGCTTCCATGAACCTGAATGAAGGTAATTTAATAGCTCA 924
 Db 221 G1yAlaPhe1ySerGln1leArg1a1leuThr1leuArg1aAsn1leuAspSerLeu 240
 QY 925 AATTAATGAACCTTCCCTTCAAAACCTGGCTGTTTACACGTCATCGGTTGATCTTG 984
 Db 241 AsnValMet1ySerTYr1leGln1yLeu1aG1yLeu1aVal1a1a1ySerLeuVal 260
 QY 985 GGAGAAATTAAGATGAAGAAAGAAATTTGAATTTTGAACCTTATCATGAAGACTA 1044
 Db 261 G1yGluPheArg1aGln1yAsn1leGln1yPheAsp1ySer1a1a1leuGln1yLeu 280
 QY 1045 TGTGATGTCACATTTGATGAGTTCAAGTTAATATCAATGAATTTTTCAGATGATAT 1104
 Db 281 CysAsnLeuThr1leGln1yPheArg1a1yTYrLeuAspTYrTYrLeuAspAsp1le 300
 QY 1105 GTTAAG---TTCCATTTGCTGGGGAATGTTTTCGCAATGCTCTCGGACGCTGATCTATA 1161
 Db 301 IleAspLeuPheAsnCysLeuThr1aAsnValSerSerPheSerLeuValSerValThr1le 320
 QY 1162 AATATATAGAGATGTTCTTAACATTTCAAAATGGCAATCCCTATCATCATTAAGATGT 1221
 Db 321 GluArgVal1yAsn1yPheSerTYrAsn1yPheG1yTYrPhe1a1leuGluLeuVal1aSerCys 340
 QY 1222 CAACATAAG-CAGTTTCCAACTGTGATCTACCTTTCTTAAAGTTTGAATTAACATATG 1280
 Db 341 TyrPheG1yGlnPheProThr1leu1yLeu1ySer1leu1yAsn1yArg1a1yThr1Ser 360
 QY 1281 AACAAAGGCTCTACATTTTAAAGATGAGCCCTACCAAGTCTCAGCTATCTTATGATCTT 1340
 Db 361 Asn1yG1yG1yAsn1aPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1341 AGTAGAAATGACCTGAGCTTTAGTGGCTGCTGTTCTTATTTGATTTGGGACAAACAGC 1400
 Db 381 SerThrGln1yLeuSerPhe1yG1yCysSerGlnSerAsn1yPheG1yThr1Ser 400
 QY 1401 CTGAGACACTTGAACCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1460
 Db 401 Leu1ySer1leuAsnProLeuSerPheAsnG1yVal1leThr1leSer1aAsn1leuG1y 420
 QY 1461 CTGAGAGCTGACGACCTGATTTTTCAGCACTCTACTTTAAAGGCTCACAGAAAT 1520
 Db 421 LeuGln1leuGln1a1y1leuAsp-PheGln1a1SerAsn1leu1yGln1leu1ySerGluPhe 440
 QY 1521 CTGAGGCTTATCCCTGAAAGACTCTTCAATGATGATGATGATGATGATGATGATGAT 1580
 Db 440 SerVal1PheLeuSer1leuArg1aAsn1y1yLeuAsp1leSer1a1Thr1a1Thr1a 460
 QY 1581 AATTGACTTGATGATATATTTCTGGCTTGAACAGTCTCAACATTAATAAATGGCTGG 1640
 Db 460 GVal1a1aPheAsnG1y1lePheAsnG1yLeuSerSer1leuGln1yVal1leu1ySer1a1aG1 480
 QY 1641 CAATTTCTTCAAAACACACCTTTCAAATGCTTTTTCACAAACAAACAACTTGACAT 1700
 Db 480 yAsnSerPheGln1yAsn1yPheProAsp1lePheThrGluLeuArg1aAsn1yThrPh 500
 QY 1701 CTTGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1760
 Db 500 IleAsn1yLeuSerGlnCysGln1leuGln1yLeuSerProThr1a1aPheAsn1yLeu 520
 QY 1761 TAGACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1820
 Db 520 rSerLeuGln1yVal1leuAsn1ySer1a1aAsn1yPheSer1leuAsp1yThr1aProTY 540
 QY 1821 TAAACAGCTGATTTCCCTCAGCACTGTGATTTGCAATTTCAATGCAATGACATGATCT-- 1878
 Db 540 r1yCys1yLeuAsn1ySer1leuGln1yVal1leuAspTYrSer1leuAsn1a1leu1yThr1Ser1y 560

QY 1879 -AAAGAAATAGTGCACATTTTCCAAAGAGTCTGACCTTCAATCTTACTAACAATTC 1937
 DB 560 slysglnglueuclnshspheproserleuvalphleuashneuthrglnasas 580
 QY 1938 TGTGCTGTATATATGTAACATCAGAAATTCCTGACATGGGTCAAGAGACAGAGT 1997
 DB 580 pphelaCytthrCysgluhtsglnserPheleuGlntrpIlelyaspglnArglnle 600
 QY 1998 CTGTGTAATGTTGAACAATGACATGTCACAACCTGTAGAGATGATGATCCTCTTACT 2057
 DB 600 ulenValGluValGluArgmetGluCysAlaThrProserAsnlysglnglyMetProva 620
 QY 2058 GTTGATTTTAAATTTCTACCTGTATATGTAACAACAATCATCTAGTGTGACAGTGT 2117
 DB 620 lleuSerleu---AsnIlethrCysgluMetAsnlysthrIlelleGlyAlaSerValle 639
 QY 2118 CAGTGTGATTTGTGTATCCACTGTAGCATTTCTGATATACACTTCAATTTTCACCTGAT 2177
 DB 639 uSerValleuValSerValSerValAlaValleuValIlelysthrPheHISleuMe 659
 QY 2178 ACTTATTTGCTGCTGTAAAGATACACAGAGAGAGAGACATCTATGATGATTTGAT 2237
 DB 659 tleuLeuAlaGlyCysIlelysthrGlyArgGlyGluAsnIleTyrAspAlaPheValII 679
 QY 2238 CTACTCGAGTCAGATGAGAGACTGGGTGAGAAATGAGCTGGTAAAGAAATTTAGAAAGG 2297
 DB 679 eTyrSerSerGlnaspGluaspIrpValArgAsnGluLeuValIlyAsnleuGluGluI 699
 QY 2298 AGTGCCTCGCTTTCACCTGCTGCTTCACTACAGAGACTTATTTCTGCTGATGCTGCT 2357
 DB 699 yValPProPheGlnleuCySleuHISlyTyrArgAspPheIleProGlyValAlaIleAl 719
 QY 2358 TGCCAAATCATCTCCAGAAAGCTTCCAAAGCCGGAAGGTATTTGCTGAGTCTAG 2417
 DB 719 aAlaAsnIlelleHISgluGlyPheHISlySerArglyValIleValValValISergI 739
 QY 2418 ACATTTATTCAGAGCGGTGTATCTTGAATATGATGATGCTCTCAACATGCGAGTT 2477
 DB 739 nhISpHeIleGlnserArgIrpCySlePheGlnIlyGluIleAlaGlnHtrPglInph 759
 QY 2478 TCTGAGAGAGCGCTGTGAGCATCTTCAATTTGCTTGAAGAGGTGAGAGTCCCTGCT 2537
 DB 759 eleuSerSerArgAlaGlyIleIlePheIleValleuGlnIlyValGluIystrIleu 779
 QY 2538 GAGCAGACAGGTGATGATTTGCTGCTTCTTGAAGAGAAACCTTACCTGGAATGGAGGA 2597
 DB 779 uArgGlnGlnValGlnleuTyrArgGluLeuSerArgsnHtrlyrleuGlnIlyrPgluAs 799
 QY 2598 CAATCTCTGGGAGAGACATCTTCTGAGAGAACTTAAATATGCCCTAATTGATGAGAA 2657
 DB 799 pSerValleuGlnlyrghISleIlePheItrPArgIleuArglyAlaIleuAspGlyly 819
 QY 2658 AGCCTCGAATCTGAGCAAA 2679
 DB 819 sSerTrpAsnProGlnIyThr 826

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 locus (TLR4).":
 RT Genome Biol. 1:RSEARCH002.1-RSEARCH002.10(2000).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP via
 CC binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; AF179220; AAF05320.1; -;
 DR EMBL; AF179218; AAF05320.1; JOINED.
 DR EMBL; AF179219; AAF05320.1; JOINED.
 DR HSP; Q15399; 1FV.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:mast cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:00045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosy. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosy. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00882; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein, Immune response, Inflammatory response,
 KW Leucine-rich repeat, Receptor, Signal, Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 839
 FT DOMAIN 24 631 Extracellular (Potential).
 FT TRANSMEM 632 652 Potential.
 FT DOMAIN 653 839 Cytoplasmic (Potential).
 FT REPEAT 52 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.
 FT REPEAT 277 303 LRR 9.
 FT REPEAT 307 330 LRR 10.
 FT REPEAT 332 350 LRR 11.
 FT REPEAT 351 372 LRR 12.

FT REPEAT 571 592 LRR 20.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 818 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 826 AA; 94678 MM; 422773185F1769 CRC64;

Alignment Scores:

Pred. No.: 1,07e-208 Length: 826
 Score: 2783.00 Matches: 554
 Percent Similarity: 79.29% Conservative: 97
 Best Local Similarity: 67.48% Mismatches: 165
 Query Match: 53.76% Indels: 6
 DB: 1 Gaps: 4

US-09-396-985b-46 (1-2951) x TIR4_PAPAN (1-826)

QY 226 CTGGCTAGACTGATCATGCACTG---TTCTTCTGCTGCTGACACGAGAGCTTG 282
 Db 7 LeuAlaGlyThrLeuIleProIleMetAlaPheLeuSerCysValaIaGProGluSerTrp 26
 QY 283 AATCCCTGACATAGAGTAGTCTTAATATTAACCTACCAATGATGATCAAGAACTGAC 342
 Db 27 GluProCysValaGluValaIProAsnIleThrTyGlnCysMetGluLeuAsnPheTyx 46
 QY 343 AAGTCCCTGATGATCTTCTTCAACCAAGAACTGATGCTGACCTTCAACCTTG 402
 Db 47 LysIleProAsnIleProPheSerThrTyAsnLeuAsnLeuSerPheAsnProLeu 66
 QY 403 AAGATCTTAAAGGCTATAGCTTCTCCAAATTTTTCAGAACTTCAAGTGGATTTATCC 462
 Db 67 ArgHisLeuGlySerTyxSerPheLeuArgPheProIleuGlnValaIleuAsnLeuSer 86
 QY 463 AAGGTGAAATTTGAAACAATTTGAAAGACAGGATGCAATGGCTTACACCACTTCAAC 522
 Db 87 ArgCysGlnIleGlnIleThrIleGluAspGlyAlaTyxGlnSerLeuSerHisLeuSerThr 106
 QY 523 TTGATTCGACAGAAACCTATCCAGATTTTCCCAAGAACTTCTGCTGACCTTCAAC 582
 Db 107 LeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlnAlaPheSerGlyLeuSer 126
 QY 583 AGTTAGACATCTGCTGCTGCTGAGACAAATTTGAGCTCTTCAAGAACTTCCATT 642
 Db 127 SerLeuGlnIleuValaIaValaGluThrAsnLeuAlaSerLeuGlnAsnPheProIle 146
 QY 643 GGAAGCTTAACTTAAAGAACTCAATGCTGCTGACAAATTTATACATTCCTGTAG 702
 Db 147 GlyHisLeuTyxThrLeuLysGlnLeuAsnValaIaHisAsnLeuIleGlnSerPheLys 166
 QY 703 TTACCTGCAATTTTCCATCTGACGACAACTAGTATGATGATCTTCTTATATAT 762
 Db 167 LeuProGluTyxPheSerAsnLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnLys 186
 QY 763 ATTCAAACTATTAAGTCAAGCACTTACAGTTTCTACGTGAAATTCACAAAGTCAATCTC 822
 Db 187 IleGlnAsnIleTyxTyxIleAsnLeuGlnValaIleuHisGlnMetProLeuProAsnLeu 206
 QY 823 TCTTTAGACATGCTTTTGAACCAATGACTTCAATGACCAAGCTTTCAGAGAT 882
 Db 207 SerLeuAsnLeuSerLeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIle 226
 QY 883 AAGCTCAGTAACTGATCTTAAGAGTAATTTAATGCTCAATATATATGAAGAACTGAC 942
 Db 227 ArgLeuHisIleuValaIleuThrLeuArgSerAsnPheAsnLeuAsnIleuValaIleuTyx 246
 QY 943 CTTCAAAACCTGCTGCTTACAGTCCATGCTGCTGATCTTGGAGAAATTTAAAGATGA 1002

Db 247 IleGlnIleuValaIleuGluValaHisArgLeuValaLeuGlnIleuPheArgAsnIle 266
 QY 1003 AGAATTTGAAATTTTGAACCTCTATCATGAGACATATGATGATGACCATGAT 1062
 Db 267 ArgAsnLeuGlnIleuPheAsnLysSerAlaLeuGlnIleuTyxAsnLeuThrIleGlu 286
 QY 1063 GAGTTCAAGTAACTATTAACAAATGATTTTCAAGATATTTGTAAG---TTCCATTGC 1119
 Db 287 GluPheArgLeuThrTyxLeuAsnTyxTyxLeuAsnIleIleAsnLeuPheAsnCys 306
 QY 1120 TTGGCAATGTTTTCGAATGCTCTGCAAGTGTATCTTAATAATCTAAGAAATGTT 1179
 Db 307 LeuAlaAsnAlaSerSerPheSerLeuValSerValaAsnIleuTyxArgValaGluAsn 326
 QY 1180 CTTAAATTTTCAAAATGCAATCTTATCATATCTTGAATGATCAACT-AAGCACTTCCA 1238
 Db 327 SerTyxAsnPheArgTyxProGlnHisLeuGlnIleuValaAsnTyxPheGlnIleuPro 346
 QY 1239 ACTGTGATCTACCCCTTTCTTAAAGTTGACCTTATCACTTATGAAACAAAGGCTATCAGT 1298
 Db 347 ThrLeuIleuLeuGlnIleuSerLeuTyxArgLeuThrPheThrAlaAsnLysGlnIleuVala 366
 QY 1299 TTTAAAGATGAGCCCTTACCAAGTCTCAGCTATCTAGATCTTATGAAATGCACTGAC 1358
 Db 367 PheSerGluValaIleuAsnLeuProSerLeuGlnPheLeuAsnLeuSerAlaAsnGlnIleuSer 386
 QY 1359 TTATGCTGCTGCTGCTTCTTATTTGATTTGGAAACAAAGCTGACCACTTATGACCTC 1418
 Db 387 PheLeuGlnIleuTyxSerGlnSerGlnSerPheGlnIleuThrThrSerLeuTyxTyxLeuAsn 406
 QY 1419 AGCTCAATGCTGCAATCATTAATGAGTCCCAATTTTCAAGTGTGCTGCAAGAGCTGACAC 1478
 Db 407 SerPheAsnAspValIleThrMetGlySerAsnPheLeuGlnIleuGlnIleuHis 426
 QY 1479 CTGGATTTTTCAGCACTCTTCTTAAAGAGTCAACAAATTTCTCAGCTGCTTATCCCT 1538
 Db 427 LeuAsn-PheGlnHisSerAsnLeuTyxGlnMetSerGlnPheSerValaIleuLeuSerIle 446
 QY 1539 TGAAGACTTACTTACTTACATCTCTTATTAATCAACCAAAATGATTCATGATGAT 1598
 Db 446 ValArgAsnLeuIleTyxLeuAsnIleSerHisThrHisIleThrValaIlePheAsnGlnIle 466
 QY 1599 ATTCTTGGCTGACCAAGTCAACCATTAATAAGTCCGCAAACTTCTTCAAGCAAA 1658
 Db 466 PheAsnArgGlyLeuLeuSerLeuTyxValaLeuLysMetAlaGlyAsnSerPheGlnGluAs 486
 QY 1659 CACCTTTTCAAAATGCTCTTTCGAAACACAAACAACTTGAATCTGATCCTTCAATATG 1718
 Db 486 nPheLeuProAsnIlePheThrAsnLeuTyxAsnLeuThrPheLeuAsnLeuSerGlnCys 506
 QY 1719 TCAATTTGAAACAATATCTTGGGGGATTTGACACCTTCATAGACTTCAATATTTAA 1778
 Db 506 GlnIleuGlnIleuLeuSerProThrAlaPheAsnThrLeuAsnIleuGlnValaLeuAs 526
 QY 1779 TATGATGACAAACAATCTATGTTTGGATTTATCCATTAATTAACAGCTGATTCCT 1838
 Db 526 nMetSerHisAsnAsnPhePheSerLeuAspValaIleuProTyxLysCysLeuProSerIle 546
 QY 1839 CACGACTTGTGATGCAATGCTTCAATGCAATGACATGCAATGCAAGAA---ATACTGACAA 1895
 Db 546 uGlnValaLeuAsnTyxSerLeuAsnHisIleMetThrSerLysAsnGlnIleuProGlnHis 566
 QY 1896 TTTTCAAAAGATCTAGCTTCTTCAATCTTATTAACAATTTCTGCTGTTATATGTA 1955
 Db 566 sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGln 586
 QY 1956 ACATCAAGAAATTCCTGCAAGTGGTCAAGAAACGAAGCTTCTTGGTGAATGTTGACAA 2015
 Db 586 uHisGlnSerPheLeuGlnIleuTyxAsnGlnIleuValaGlnIleuValaGlnIleuVala 606
 QY 2016 AATGACATGTCGAACCTGTGATGATGAATATACCTCTTATGTTGATTTTATATATTC 2075

Db 640 eThrValLeuLeuValPheLeuValValLeuValTyrLysePheThyPheHisLeuLeu 660
 Qy 2178 ACTTATGCTGCTGCTGTAAGTAACAGAGAGAGAGATCTATATGATCTTGGAT 2237
 Db 660 tLeuLeuAlaGlyCysLeuYsYrYsSerArgGlyGlyuSerThyTyrAspAlaPheVal11 680
 Qy 2238 CTACTCGAGTCAGATGAGAGCTGGGTGAGAAATAGACTGGTAAAGATTAGAGAGG 2297
 Db 680 eTyYrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 700
 Qy 2298 AGTCCCGCGCTTTCACCTGCTGCTTCACTACAGAGACTTATTCCTGCTGAGCATTCG 2357
 Db 700 yValProProPheGlnLeuGlySerLeuHisTyrArgAspPheIleProGlyAlaAla1eal 720
 Qy 2358 TGGCAATCATCATCAGAGAGCTTCCACAGAGCGGAGAGTTATTTGGTAGCTAG 2417
 Db 720 aAlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValAlaSerG1 740
 Qy 2418 ACACTTATTCAGAGCGGTGTGTATCTTGAATATGAGATTGCTCAACATGCGAGTT 2477
 Db 740 nhIsPheIleGlnSerArgTrpCysIlePheGlnTyrGlyIleAlaGlnThrTrpGlnPh 760
 Qy 2478 TCTGAGAGCGCGCTGTCGATCATCTTCAATTTGCTTGAAGAGTTGAGAGTCCCTGCT 2537
 Db 760 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLe 780
 Qy 2538 GAGGACAGAGTGAATTTGATGCTTCTTGAAGAGAGACCTTGAATTTGAGAGG 2597
 Db 780 uArgGlnGlnValGlnLeuTyrArgLysLeuLeuAsnArgAsnThrTyrLeuGlnTyrGlnAs 800
 Qy 2598 CAATCCTCTGGGAGGAGACATCTTCTGAGAGAGACTTACCTTATGATGAGAGAA 2657
 Db 800 pSerValLeuGlnArgHisIlePheTrpArgLysLeuArgLysAlaLeuLeuAspGlyLy 820
 Qy 2658 AGCCTCGAATCTTGAGCAACAGCAGAGAGAGAA 2691
 Db 820 sProArgCysProGlnGlyMetAlaAspAlaGln 831
 RESULT 10
 Q8SPER PRELIMINARY; PRT; 837 AA.
 AC Q8SPER;
 DT 01-JUN-2002 (TREMBlurel. 21, Created)
 DT 01-JUN-2002 (TREMBlurel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlurel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21405531; PubMed=11514453;
 RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 in humans";
 RL Genetics 158:1657-1664(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF497565; AA018617.1; -
 DR EMBL; AF497565; AA018617.1; JOINED.
 DR HSSP; O60603; 1077.
 DR GO; GO:0046666; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007204; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:mast cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO; GO:0045672; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00369; LRR_Typ; 2.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KM Receptor.
 SQ SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;
 Alignment Scores:
 Pred. No.: 2.38e-206 Length: 837
 Score: 2753.00 Matches: 553
 Percent Similarity: 78.86% Conservative: 100
 Best Local Similarity: 66.79% Mismatches: 168
 Query Match: 53.18% Indels: 8
 DB: 2 Gaps: 5
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 Db 1 MecMesSerAlaSerArgLeuAlaGlyThrLeuIleProAlaPheLeuSerCys 20
 Qy 265 CTGACACAGAGAGCTTGAATCCCTGCATGAGGTAGTTCCTATATATTAACCAATGC 324
 Db 21 ValArgProGlnSerTrpGlnProCys-----ValValProAsnIleThrTyrGlnCys 38
 Qy 325 ATGATCAGAAACTCAGCAAGATCCCTGATGACATTCCTTCCACCAAGACATATGAT 384
 Db 39 MecGlnLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 58
 Qy 385 CTGAGCTCAACCCCTTGAAGATCTTAAAGCATATGCTTCCATTTTTCAGAACTT 444
 Db 59 LeuSerPheAsnProLeuArgHisLysGlySerTyrSerPhePheSerPheProGlnLeu 78
 Qy 445 CAGTGCCTGATTTATTCAGAGTGTGAATTAAGAAACATTAAGAGAGAGATGCATGCG 504
 Db 79 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 98
 Qy 505 TTACACCACTCTCAAACTTGATTAAGTGAAGAGAAACCTTATCCAGAGTTTTCACAG 564
 Db 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 118
 Qy 565 AGTTTCTGAGACTTAACAATTTAGACAACCTGCTGCTGAGAGAAATGGCCCTT 624
 Db 119 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 138
 Qy 625 CTGAAGAGCTTCCCTATTTGAGACAGTGTATTAACCTTAAGAAGACCAATGTGCTCAAT 684
 Db 139 LeuGlnAsnPheProIleGlyHisLysLeuThrLeuLysGlnLeuAsnValAlaHisAsn 158
 Qy 685 TTATATACATTCCTGTAAGTTAAGTCAATTTTTCATGTGAGAACTTAGATCATGTG 744
 Db 159 LeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnTyrLeu 178
 Qy 745 GATTTTCTTATATCACTATTAATTAAGTCAAGTCAAGTCAAGTCAAGTTCAGTGA 804
 Db 179 AspLeuSerSerLeuLysIleGlnSerIleTyrCysThrAspLeuValLeuHisGln 198
 Qy 805 AATCCAGAGTCATCTCTTATGACATGCTTGAACCAATTAAGTCAATTCATTCAGAGAC 864

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Db      199 MetProLeuLeuAsnLeuSerLeuAsnProMetThrPheIleGlnPro 218
      865 CAAGCCTTTCAGGAATTAAGCTCATGACGATCTTAAGAGTAATTTAATATGCTCA 924
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      925 AATATAATGAATAACTTGCTCAAAACCTGGCTGTATTAACAGCTCCATCGGTGATCTTG 984
Db      239 AsnValMetLysThrCysIleGlnIleuAlaGlyLeuGlnValArgArgLeuValLeu 258
      985 GAGAGATTTAAAGATGAAGAAGAAATCTGAAAATTTTGAACCTCTATCATGGAAGACTA 1044
Db      259 GlyCysPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 278
      1045 TGTGATGTGACCATGATGAGTTCAGCTTACATATACAAATGATTTTTCAGATGATTT 1104
Db      279 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyIleuAspTyIleuAspAspIle 298
      1105 GTTAAG--TTCCATTGGCTGGCGAATGTTCTGCATATGTCCTGGCAGGTGATCTATA 1161
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Db      319 GluArgValLysAspPheSerTyIleAsnGlyIleGlnIleuValAsnGly 338
      1222 CAACTAAG-CAGTTTCAACTCTGATCTTACCTTTTAAAGTTGACTTTAATCTATG 1280
Db      339 LysPheGlyGlnPheProThrLeuLysLysSerLeuLysArgLeuThrPheThrSer 358
      1281 AACAAAGGCTATAGTTTAAATAAGTCCACCAAGCTTCAGTATCTAGATCTT 1340
Db      359 AsnLysGlyGlyAsnAlaPheSerIleValAspLeuProSerLeuGlnPheLeuAspLeu 378
      1341 AGTAAATGACACTGAGCTTTAGTGTGCTGTTCTTATCTGATTTGGCAACAAACAGC 1400
Db      379 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 398
      1401 CTGAGACACTTAAGACTCAGCTTCAATGGTGCATCATTAAGAGTGCATTTCAATG 1460
Db      399 LeuLysTyIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 418
      1461 CTAGAAGAGCTGACGACCTGATTTTTCAGACACTCTTAATAAAGCTCACAGATTT 1520
Db      419 LeuGlnGlnLeuGlnLysLeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 438
      1521 CTCAGCGTTCTTAATCCCTTGAAGAACTACTTACCTTGAACATCTTCTTAAACACCA 1580
Db      438 eSerValPheLeuSerLeuArgAsnLeuIleTyIleuAspIleSerHisThrHisThrArg 458
      1581 AATTGACTTCGATGGTATATTTCTTGCTTGAACAGTCTCAACACATTTAAATAGGCTGG 1640
Db      458 GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 478
      1641 CAATTCTTTCAAAAGACACACCTTTTCAATGCTTTGCAAAACACAACTTGACATTT 1700
Db      478 YAsnSerPheGlnGlnLeuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 498
      1701 CCTGATTCCTCTTAATATGTAATGTAACAATATCTGGGGGGGTATTTGACACCTCTCA 1760
Db      498 eLeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSe 518
      1761 TAGACTTCATTTAATTAATATGAGTCACACAAATCTATTTGTTTGAATTCATCCCATTA 1820
Db      518 rSerLeuGlnValIleuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 538
      1821 TAACCAAGTGTATTCCTCAGACACTCTGATGAGTTCAGATTCATGACATGACATCT-- 1878
Db      538 rLysCysLeuAsnSerLeuArgValLeuAspLysSerLeuAsnHisIleMetCThrSerLys 558
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Db      558 sLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 578
      1938 TGTTCCTGTATATGTAACAATTCCTGACAGGGGTCAAGAGACAGAGAGCTT 1997
Db      578 pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLe 598
      1998 CTGTGTAATGTTGAACAAATGACATGTGCAACACCTGTGAGATGTAATACCTCCTTGT 2057
Db      598 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerSerLysGlnGlnMetProVa 618
      2058 GTTGCAATTTAATAATTTCTACTCTGTATATGATGTAACAACATCATCATGCTGTGCA 2117
Db      618 lLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValle 637
      2118 CAGTGTATGTGGTATTCACCTGTAAGATTTCTGATATCCACTTATTTTCACTGAT 2177
Db      637 uSerValLeuValSerValValAlaValLeuValTyIleSerPheTyIlePheHisLeuMe 657
      2178 ACTTATTTGCTGGCTGTAAAAAGTACACAGAGAGAAAGCATCTATGATGCAATTTGTGAT 2237
Db      657 tLeuLeuAlaGlyCysIleLysTyIleArgGlyGlnAsnValTyIleAspAlaPheValI 677
      2238 CTACTGAGTCAAGATGAGACTGCGGTGAGAATGAGCTGGTAAAGATTTAGAAAGG 2297
Db      677 eTyIleSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 697
      2298 AGTCCCGGCTTCACTCTGCTTCACTACACAGACATTTATCTCTGTGTAGCCATTCG 2357
Db      697 yValProPheGlnLeuCysLeuH1sTyIleArgAspPheIleProGlyValAlaIleAl 717
      2358 TGCCACATCATCCAGAGAGGCTTCCACAGAGCGGAGAGGTTATTTGGTATGCTGATG 2417
Db      717 AlaAsnIleIleHisGlnGlnPheHisLysSerArgLysValIleValValValSerGly 737
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Db      737 nHisPheIleGlnSerArgTrpCysIlePheGlnTyIleGlnIleAlaGlnThrTrpGlnPhe 757
      2478 TCTGAGACCGGCTCTGCGATCATCTTCATTTGCTTGAAGAGTTGAGAAAGTCCCTGCT 2537
Db      757 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLe 777
      2538 GAGGACAGAGTGAATTTGATGCTTCTTGAAGAAACCTTACCTGGAATGGAGAGA 2597
Db      777 uArgGlnGlnValGlnLeuTyIleArgLysLeuSerArgAsnThrTyIleuGlnLysPhe 797
      2598 CAATCTCTGGGAGGACACATCTTCTGAGAGAGACTTAAATAATGCCCTATTTGATGAGA 2657
Db      797 pSerValLeuGlyArgHisIlePheThrArgArgLysAlaLeuLeuAspGlyLys 817
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Db      817 sSerTrpAsnProGlnGlyThr 824

RESULT 11
TLR4_PONFY
ID TLR4_PONFY STANDARD; PRT; 828 AA.
AC Q8SPB9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21405531; PubMed=11514453;
RA Saitou N., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans."

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RL Genetics 158:1657-1664(2001).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAF4 via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, AF497562; AAM18616.1; -
 DR EMBL, AF497560; AAM18616.1; JOINED.
 DR EMBL, AF497561; AAM18616.1; JOINED.
 DR HSPB, O60603.1; PFM.
 DR GO, GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO, GO:0001530; P:lipopolysaccharide binding; ISS.
 DR GO, GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO, GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO, GO:0016046; P:detection of fungi; ISS.
 DR GO, GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO, GO:0042116; P:macrophage activation; ISS.
 DR GO, GO:0045576; P:macrophage activation; ISS.
 DR GO, GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO, GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO, GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO, GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO, GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO, GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro, IPR001611; LRR.
 DR InterPro, IPR000483; LRR_Cterm.
 DR InterPro, IPR003591; LRR_Typ.
 DR InterPro, IPR000157; TIR.
 DR Pfam, PF00560; LRR_12.
 DR Pfam, PF01463; LRRCT_1.
 DR Pfam, PF01582; TIR_1.
 DR PRINTS, PR00019; LEURICHRPT.
 DR SMART, SM00369; LRR_TYP_1.
 DR SMART, SM00082; LRRCT_1.
 DR SMART, SM00255; TIR_1.
 DR PROSITE, PS01004; TIR_1.
 DR GlycoProtein, Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 828 Toll-like receptor 4.
 FT DOMAIN 630 650 Extracellular (Potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 651 828 Cytoplasmic (Potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.
 FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.

FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.
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 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DF CRC64;
 Alignment Scores:
 Pred. No.: 3,4e-206 Length: 828
 Score: 2751.00 Matches: 551
 Percent Similarity: 78.74% Conservative: 101
 Best Local Similarity: 66.55% Mismatches: 169
 Query Match: 53.14% Indels: 8
 DB: 1 Gaps: 5
 US-09-396-985b-46 (1-2951) x TLR4_PONPY (1-828)
 QY 208 ATGATGCTCCCTGGCTCTGCTGAGACTCTGATCATGCACTG---TTCTTCTCTGTC 264
 Db 1 MetMeiserLaseArGleuIaGlyThleuIleProIaMetLaPheLeuSerCys 20
 QY 265 CTGACACGAGAGCTTGAATCCCTGATGAGAGTGGTCTTAATATTAACCTCAATGTC 324
 Db 21 ValArProGluSerThrGluProCys-----ValValProSerIleThrGlnCys 38
 QY 325 ATGATGAGAAAGCTCAGCAAGTCCCTGATGATTCCTTTCACACGAAACATAGAT 384
 Db 39 MetGluLeuSerPheThrIleProAspAsnLeuProPheSerThrIleValAsnLeuAsp 58
 QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTTCCAAATTTTCAAGACT 444
 Db 59 LeuSerPheAsnProLeuArGlnIleGluIleSerIlePheSerPheProGluLeu 78
 QY 445 CAGTGGCTGATTTATTCAGAGTGAATGAAGCAATTAAGCAAGATGGCATGGC 504
 Db 79 GlnValLeuAspLeuSerArGysGluIleGlnThrIleGluAspGluAlaIleGlnSer 98
 QY 505 TTACACACACCTTCAACCTTGAATGATGACAGCAAGAACCTATCCAGAGTTTCCCGCAGA 564
 Db 99 LeuSerIleLeuSerThrIleLeuThrGluAsnProIleGlnAsnLeuAlaLeuGly 118
 QY 565 AGTTTCTTGACATCAACAGATTGACACATCTGGTGGCTGTGAGACAAAATTGGCCTCT 624
 Db 119 AlaPheSerGlyLeuSerSerIleGlnIleValAlaValGluThrAsnLeuAlaSer 138
 QY 625 CTAAAGAGCTTCCCTATTTGACAGCTTAAAGCAATTAAGCAAGCTATGGGCTCACAAT 684
 Db 139 LeuIleAsnProIleGlnIleValIleValIleValIleValIleValIleValIleVal 158
 QY 685 TTTATACATTCCTGTAAGTATCACTGATATTTTTCATGCAAGCACTAGTACATGTG 744
 Db 159 LeuIleGlnSerPheIleValProGluIlePheSerAsnLeuThrAsnLeuGlnIleVal 178
 QY 745 GATCTTTCTTAATACATATTAATCAATTAATCAATCAATCAATCAATCAATCAATCAAT 804
 Db 179 AspLeuSerSerIleValIleGlnSerIleValIleValIleValIleValIleValIleVal 198
 QY 805 AATCCACAAGTCAATCTCTTGAACATGCTTGAACCAATTAATGATCACTCAAGAC 864
 Db 199 MetProIleuLeuSerLeuSerLeuAspLeuSerLeuAsnAlaMetAsnPheIleGlnPro 218

OY	865	CAAGCGTCTGAGGAATTAAGCTCCATGACATGACCTTAAGGGTAATTTTAAATGGCA	924
Db	219	GtAlaAphEuLySGluIleArgLeuHnIStyBLeuHnTrpLeuAlaGAsnSerPheAspSerLeu	238
OY	925	AATATAATGAAAACTTGCCCTTCMAAACCTGGCTGGTTTACAGCTCCATCGGTGAATCTTG	984
Db	239	AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHnHnIleValLeu	258
OY	965	GGAGAAATTTAAAGATGAAAGGAATCTGGAAATTTTGAACCTCTATCAATGAGAGACTA	1044
Db	259	GlyGluPheArgAsnGlnLysAsnLeuGlnLysPheAspThrSerAlaLeuGlnGlyLeu	278
OY	1045	TGTGATGTGACCATGATGAGTTCAGCTTACATATATACAAATGATTTTTCAGATGATAT	1104
Db	279	CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle	298
OY	1105	GTTAAG--TTCCATTTGCTGGCCGAAATGTTTCTGCAATGCTCTGCGAGTATCACTTA	1166
Db	289	IleAspLeuPheAsnCysLeuAlaAsnValSerSerPheSerLeuValSerValThrIle	318
OY	1162	AAATATCTAGAAGATGTTCTTAACATTTCAATGGCAATCCTTATCAATCATTAATGAT	1222
Db	319	LysSerValLysAspPheSerTyrAsnPheGlyTyrGlnHnIleSteuGlnLeuValAsnCys	338
OY	1222	CAACTAAG-CAGCTTCCAACTCTGATCTACCCCTTTCTTAAAGTTTGACTTTAACTATG	1282
Db	339	LysPheGlyGlnPheProThrLeuGlnLeuLysSerLeuLysArgLeuThrPheThrAla	358
OY	1281	AACAAAGGGTCTATCAGTTTAAAAAAGGTGGCCCTACCAAGCTCAGCATCTACATCTT	1340
Db	359	AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu	378
OY	1341	AGTAGAAATGCACTGAGCTTTAAGTGGCTGTTCTTATTTCTGATTTGGGAACAAAACGC	1400
Db	379	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	398
OY	1401	CTGAGACACTTGAACCTCAGCTTCAATGCTGCCATCTAATGAGTCCAAATTTACGGGT	1460
Db	399	LeuLysTyrLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly	418
OY	1461	CTAGAAGAGCTGCAGCACCTGGAATTTTCAGACACTCTTATTAAGGAGGACAGAAAT	1520
Db	419	LeuGlnGlnLeuGlnHnIleuAsp-PheGlnHnIleSerAsnLeuLysGlnMetSerGlnP	438
OY	1521	CTCAGCGTTCTTATCCCTTGAAGAGCTTACCTTACATCTCTTATTAACAACA	1580
Db	438	eSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHnIleThrHnIleThrAr	458
OY	1581	AATTGACTTCGATGGTATATATTTCTTGGCTTGACACAGTCTCAACACATTAAATGGCTGG	1640
Db	458	GValAlaPheHnAsnGlyIlePheAsnGlyLeuSerSerLeuLysValLeuLysMetAlaG	478
OY	1641	CAATTTCTTCAAAAGACACACCCCTTTCAAATGCTCTTGCAACACACAAACTTGACATT	1700
Db	478	YAsnSerPheGlnGlnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPh	498
OY	1701	CCTGGATCCCTTAATATGTCAATTGGAACAATCTTGGGGGGATTTTGAACCCCTCA	1760
Db	498	eLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSe	518
OY	1761	TAGACTTCATTTAATTAATATGAGTCACACAAATCTATGTTTTTGGATTCATCCCATTA	1820
Db	518	rSerLeuGlnValLeuAsnMetSerHnIleAsnAsnPheSerLeuAspThrPheProTyr	538
OY	1821	TAACCAGCTGATTCCTCCACACACTCTTGATTTGACAGTTTCAATGGCAATGACATCT--	1878
Db	538	rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHnIleMetThrSerLys	558
OY	1879	-AAGGAATACTGGCAACTTTTCCAAAGAGCTAGCCTTCTTCACTTACTTAACAATTC	1937
Db	558	StyGlnGlnLeuGlnHnIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs	578
OY	1938	TGTTGCTTGTAATGTGAACATCAGAAATTCCTGACGTGGGTCAAGAAACAGACGTT	1997

QY	Db	Sequence	Accession	Length
QY	Db	578 pphelaCythrCysgluHisGlnSerPheLeuGlnTrpIleYasAspGlnArgIle	598	1998
QY	Db	1998 CTTGGTGAATGTTGAACAAATGACATGTGCAACACCTGTAGAGATGAATACCTCTT	2057	598
QY	Db	598 uLeuValGluValGluArgMetGluCysAlaThrProSerAspIysGlnIleMetProVa	618	2058
QY	Db	2058 GTTGGATTTTAATTAATCTTACCTGTTATATGATCAAGACATCATCTAGCTGTGAGTGT	2117	618
QY	Db	618 lLeuSerLeu---AsnIleThrCysGlnMetAsnIlyThrValIleGlyValSerValPh	637	2118
QY	Db	2118 CAGGTGATATGTTGGTATTCACCTGTAGAGATTTTGATATACACTTCATATTTTACCTGAT	2177	637
QY	Db	637 eSerValLeuValValSerValValAlaValIleValIlyTrpSerThrPheThrSerLeuMe	657	2178
QY	Db	2178 ACTATTTCTGGCTGTGTAAAAAGTACAGCAAGAGAGAAAGATCATATGATCATTTTGAT	2237	657
QY	Db	657 tLeuLeuAlaGlyCysIleIleYsTrpGlyArgGlyGluAsnThrTrpSerPheAlaPheValI	677	2238
QY	Db	2238 CTACTCGAGTCAGATGAGAGACTGGGTGAGAAATAGCTGGTAAAGATTTTGAAGAAGC	2297	677
QY	Db	677 eIySerSerSerGlnAspTrpIubAspTrpValArgAsnGluLeuValIlyAsnLeuGluGlu	697	2298
QY	Db	2298 AGTGGCCCCGCTTTCACCTCTGCTTCTACCTACAGAGACTTATTTCTGTGTAGCCATTGC	2357	697
QY	Db	697 yValProThrPheGlnIleuCysLeuHisTrpArgAspPheIleProGlyAlaAlaIleAl	717	2358
QY	Db	2358 TGCCACATCATTCACAGAGAGGCTTCCACAGAGCGGAGAGGTTATTTGGTAGTGTCTAG	2417	717
QY	Db	717 aAlaAsnIleIleHisGlnGluIlyPheHisIlySerArgIlyValIleValValAlaSerG	737	2418
QY	Db	2418 ACACCTTATTACAGACCGGTGGTGTATCTTTGAATATGAGATTGCTCAACATGGCAGTT	2477	737
QY	Db	737 nHisPheIleGlnSerArgTrpCysIlePheGluIlyTrpGluIleAlaGlnThrTrpGlnPh	757	2478
QY	Db	2478 TCTGAGCAGACCGCTCTGTGCAATCATCTTATTTGTCCTTGAGAGAGTTGAGAAAGTCCCTGCT	2537	757
QY	Db	757 eLeuSerSerArgAlaGlyIleIlePheIleValIleGluIlyValGluIlySerThrLeu	777	2538
QY	Db	2538 GAGGACACGAGGTGAATTTATGAGCCCTTTAGACAGAAACACCTACCTGGAAATGGGAGAG	2597	777
QY	Db	777 uArgGlnGlnValGluIleuTrpArgLeuLeuSerArgAsnThrTrpIleuGluIlyTrpGluAs	797	2598
QY	Db	2598 CAATCCTCTGGGGAGGACATCTTCTGTGAGAGAGCTTAAATAATGCCCTATTGGATGAGAA	2657	797
QY	Db	797 pSerValLeuGlyArgHisIleIlePheTrpArgIleuArgIlyAlaIleuLeuAspGlyIly	817	2658
QY	Db	2658 AGCCTCGAATCTGAGCAACA 2679		817
QY	Db	817 sSerTrpAsnProGluIlyThr 824		
RESULT 12				
TLR4 BOVIN				
AC	Q9GLB5;	STANDARD;	PRT;	841 AA.
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor.			
GN	Name=TLR4;			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovine; Bos.			
CC	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Guionaud C.T., Dubey C., Jungi T.W.;			
RT	"Bovine Toll-like receptor 4 (TLR4)."			
RL	Submitted (NDV-2001) to the EMBL/GenBank/DBJ database.			
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate			
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via			
CC	MYD88, TIRAP and TRAM6, leading to NF-kappa-B activation, cytokine			

CC	SECTION: and the inflammatory response (By similarity).
CC	- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC	multi-protein complex containing at least CD14, LY96 and TLR4.
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC	their respective TIR domains (By similarity).
CC	- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	- SIMILARITY: Belongs to the Toll-like receptor family.
CC	- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
CC	- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its use by
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF310952; AAG32061.2; --
DR	HSBP, O60603, 1FPX.
DR	GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR	GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR	GO; GO:0007250; F:activation of NF-kappa-inducing kinase; ISS.
DR	GO; GO:0016046; F:detection of fungi; ISS.
DR	GO; GO:0009598; F:detection of pathogenic bacteria; ISS.
DR	GO; GO:0042116; F:macrophage activation; ISS.
DR	GO; GO:0045576; F:macrophage activation; ISS.
DR	GO; GO:0045671; F:negative regulation of osteoclast different. ; ISS.
DR	GO; GO:0045084; F:positive regulation of interleukin-1 biosyn. ; ISS.
DR	GO; GO:0045366; F:positive regulation of interleukin-12 biosyn. ; ISS.
DR	GO; GO:0054410; F:positive regulation of interleukin-13 biosyn. ; ISS.
DR	GO; GO:0024088; F:T-helper 1 type immune response; ISS.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR003591; LRR_Typ.
DR	InterPro; IPR00157; TIR.
DR	Pfam; PF00560; LRR_13.
DR	Pfam; PF01463; LRRCT; 1.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICRPT.
DR	SMART; SM00369; LRR_TYP; 1.
DR	SMART; SM00082; LRRCT; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response;
KW	leucine-rich repeat; Receptor; Receptor; Signal; Transmembrane.
FT	SIGNAL 1 23 Potential.
FT	CHAIN 24 841 Toll-like receptor 4.
FT	DOMAIN 24 632 Extracellular (Potential).
FT	TRANSMEM 633 653 Cytoplasmic (Potential).
FT	DOMAIN 654 841 LRR 1.
FT	REPEAT 53 76 LRR 2.
FT	REPEAT 77 100 LRR 3.
FT	REPEAT 102 124 LRR 4.
FT	REPEAT 149 173 LRR 5.
FT	REPEAT 174 197 LRR 6.
FT	REPEAT 203 225 LRR 7.
FT	REPEAT 277 300 LRR 8.
FT	REPEAT 310 334 LRR 9.
FT	REPEAT 350 372 LRR 10.
FT	REPEAT 373 398 LRR 11.
FT	REPEAT 400 421 LRR 12.
FT	REPEAT 422 445 LRR 13.
FT	REPEAT 446 469 LRR 14.
FT	REPEAT 471 494 LRR 15.
FT	REPEAT 495 518 LRR 16.
FT	REPEAT 520 542 LRR 17.
FT	REPEAT 544 566 LRR 18.
FT	REPEAT 568 592 TIR.
FT	DOMAIN 673 819 N-linked (GlcNAc . .) (Potential).
FT	CARBOHYD 35 35

[illegible]

QY 985 GGAGATTGAAGTGAAGGATCTGGAATTTTGAACCCCTCATCATGGAAGACTA 1044
 Db 261 G1ygluPheLysasnGluArgLysLeuGlnArgPheAspArgSerPheLeuGluGlyLeu 280
 QY 1045 TGTGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
 Db 281 CysasnLeuThrLysGluGlnPheArgLysLeuAlaLysLeuAspLysPheSerGlyAspAsp 300
 QY 1102 ATTGTGAATCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1161
 Db 301 ThrAspLeuPheAsnGlySerLeuAlaAsnValSerValLysSerLeuSerLysLeu 320
 QY 1162 AAATATCTGAGAAGATGTTCTTAAACATTTCAATGCGCATCTTATCATCATGATG 1221
 Db 321 GlySerLeuGlnAlaLeuLysAspPheArgTrpGlnLysLeuGluLeuLysAsnGly 340
 QY 1222 CAATTAAG-CAGTTTCCACTCTGAGTATCCTCTTCTTAAAGTTGACCTTAACTATG 1280
 Db 341 AspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPheValPheThrAsp 360
 QY 1281 AACAAAGGGTCTATCAGTTTAAAGTGGCCCTACCAAGTCTCAGCTATCTAGTCTT 1340
 Db 361 AsnLysAspLysSerThrPheThrGluPheGlnLeuProSerLeuGlnLysLeuAspLeu 380
 QY 1341 AGTGAATATGCACTGAGCTTATGAGTGGCTGTTCTTATCTGATTTGGGAACAAGCAGC 1400
 Db 381 LysArgAsnLysLeuSerPheLysGlyCysCysSerHisThrAspPheGlyThrThrAsn 400
 QY 1401 CTGAGACCTTAAACCTCAGCTTCAATGCTGCCATCATTAATGAGTCCCAATTTCAAGGT 1460
 Db 401 LeuLysHisLeuAspLeuSerPheAsnAspValLysLeuGlnLysSerAspPheMetGly 420
 QY 1461 CTAGAAGCTGCGACCTGAGTATTTTCAACACTTAAAGGTCACAGACT 1520
 Db 421 LeuGlnGlnLeuGlnLysLeuAsp-PheGlnHisSerThrLeuLysGlnLysLeuAlaPhe 440
 QY 1521 CTGACGCTTCTTATCCTTGAAGGCTACTTACCTTGAACATCTTATTAACAACCA 1580
 Db 440 eSerAlaPheLeuSerLeuArgAsnLeuArgLysLeuAspLysSerLysThrAsnLysLeu 460
 QY 1581 AATTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 Db 460 G1LeuAlaPheHisGlyLysPheThrGlyLeuValSerLeuGlnLysLeuLysMetAlaG1 480
 QY 1641 CAATTCTTGAAGACCAACCCCTTCAATGCTTGAACAACAACAACCAATCTGAGATT 1700
 Db 480 YasnSerPheGlnAsnAsnLeuLeuProAspLysPheThrGlyLeuThrAsnLeuThrAs 500
 QY 1701 CTTGATCTCTTAAATGCTCAATGGAACAATATCTTGGGGGCTATTTGACACCTCA 1760
 Db 500 LLeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPheHisSerLeuSe 520
 QY 1761 TAGACTTCAATTAATTAATGAGTCAACAACATCTATGTTTGGATTCATCCATTA 1820
 Db 520 rSerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeuAspThrPheLeuLys 540
 QY 1821 TAAACAGCTGATCTCTGACGACTCTTGAATGAGTTCAATGGCATAGAGACTTAA 1880
 Db 540 rGluPheLeuHisSerLeuArgLysLeuAspCysSerPheAsnArgLysLeuMetAlaSerLys 560
 QY 1881 A--GGAATACCTGACATTTTCCAAAGAGCTAGCTCTTCAATCTTCAATCAATTC 1937
 Db 560 sGluGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsnLeuThrGlnAla 580
 QY 1938 TGTTCCTTGTATATGTAACATCAGAAATCTCTGACGTGGCTCAAGGAAGAAGAGCTT 1997
 Db 580 aPheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgLysLeu 600
 QY 1998 CTTCGTGAATCTTGAACAATGACATGTCGAACCTCTGAGATGATGATGATGATGAT 2057
 Db 600 uLeuValGlyAlaGlnGlnMetCysAlaGlnProLeuAspMetGlnAspMetProVal 620
 QY 2058 GTTGATTTTAATTAATCTACTGTATATGTAACAACAATCATCATGATGCTGATGCT 2117

Db 620 LLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrLysLeuSerValSerVal 640
 QY 2118 CAGTGTATGTTGTATATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 2177
 Db 640 LThrValLeuLeuValSerValValGlyValLeuValLysLysPheThrPheHisLeuSe 660
 QY 2178 ACTTATGCTGCTGTAAAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2237
 Db 660 tLeuLeuAlaGlyCysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 680
 QY 2238 CTACTGATGTCAGATGAGAGATCTGGTGAAGATGACCTGGTAAAGATTTAGAGAAGG 2297
 Db 680 eLysSerSerGlnAspLysLysLysLysLysLysLysLysLysLysLysLysLysLys 700
 QY 2298 AGTCCCGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2357
 Db 700 YValProProPheGlnLeuLysLeuLysLysLysLysLysLysLysLysLysLysLys 720
 QY 2358 TGCCACATCATCCAG 2417
 Db 720 AlaAlaSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 740
 QY 2418 ACACTTATTCAGAGCGGTGCTGATCTTGAATGAGATGCTCAACATGCGAGCTT 2477
 Db 740 nHisPheLysGlnSerArgTrpCysLysPheGlnLysLysLysLysLysLysLysLys 760
 QY 2478 TCTGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2537
 Db 760 eLeuSerSerArgAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLys 780
 QY 2538 GAGGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2597
 Db 780 uArgGlnGlnValGlnLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 800
 QY 2598 CAATCTCTGAG 2657
 Db 800 pSerValLeuGlyLysHisValPheTrpArgLysLysLysLysLysLysLysLysLys 820
 QY 2658 AGCTGCAATCTGAG 2717
 Db 820 sProGlnSerProGlnLysLysLysLysLysLysLysLysLysLysLysLysLys 840
 QY 2717 GACC 2712
 Db 840 rThr 841
 RESULT 13
 Q8S055 PRELIMINARY; PRT; 841 AA.
 AC Q8S055;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ito T., Morimatsu M.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056444; BAB86840.1; -.
 DR HSP: O60603; 1077
 DR GO: GO:004696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macr cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO; GO:0042068; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR001571; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 DR RecProt.
 DR SQUENCE 841 AA; 96054 MW; E08DCA840EAL2DEF CRC64;
 Alignment Scores:
 Pred. No.: 7,29e-205 Length: 841
 Score: 2734.00 Matches: 547
 Percent Similarity: 77.20% Conservative: 103
 Best Local Similarity: 64.96% Mismatches: 185
 Query Match: 52.81% Indels: 8
 DB: 2 Gaps: 4
 US-09-396-985b-46 (1-2951) x Q8SQ55 (1-841)
 QY 208 ATGATGCTCCCTGGCTCTGAGTGAAGCTGATGCA---CTGTTCTTCTCTGC 264
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaLeuLeuProAlaThrAlaLeuSerCys 20
 QY 265 CTGACACGAGAGCTGAAATCCCTGATGAGTAGTCTATATTACTTACCTACGATGC 324
 Db 21 LeuArgThrGluSerThrPheProCysValGlnValProAlaIleSerTyrGlnCys 40
 QY 325 ATGATGAGAAACTCAGCAAAAGCTGATGACATCTCTTCTTCAACCAAGAACTAGAT 384
 Db 41 MetGluLeuLeuLeuTyrGlnIleProAspAsnIleProIleSerThrIlyMetLeuAsp 60
 QY 385 CTGAGCTTCAACCCCTGGAAGATCTTAAAGCTATAGCTTTCGCAATTTTCAAACTT 444
 Db 61 LeuSerPheAsnTyrLeuArgGlnIleGlnIleGlnValAspThrPheGlnGly 80
 QY 445 CAGTGGCTGATTTATTCAGGTGTGAATTGAACATTTGAAGAACAAGGATGGCATGGC 504
 Db 81 GlnAlaLeuSerLeuSerArgCysGlnIleLeuIleIleGlnValAspThrPheGlnGly 100
 QY 505 TTACACCACTCTCAAACTGATGATGACAGAAACCTATCCAGAGTTTTCGCCAGGA 564
 Db 101 LeuAsnIleLeuSerThrLeuIleLeuThrGlnAsnProIleGlnIleLeuAlaIleTyrGly 120
 QY 565 AGTTTCTGTGAGTACAGATTTAGACATCTGTGCTGTGAGACAAAATGGCCCTT 624
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIlySerValAlaValGlnThrAsnIleValSer 140
 QY 625 CTAAAGAGCTTCCCTATTTGACAGCTTATACCTTAAAGAAACCAATGGCTCAGAT 684
 Db 141 LeuAsnAspPheProIleGlyIleLeuIlyAsnLeuArgGlnLeuAsnValAlaIleIleAsn 160
 QY 685 TTATACATCTCTTAAGTACTGACATATTTTCCATCTGACGAAACCTAGTATG 744
 Db 161 PheIleIleSerPheIlySerLeuProGlnTyrPheSerAsnLeuProAsnIleGlnIleIleu 180
 QY 745 GATCTTTCTTATTAATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
 Db 181 AspLeuSerAsnAsnIlyIleGlnAsnIleTyrTyrGlnAspValIlyValIleAsnIleGln 200

QY 805 AATCCAAAGTCAATCTCTTTAGACATGTCTTTGAACCAATGACTTCAAGAC 864
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAsnProIleGlnPro 220
 QY 865 CAAGCTTTGAGGAATTAAGCTCCATGAACCTGACTTGAAGCAATTTAATAGCTCA 924
 Db 221 GlyThrPheGlnIleLeuIlySerLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSer 240
 QY 925 AATATATGAAGAACTTCCCTTCAAAACCTGGCGGTTCACGTCATCGGTGATCTTG 984
 Db 241 HisValMetLeuThrTyrIleGlnGlyLeuAlaGlyLeuIlyThrAsnArgLeuValLeu 260
 QY 985 GGAGATTTTAAAGATGAAGAAATTTGAACCTCTATCAATGAGGAGCTA 1044
 Db 261 GlyGluPheIlySerGlnIlyArgIlySerGlnArgPheAspArgSerPheLeuGlnIlyLeu 280
 QY 1045 TGTGATGTGACCAATGATGAGTTCAGGTTAACTATTAACAATGATTTTCA--GATGAT 1101
 Db 281 CysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspIlySerSerGlyAspAsp 300
 QY 1102 ATGTGTAAGTCCATTCCTTGGGAAATGTTTGCAGATGCTGCGAGGTGATGATATA 1161
 Db 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeuSerIleSerLeu 320
 QY 1162 AATATATGAGATGTTCTTAAACATTTCAATGAGCAATCTTATCAATCATTTAGATGT 1221
 Db 321 GlySerLeuGlnIleLeuLeuIlyAspPheArgTyrGlnIleIleLeuGlnIleLeuAsnCys 340
 QY 1222 CAACATAAG-CAGTTTCCAACTGGAATCTACCTTTCTTAAAGTTGACTTTAATGATG 1280
 Db 341 AspPheAspIlySerPheProAlaLeuIlyLeuSerSerIlySerIlyAspValPheThrAsp 360
 QY 1281 AACAAGGCTCTACGATTTTAAAGAGCGCCCTCAAGTCTCAGCTATCTAGATCTT 1340
 Db 361 AsnIlyAspIleSerThrPheThrGlnPheGlnLeuProSerLeuGlnIlyLeuAspLeu 380
 QY 1341 AGTAAAGATCAGCTGAGCTTTAGTGGCTGTCTTATCTGATTTGGGAAACAAGCAGC 1400
 Db 381 LysArgAsnIleLeuSerPheIlySerGlyCysCysSerIleThrAspPheGlyThrAsn 400
 QY 1401 CTGAGACATTTAGACCTCAGCTTCAATGATGTCATATTAAGTGGCCAAATTCATGGT 1460
 Db 401 LeuIleIleIleuSerLeuSerPheAsnAspValIleThrLeuGlnSerAsnPheMetGly 420
 QY 1461 CTGAGAGCTGACGACCTGGAATTTTTCAGCTCTACCTTAAAGGCTCAGAAAT 1520
 Db 421 LeuGlnIleLeuGlnIleLeuAsp-PheGlnIleSerThrLeuIlyGlnIleAsnAlaPhe 440
 QY 1521 CTGAGCTTCTTATCCCTGAAAGACTTATCTTACCTGACATCTCTTATCAACCAAA 1580
 Db 440 AsnIlePheLeuSerLeuArgAsnLeuAlaGlyTyrLeuAspIleSerTyrThrAsnIleArg 460
 QY 1581 AATGACTTGAATGATATATTTCTGGCTTACCAAGCTCAACACATTAATAATGGCTGG 1640
 Db 460 GlyLeuAlaPheIleGlyIlePheThrGlyLeuValIleSerLeuGlnIleThrLeuIlyMetAlaGly 480
 QY 1641 CAATCTTTCAAGACAAACCTTTCAAATGCTTTTGCAAAACAACAATGATTAAT 1700
 Db 480 ValSerPheGlnAsnAsnLeuLeuProAspIlePheThrGlyLeuThrAsnLeuThrIleVal 500
 QY 1701 CTTGAGCTTCTTAAATGATCAATTTGAAACAATATCTGGGGGATTTTGAACCTTCA 1760
 Db 500 IlyLeuAspLeuSerIlySerGlnIleuGlnIleValAlaGlnIleThrAlaPheIleSerLeu 520
 QY 1761 TAGACTTCAATTAATAATAGACTCAACAATGATATGTTTGGATTCATCCATTA 1820
 Db 520 rSerLeuGlnValLeuAsnMetSerIleAsnIlyLeuLeuSerLeuAspThrPheLeuIly 540
 QY 1821 TAACCACTGATATCCCTCAGCACTCTTGAATGAGATTTCAATGGCATAGAGATCTTA 1880
 Db 540 rGluProLeuIleIleSerLeuArgIleLeuAspCysSerPheAsnArgIleMetAlaSerIly 560

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NC NCB1 TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Nornick J.E.;
 RT "haplotype variation in bovine TOLL-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369 (2003).
 DR EMBL; AY297043; AA062701.1; -
 DR EMBL; AY297041; AA062701.1; JOINED.
 DR EMBL; AY297042; AA062701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0040888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_cybt.
 DR InterPro; IPR003591; LRR_type.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 12.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00365; LRR_SD22; 6.
 DR SMART; SM00369; LRR_type; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 95954 MW; ADE006ACFE44CC91 CRC64;

Alignment Scores:

Pred. No.: 1.5e-204 Length: 841
 Score: 2730.00 Matches: 547
 Percent Similarity: 77.08% Conservative: 102
 Best Local Similarity: 64.96% Mismatches: 186
 Query Match: 52.73% Indels: 8
 Gaps: 4

US-09-396-985b-46 (1-2951) x Q6WCD4 (1-841)

QY 208 ATGATGCTCCCTGCTGCTGCTAGACTGATCATGCA---CTGTTCTTCTCTGCTC 264
 DB 1 MetMetAlaArgAlaArgLeuAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
 QY 265 CTGACACGAGGAAGCTTGAATCCCTGCATAGAGTAGTTCCTAATATTACCTACCATGTC 324
 DB 21 LeuAlaGlnArgIleSerThrPheProCysValGlnValProAlaIleSerThrIleGlnCys 40
 QY 325 ATGATGACGAAACTGACGAAAGTCCGATGATGATCTCTTCTTCAACGAAAGCATAGAT 384
 DB 41 MetGlnLeuAlaLeuIleThrIleProAlaPheIleProIleSerThrIleMetLeuSerP 60
 QY 385 CTGAGCTTCAACCTTGAAGATCTTAAAGCTATAGCTTCTCAATTTTTCAGAACTT 444
 DB 61 LeuSerPheAsnIleLeuAlaArgIleLeuGlnSerHisAsnPheSerSerPheProGlnLeu 80
 QY 445 CAGTGGCTGATTTTATCCAGGTGTGAATGAAATGAAACATTTGAAGACGAGCATGGATGCG 504
 DB 81 GlnValLeuAspLeuSerThrGlySerIleLeuValIleGlnAspAspThrPheGlnIle 100
 QY 505 TTACACCACTCTCAACTGTATGATGACGAGAAACCTATCCAGAGTTTTCCTCCACAGA 564
 DB 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlnAsnProIleGlnSerLeuAlaThrGly 120
 QY 565 AGTTTCTCTGACATACAGATTGACAACTGTGGTGGCTGTGGAGACAAATGGCTCTT 624
 DB 121 AlaPheSerGlnLeuSerSerLeuGlnIleValAlaValGlnThrAsnIleValSer 140
 QY 625 CTAGAAAGCTTCCATTGACAGCTTAATTAACCTTAAGAAACGAACTGAATGTGCTCAAT 684

DB 141 LeuAsnAspPheProIleGlnHisLeuIleAsnLeuIleGlnLeuAlaHisAsn 160
 QY 685 TTTATACATTCCTAGATTACCTGCATATTTTCCATCTGACGAACTGATCATGTG 744
 DB 161 PheIleHisSerPheIleuPro****PheSerAsnLeuProAlaLeuGlnHisLeu 180
 QY 745 GATTTCTTATATACATTAATTTCAAACTTACTGTCAACGACTTACAGTTTCTACGTGA 804
 DB 181 AsnLeuSerAsnAsnIleGlnAsnIleIleTyrGlnAspValIleValLeuHisGln 200
 QY 805 AATCCACAGCTCAATCTCTCTTTAGACATGTCTTGAACCCATGACCTTATTCAGAC 864
 DB 201 MetProLeuAlaLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 865 CAACCTTTCAGGAAATTAAGCTTCACGATGACCTGATTAAGAGTATTTAATAGCTCA 924
 DB 221 GlyThrPheIleGlnIleLeuAsnGlnIleuThrLeuIleArgSerAsnPheAsnSerSer 240
 QY 925 AATATTAATGAAGAACTGCTTCACAAACCTGGCTGGTTTACAGCTCACTGGTATCTTG 984
 DB 241 HisValMetIleIleThrCysIleGlnGlnIleuAlaGlnIleuIleuIleuIleuValIleu 260
 QY 985 GGAGAAATTTAAGATGAAGAAAGATCTGGAATTTTGAACCTCTATCATGGAAGACTA 1044
 DB 261 GlnIleuPheIleuAsnGlnIleuArgIleuGlnIleuArgPheAspArgSerPheLeuGlnIleu 280
 QY 1045 TGTGATGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
 DB 281 CysAsnLeuThrIleGlnGlnIleuPheArgIleuAlaIleuIleuIleuIleuIleuIleuIleu 300
 QY 1102 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
 DB 301 ThrAspLeuPheAsnIleuAlaAsnValSerValIleSerLeuLeuSerIleSerLeu 320
 QY 1162 AATATATGAGAGATGCTTCTTAAACATTTCAATGAGCAATCTTATCATGATGATGAT 1221
 DB 321 GlnIleuLeuGlnAlaLeuLeuIleuAspPheArgIleuGlnIleuIleuIleuIleuIleuIleu 340
 QY 1222 CAACCTAAG-CAGTTTCCACCTGAGATCTACCTCTTCTTAAAGTTGACCTTAACTATG 1280
 DB 341 AspPheAspIleuPheProAlaLeuIleuLeuSerSerIleuIleuIleuIleuIleuIleuIleu 360
 QY 1281 AACAAAGGCTCATCAGTTTAAAGAGTGGCCCTTCAACCAATCTCAGCTATCTGATGAT 1340
 DB 361 AsnIleAspIleSerThrPheThrGlnPheGlnLeuProSerLeuGlnIleuIleuAspLeu 380
 QY 1341 AGTGAATATGCACTGACCTTATAGTGGCTGCTGTTCTTATTTGATTTGGGAAACAAACGC 1400
 DB 381 LysArgAsnHisLeuSerPheIleGlnCysCysSerHisThrAspPheGlnIleuThrAsn 400
 QY 1401 CTGAGACACTTGAACCTCAGCTTCAATGAGGCCATCATATGAGTGCATTTGATGGGT 1460
 DB 401 LeuIleHisLeuAspLeuSerPheAsnAspValIleThrIleuGlnIleuIleuIleuIleuIleu 420
 QY 1461 CTAGAAGAGCTGACGACCTGATTTTTCAGACCTTACTTAATAAAGGTCACAGAAAT 1520
 DB 421 LeuGlnGlnLeuGlnHisLeuAsp-PheGlnHisSerThrIleuIleuGlnIleuAlaPhe 440
 QY 440 eSerAlaPheLeuSerLeuArgAsnLeuArgTyrLeuAspIleSerTyrThrAsnIleArg 460
 QY 1581 AATGACTTGCATGATATTTTCTTGGCTTACACAGCTCAACACATTTAAATGGCTGG 1640
 DB 460 GlnLeuAlaPheHisGlnIlePheThrGlnIleuValSerLeuGlnIleuIleuIleuIleuIleu 480
 QY 1641 CAATTTCTTGAAGACAAACCTTGAATGTCTTGAACAAACAACTTGAACAT 1700
 DB 480 YAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGlnLeuThrAsnLeuIleuVal 500
 QY 1701 CTTGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1760

Db 500 lleuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPheHisSerLeuSe 520
QY 1761 TAGACTTCATTAATTAATAGTCAACAATCTATGTTTGGATTCATCCCATTA 1820
Db 520 rSerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeuAspThrPheLeuTy 540
QY 1821 TAACCAAGCTGATTCCTCAGACACTTGTGATTGCAAGTTTCATTCGATAGACATCTAA 1880
Db 540 rGluProLeuHisSerLeuHisrGlnLeuAspCysSerPheAsnHrGlnMetAlaSerLys 560
QY 1881 A---GGAAATCTGCAACATTTCCAAAGAGCTTAGCTTCTCAATCTTACTAACAATTC 1937
Db 560 sGlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsnLeuThrGlnAsnAl 580
QY 1938 TGTTGCTGTATATGTGACATCAGAAATTCCTGACAGGGGTCAAGGACAGAAAGCAGT 1997
Db 580 aPheAlaCysValCysGlnHisSerPheLeuGlnTrpValLysAspGlnArgGlnLe 600
QY 1998 CTGTGTAATGTGTAACAAATGACATGTGCAACACTGTAGAGATGAATACCTCTTAGT 2057
Db 600 uLeuValGlyAlaGlnGlnMetCysAlaGlnProLeuAspMetGlnAspMetProVa 620
QY 2058 GTTGGATTTAATTAATCTTACTGTATATGATGACAGACATCATCATGCTGTAGTGT 2117
Db 620 lLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleSerValSerValVa 640
QY 2118 CAGTGTATGTGTGATCCACTGTAGCATTTCTGATATACCACTTCTATTTTCACTGAT 2177
Db 640 lThrValLeuLeuValSerValValGlyValLeuValTyIlyPheTyIlyPheHisLeuMe 660
QY 2178 ACTTATTTCTGGCTGTAAAAAGTACACAGACAGAGAAAGCATCTATGATGATTTGTGAT 2237
Db 660 tLeuLeuAlaGlyCysLeuLysTyIlyArgGlyGlnSerIleTyIlyAspAlaPheValIl 680
QY 2238 CTACTCGATGACATGAGACTGCGGTGAGAAATGACCTGTAAAGATTTAGAGAGG 2297
Db 680 eTyIlySerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGl 700
QY 2298 AGTGGCCCGGCTTCACTGCTGCTTCACTACAGAGACTTATCTGTGTAGGCATGTC 2357
Db 700 yValProProPheGlnLeuCysLeuHisTyIlyArgAspPheIleProGlyValAlaIleAl 720
QY 2358 TGCCACATCATCCAGAGAGGCTTCCACAAGAGCCGGAAGGTATTTGTGTAGTGTCTAG 2417
Db 720 aAlaAsnIleIleGlnGlnGlnPheHisLysSerArgLysValIlleValValValSerGl 740
QY 2418 ACACCTTATTCAGAGCCGTTGGTGTATCTTGAATATGAGATGCTCAACATGGCAGTT 2477
Db 740 nHisPheIleGlnSerArgTrpCysIlePheGlnTyIlyIleAlaGlnThrTrpGlnPh 760
QY 2478 TCTGAGACGCGGCTCTGGCATCATCTTCATTTGCTTGAAGAGGTGAGAAAGTCCCTGCT 2537
Db 760 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLe 780
QY 2538 GAGGACAGAGGTGGAATTTGATTCGCTTTAGAGAAACACTTACTGGAATGGAGAGA 2597
Db 780 uArgGlnGlnValGlnLeuTyIlyArgLeuLeuSerArgAsnThrTyIlyLeuGlnuTrpGlnAs 800
QY 2598 CAATCTCTGGGAGGACATCTTCTGGAGAAACTTAATAATGCCCTATTTGATGGAAA 2657
Db 800 pSerValLeuGlnLysArgHisValPheTrpArgArgLeuArgLysAlaLeuLeuAlaGlyLy 820
QY 2658 AGCCTCGAATCTGACGAAACAGAGAGAGAA-----CAAGAAACGGCAACTTG 2708
Db 820 sProGlnSerProGlnGlnThrAlaAspAlaGlnThrAsnProGlnGlnuAlaThrThrSe 840
QY 2709 GACC 2712
Db 840 rThr 841

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 755 Seconds
(without alignments)
19454.816 Million cell updates/sec

Title: US-09-396-985B-47

Perfect score: 33065
Sequence: 1 tccccctactcttcacatt.....catgaabdcabdcabdc 18989

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlh
-Q=cg22_1/USFT0.spool/US0939685/Runat_28032005_155742_21135/app_query.fasta.1.85098
-DB=A_Geneseq_16Dec04 -Qfmt=fasta -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=PCT -NORM=EXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US0939685 @CGN 1.1 4007 @runat_28032005_155742_21135 -NCPU=6 -ICPU=3
-NO MAP -LARGESQDBRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3905.5	11.8	839	ABU04773	Human exp
2	3905.5	11.8	839	ABU04774	Human exp
3	3905.5	11.8	839	ABU04775	Human exp
4	3905.5	11.8	839	ADG78785	Human PRO
5	3905.5	11.8	839	ADG78785	Human PRO
6	3903.5	11.8	799	AAW86352	Human DNA
7	3903.5	11.8	799	AAE16093	Human DNA
8	3903.5	11.8	799	ABR83162	Human Tol
9	3903.5	11.8	799	ABR42963	Human Tol
10	3903.5	11.8	799	ADB39121	Human tol

11	3903.5	11.8	799	8	ADP56656	Adp56656 Human Tol
12	3903.5	11.8	799	8	ADP48597	Adp48597 Human Tol
13	3903.5	11.8	837	2	AAW86361	AAW86361 Human DNA
14	3903.5	11.8	837	5	AAE16102	AAE16102 Human DNA
15	3903.5	11.8	837	6	ABU04776	ABU04776 Human exp
16	3896.5	11.8	837	5	AAE16116	AAE16116 Human DNA
17	3889.5	11.7	808	8	ADOS7782	Ados7782 Chimpanze
18	3878.5	11.7	808	8	ADOS7785	Ados7785 Gorilla t
19	3875.5	11.5	808	8	ADOS7803	Ados7803 Chimpanze
20	3794	11.5	728	8	ADP29455	Adp29455 Human sec
21	3751.5	11.3	801	8	ADOS7788	Ados7788 Gibbon to
22	3629.5	11.0	795	8	ADOS7791	Ados7791 Rhesus mo
23	3612.5	10.9	795	8	ADOS7800	Ados7800 Hamadryas
24	3544.5	10.7	801	8	ADOS7797	Ados7797 Squirrel
25	3501	10.6	745	8	ADOS7794	Ados7794 White-fac
26	1090	3.3	208	8	AAW8059	AAW8059 Human Tol
27	919	2.8	178	8	ADN12270	Adn12270 IL-1R/TLR
28	785	2.4	179	7	ADG42707	Adg42707 Murine To
29	561.5	1.7	784	2	AAW86350	AAW86350 Human DNA
30	561.5	1.7	784	5	AAE16091	AAE16091 Human DNA
31	561.5	1.7	784	5	ABR83161	ABR83161 Human Tol
32	561.5	1.7	784	8	ADN02005	Adn02005 Human inf
33	560.5	1.7	784	2	AAV05869	AAV05869 Human Tol
34	560.5	1.7	784	6	ABU61956	ABU61956 Human Tol
35	560.5	1.7	784	7	ADL15005	Adl15005 Human Tol
36	560.5	1.7	784	8	ADP48593	Adp48593 Human Tol
37	560.5	1.7	784	8	ADP48593	Adp48593 Human Tol
38	560.5	1.7	784	8	ADQ66397	Adq66397 Novel hum
39	560.5	1.7	784	8	ADP23787	Adp23787 PRO polyp
40	560.5	1.7	784	8	ADQ39727	Adq39727 Human myo
41	560.5	1.7	784	8	ADQ39728	Adq39728 Human myo
42	557.5	1.7	784	2	AAW48245	AAW48245 Human pro
43	557.5	1.7	784	4	AAW90069	AAW90069 Human TNF
44	557.5	1.7	784	5	ABG73879	Abg73879 Human tun
45	557.5	1.7	784	5	AAW50618	AAW50618 Human tun

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
AC	ABU04773;	
DT	29-JAN-2003	(first entry)
DE	Human expressed protein tag (EPT) #1439.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200278524-A2.	
XX	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US009671.	
XX	28-MAR-2001; 2001US-0279495P.	
XX	21-MAY-2001; 2001US-0292444P.	
XX	08-AUG-2001; 2001US-0310801P.	
XX	01-OCT-2001; 2001US-0326370P.	
XX	04-DEC-2001; 2001US-0336780P.	
XX	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCO INC.	
XX	Chicz RM, Tomlinson AJ, Urban RG;	

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XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX tracing cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1439; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX melanoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIP0 at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 839 AA:

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 3905.50 Matches: 773
Percent Similarity: 93.46% Conservative: 13
Best Local Similarity: 91.91% Mismatches: 20
Query Match: 11.81% Indels: 35
DB: Gaps: 6

US-09-396-985b-47 (1-18989) x ABU04773 (1-839)
QY 11992 TGCTTATGATGATGCTTAACATGACAAAAAGAGCTTATCATTCGACCAATATGATTA 12051
DB 29 CysValAluValAlProAsnIleThrTyGlnCysMetGluLeuAsn----- 44
QY 12052 TACTCATCTGTGGGGCTTCTATTGCTT-----ATTCATCATCATCTGTCTG 12102
DB 45 -----PheTyLysIleProAspAsnLeuProPheSerThrLysAsn 58
QY 12103 CTGATGCTCTTGGCTATGACATCATATGACCCA---TCACATCTGTATGAAGAGCTG 12159
DB 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
QY 12160 GATGACAGTAAATATTTCTATTATAGTTCTTATTC---GCAGAAATATTAGATTAAT 12216
DB 69 -----LeuGlySerTySerPhePheSerPheProGluLeu 80
QY 12217 CAATGCTTTTATTCCTGTAAGTGTAATCCAGCAATTAAGAGGGGACATATCAGA 12276
DB 81 GluValIleuAspLeu--SerArgCysGluIleGlnIleGlnIleGlnIleGlnIleGlnIle 100
QY 12277 GCCTAAGCCACCTCTACCTTATATTTAGACAGAAACCCCATCCAGAGTTTACCTCGG 12336
DB 100 erLeuSerHisLeuSerThrIleuIleuThrGlyAsnProIleGlnSerIleuAlaLeuG 120
QY 12337 GAGCCTTTTCTGACATCAAGATTACAGAAAGCTGTGGCTGTGGAGACAAATTCATCAT 12396
DB 120 lylAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValAluThrAsnLeuAlaS 140
QY 12397 CTCTAGAGAACTTCCCATTTGAGACATCTCAAAACTTTGAAAGAACTTAATGTGCTACA 12456
DB 140 erLeuGluAsnPheProIleGlyHisLeuLysThrIleuLysGluLeuAsnAlaAlaHisA 160
QY 12457 ATCTTATCAATCTTTCAAAATTACCTGAGTATTTTCTAATCTGACCAATCTAGAGACT 12516

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DB 160 snLeuIleGlnSerPheLysLeuProGluTyPheSerArgAsnLeuThrAsnLeuGlnHisL 180
QY 12517 TGGACCTTTCCAGCAACAAAGATTTCAAGATTTATTTGACACAGCTTGGGGTTTACATC 12576
DB 180 euAspLeuSerSerAsnLysIleGlnSerIleTyrcTySerHisPheLeuArgValLeuHisG 200
QY 12577 AAATGCCCTTACATCTCTCTTTAGACCTGTCCCTGAACCCCTGAACCTTATATCCAAAC 12636
DB 200 lmeMetProLeuLeuAsnLeuSerIleuAspLeuSerIleuAsnProMetAsnPheIleGlnP 220
QY 12637 CAGGTGCATTTAAAGAAATTAAGGCTTCATAGCTGACTTTAAAGAAATTTGATAGTT 12696
DB 220 rodLylAlaPheLysGluIleArgLeuHisLysLeuThrIleuArgAsnAsnPheAspSerL 240
QY 12697 TAAATGTATGAAGAACTGTGATTTCAAGGCTCGGCTGTGTTAAGACCCATCGTTGGTTC 12756
DB 240 euAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValL 260
QY 12757 TGGGAAATTTTGAATGAAGAACTTGAAAGAAAGTTTGACAAATCTGCTTAGAGAGGCC 12816
DB 260 euGlyGluPheArgAsnGlnGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyL 280
QY 12817 TGTCAATTTGACCATTTGAAGAAATTCGATTAAGCATATTAAGATTAATCTGATGATGA 12876
DB 280 euCysAsnLeuThrIleGlnGluPheArgLeuAlaTyIleuAspTyTyTyLeuAspAspI 300
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DB 300 lrlleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAGAGGTAAAGAACTTTCTTATTAATTTGATGAGCAACTTATTAAGATTAATTAAGT 12996
DB 320 lrdLysArgValLysAspPheSerTyAsnPheGlyTyProGlnHisLeuGluLeuValAsn 340
QY 12997 GTAAATTTTGACAGTTTCCCACTTGAATCTCAAAATCTCTCAAAAGGCTTACTTCACTT 13056
DB 340 yslYspPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrS 360
QY 13057 CCNACAAAGTGGGAATGCTTTTTCAGAGTGTGATTCACCAAGCTTGAAGTTTCTTGAATC 13116
DB 360 exrAsnLysGlyLysAlaAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspI 380
QY 13117 TCAGTGAAGATGCTGAGTTTCAAGAGTTGCTGTTCTCAAGAGTAAATTTGGGACAACA 13176
DB 380 euSerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrs 400
QY 13177 GCCTAAAGATTTAGATCTGAGCTTCATGCTGTATTAATCAATGAGTTCAAACTTCTGG 13236
DB 400 erLeuLysTyIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420
QY 13237 GCTTAAGACAACTGAACATCTGGATTTCCAGATTCCAATTTGAAACAAATGAGTGAAGT 13296
DB 420 lylLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlu 440
QY 13297 TTTCAAGATTCATATCAGTACAGAACTCATTAATCACTTGAATTTCTCATATCTCACACCA 13356
DB 440 heserValPheLeuSerLeuArgAsnLeuIleTyIleuAspIleSerHisThrHisThrA 460
QY 13357 GAGTTCCTTTCAATGTCATCTTCAATGCTTGTCCAGTCTCGAAGCTTGAAGAAATGGCTG 13416
DB 460 rglValAlaPheAsnGlnLysPheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
QY 13417 GCAATTCCTTCCAGAAAACTTCTCTCCAGATATCTTCACAGAGCTGAGAAACTTGAACCT 13476
DB 480 lYAsnSerPheGlnGlnLysPheLeuProAspIlePheThrGlnLeuAspAsnLeuThrP 500
QY 13477 TCCGTGACCTCTCTCAGTGCATCTGAGAGAGTGTCTCAACAGAGATTTAATCTCACTCT 13536
DB 500 heLeuAspLeuSerGlnCysGlnLeuGlnLysLeuSerProThrAlaPheAsnSerLeuS 520
QY 13537 CCAAGCTTCAGTACTAATATATGAGCACAAACTTCTTTTCATTTGATGATACGTTTCTT 13596

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Db 520 eSerLeuGlnValLeuAsnMetSerHisAsnAspPheSerLeuAspThrPhePro 540
QY 13597 ATAAGTGTGAATCCCTCAGGTTCTGTATTAAGTCAATCAATATGACTTCCA 13656
Db 540 YrlyeCyLeuAsnSerLeuGlnValLeuAspYrlySerLeuAsnHisIleThrSerL 560
QY 13657 AAAACAGCAACTACAGCATTTTCCAGTAGTCTTCTTAATCTTACTCAGATG 13716
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QY 13717 ACTTGTCTTACTTGTGAACACCAAGTTTCTGTCAATGAGATCAGACCAAGCAGC 13776
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QY 13777 TCTTGGGAAAGTTGAACGAATGGAGTGCACACTTCAATACAGAGGAGTGCCTG 13836
Db 600 eueuValGlnValGlnArgMetGlnCysAlaThrProSerAspYrGlnGlyMetPro 620
QY 13837 TGCTGAGTTGAATATACCTGTCAGATGATGAAGACATCATGTGTGCTGCTCTCA 13896
Db 620 aLeuSerLeuAsnIleThrCyGlnMetAsnYrThrIleGlyValSerValLeuS 640
QY 13897 GTGTGCTGTAGATCTGTGTGAGCACTTGTGCTATTAAGTTCTATTTTCACTGATGC 13956
Db 640 eValLeuValValSerValValAlaValLeuValYrYrAspPheYrPheHisIleMetL 660
QY 13957 TTTTGTGCTGCTCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 14016
Db 660 eueuValGlyCyThrIleYrGlyYrGlyValGlyValGlnIleYrAspAlaPheAlaIleT 680
QY 14017 ACTCAAGCCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 14076
Db 680 YrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValYrAsnLeuGlnGlnGly 700
QY 14077 TGCTTCATTTGAGTCTGTGCTTCACTACAGACATTTATCCCGGTGAGCATGCTG 14136
Db 700 aLProProPheGlnLeuCyLeuHisIleYrArgAspPheIleProGlyValAlaIleAla 720
QY 14137 CCAACATCATCCATGAAAGTTTCCATTAAGCCGAAAGGATGATGATGATGATGATGATG 14196
Db 720 IaAsnIleIleHisGlnGlyPheHisIleYrSerTrpValIleValValValSerGlnH 740
QY 14197 ACTTCATCCAGACCGCTGTGTATCTTATATATGATGATGATGATGATGATGATGATG 14256
Db 740 IAspHeIleGlnSerArgTrpCyAllePheGlnIleYrGlnIleAlaGlnThrTrpGlnPhe 760
QY 14257 TGAGCAGTGTGTGTATCATTTATGCTGTGAGAGATGAGAGATGAGAGATGAGTCA 14316
Db 760 euserSerArgAlaGlyIleIlePheIleValLeuGlnYrValGlnYrThrLeuLeuH 780
QY 14317 GGCAGCAGGTGGAGCTGTACCGCTTCTGACGAGAAACATTTACCTGAGTGGAGGACA 14376
Db 780 rGlnGlnValGlnLeuYrArgLeuLeuSerArgAsnThrYrLeuGlnTrpGlnAspS 800
QY 14377 GTGTCTGGGGGCGGACATTTCTGAGAGACATCGAAGAAAGCCGTGATGATGATAAT 14436
Db 800 eValLeuGlnYrGlnHisIlePheTrpArgArgLeuArgYrValAlaLeuLeuAspGlyLys 820
QY 14437 CATGAATCCAGAGAGAAAGATGGGTACAGATGCAATTTGGCAGAGAAACATCTATC 14495
Db 820 eTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839

```

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KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS Homo sapiens.
PN WO200278524-A2.
PD 10-OCT-2002.
PF 28-MAR-2002; 2002WO-US009671.
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOs INC.
PA Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1440; 134bp; English.
PS The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 839 AA;
XX
XX Alignment Scores:
Pred. No.: 0 Length: 839
Score: 3905.50 Matches: 773
Percent Similarity: 93.468 Conservative: 13
Best Local Similarity: 91.918 Mismatches: 20
Query Match: 11.818 Indels: 35
DB: Gaps: 6
US-09-396-985b-47 (1-18989) x ABU04774 (1-839)
QY 11992 TGTATATCATGATGCTTAACATGACAAAGAGCTATTCAGACCAAGATGATTA 12051
Db 29 CysValGlnValValProAsnIleThrYrGlnCysMetGlnLeuAsn----- 44
QY 12052 TACTCAGTGTGTGGGCTTCTTATTTGCTT-----ATTGCATCATCATCTGTCTG 12102
Db 45 -----PheYrYrIleProAsnLeuProPheSerThrYrAsn 58
QY 12103 CTTGATGCTTTTGCCATATGACATGATGACCA---TCACTGTGATGAAGAGCTG 12159

```

Db 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
QY 12160 GATGACTAGAGATTAAATTCATATTAGGTCCTATTCA---GCAGAAATATATAGATAT 12216
Db 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 12217 CAATGCTTTTATTCCTGAGGTGTGAATCCAGACAATGGAAATGGGACATATCAGA 12276
Db 81 GlnValLeuAspLeu---SerArgCysGlnIleGlnIleThrIleGlnAspGlyAlaTyrGlnHis 100
QY 12277 GCTTAAGCCACTCTCTACCTTAAATTTGACAGAAACCCCATCCAGAGTTTATGCCCTGG 12336
Db 100 etLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleGln 120
QY 12337 GAGCCTTTCTGGACATATCAAGTTTACAGAGCTGGGTGGTGGAGACAATCTAGCAT 12396
Db 120 LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 140
QY 12397 CTCTAGAGAACTTCCCATTTGGACATCTCAAAACTTTGAAAGAACTTAAATGTGGCTCAGA 12456
Db 140 etLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsp 160
QY 12457 ATCTTATCCAAATTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACT 12516
Db 160 snLeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisIle 180
QY 12517 TGGACCTTTCCAGCAACAAGATTCAAGATTTATTTGACAGACTGGCGGTCTTCAATC 12576
Db 180 euAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLysValLeuHisG 200
QY 12577 AAAATGCCCTACTCAATCTCTCTTAGACCTGTCCCTGAACCCCTATGAACCTTATTCACAC 12636
Db 200 lmePProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnP 220
QY 12637 CAGGTGCATTTAAAGAAATTTAGGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTT 12696
Db 220 rGgIyAlaPheLysGlnIleArgLeuHisIleLysLeuThrLeuArgAsnPheAspSerI 240
QY 12697 TAAATGTAAATGAACCTTGATATCAAGTCTGGCTGGTTTAGAAGTCCATGCTTGGTTC 12756
Db 240 euAsnAlaIleCysIleTyrIleGlnGlyLeuAlaGlyLeuGlnValHisAspGlyLeuVal 260
QY 12757 TGGAGAAATTTAGAAATGAAGAACTTGGAAAAGTTTGAACAATCTGCTTAGAGAGGC 12816
Db 260 euGlyIlePheArgAsnGlnLysAsnLeuGlnLysPheAspLysSerAlaLeuGlnGly 280
QY 12817 TGTGCATTTGACATTTGAAGAATTCGATTAGCAATCTTGAAGCTTACTGATGATTA 12876
Db 280 euCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspI 300
QY 12877 TTAATGACTTAATTAATTTGTTGACAAATGTTTCTCATTTTCCCTGGTGAAGTGTGACTTA 12936
Db 300 lLeIleAspLeuPheAsnCysLeuThrAsnAlaSerSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAAGGGTAAAGAATTTTCTTAATATTTCCGATGGCAACATTTAGAAATTAAGTTAACT 12996
Db 320 lGgIyArgValLysAspPheSerTyrAsnPheGlyIleArgIleHisLeuGlnLeuValAsn 340
QY 12997 GTTAAATTTGACAGTTTCCCACTTGAACATCTCAAAATCTTCAAAAGGCTTACTTCACTT 13056
Db 340 yAlaPheGlnGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrHis 360
QY 13057 CCAACAAAGGTGGAGATGCTTTTTCAGAGTTGATCTACCAAGCCTTGAAGTTCTTAGATC 13116
Db 360 etAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspI 380
QY 13117 TCAGTGAAGATGGCTTGAAGTTTCAAAAGTGTGCTGTTCTCAAGATGATTTTGGGACAACA 13176
Db 380 euSerIleArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrHis 400
QY 13177 GCCTAAAGATTTATGATCTGAGCTTCAATGTGTGTTATTCACATGAGTTCAAACTTCTTGG 13236
Db 400 etLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420

QY 13237 GCTTAGAACCACTAGAACATCTGGAATTCACACATTCCAATTTGAAAACAATGAGTACT 13296
Db 420 LysLeuGlnIleuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnImeSerGlnP 440
QY 13297 TTTCAATATTCCTATCACTCAGAAAACCTTATTAACCTTGAACATTTCTCACTACTCACCA 13356
Db 440 heSerValPheLeuSerLeuAlaGlnLeuIleTyrLeuAspIleSerHisThrHisThrA 460
QY 13357 GAGTTCCTTTCAATGGCATCTTCAATGGCTTGTCCAGTCTCCAGATCTTGAAAATGGCTGG 13416
Db 460 rGValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
QY 13417 GCAATTCCTTTCCAGGAAAACCTTCCCTCCAGATATCTTCAAGAGCTGAGAAAACCTGACCT 13476
Db 480 LysAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuAspAsnLeuThrP 500
QY 13477 TCTTGACCTCTCTCAGTGTCAACTGAGACAGTGTCTTCCAAACAGCATTTAACTCACTCT 13536
Db 500 heLeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuS 520
QY 13537 CCAAGTCTTCAAGTACTAAATATAGACCCACAACAATCTTTCATTGATAGTTTCCTT 13596
Db 520 etSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProT 540
QY 13597 ATTAAGTGTGAAACTCCCTCCAGAGTCTTGATTAAGTCAAGTCAATCAATATGACTTCCA 13656
Db 540 TyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerL 560
QY 13657 AAAAACAGGAATTAACAGATTTTCCAAAGTACTAGCTTTCTTAAATCTTACTCAGAAATG 13716
Db 560 yAlaGlnGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnA 580
QY 13717 ACTTTGCTTGATCTTGTGAACCCAGAGTTCCTGCAATGATTCAGAGACCCAGAGCAAC 13776
Db 580 spPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrLysAspGlnArgGln 600
QY 13777 TCTTGTTGGAAGTTGAACGAATGTGGAATGTGCAACACCTTCAATTAAGCGGGCATCTCG 13836
Db 600 euLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnLysMetProV 620
QY 13837 TGTGAGTTGGAATATCACTCTGACATGATGAATGAACCATCATTTGGTGTGTGCTCTCA 13896
Db 620 alLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuS 640
QY 13897 GTGTGCTTGTACTATCTGTGTGAGCAATCTGTGTCTATTAAGTTCTTATTTCACTGATGC 13956
Db 640 etValLeuValValSerValAlaValLeuValTyrLysPheTyrPheHisLeuMetL 660
QY 13957 TTTCTGCTGGCTGAATAAGTATGGTAGAGTGAAGAAACATCTATGATGCTTTGTTATCT 14016
Db 660 euLeuAlaGlyCysIleLysTyrGlyArgGlyLysAsnIleTyrAspAlaPheValIleT 680
QY 14017 ACTCAAGCCAGGATGAGACTGCGGTGAAGGAATGAGCTAGTAAAGATTTAGAAAGGGG 14076
Db 680 ySerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGlnLys 700
QY 14077 TGCCTTCATTTAGCTTCGCTTCACTACAGAGACTTATATCCCGGTGGCCATTTGCTG 14136
Db 700 alProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleHisA 720
QY 14137 CCAACATATCCATGAAGGTTTCCATTAAGCCGAAAGGTGATTTGTGGTGGTCCCAAC 14196
Db 720 lAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGlnH 740
QY 14197 ACTTCATCCAGACCGCTGTGTATCTTGAATATGAGATTTGCTGACCTGGCAGTTTC 14256
Db 740 lPheIleGlnSerThrArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPhe 760
QY 14257 TGAAGATGTGTCTGGATCATCTTCATTTGCTGTGCAAGAGGTGAGAAAGACCTGTGCTCA 14316
Db 760 euSerSerArgLacGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuA 780

QY 12877 TTAATGACTATTAAATGTTTGACAAGATGTTCTTCAATTTCCCTGGTGAAGTGTGACTA 12936
Db 300 l e l l e a p l e u p h e a n c y b l e u t h r a n v a l s e r s e r p h e s e r l e u v a l s e r v a l t h r i 320
QY 12937 TTGAAAGGGTAAAGACTTTTCTTAATAATTCGGATGGCAACATTAGAATTAAGTTAACT 12996
Db 320 l e g u a r v a l l y a s p h e s e r t y r a s n p h e g l y t r p g l n h i s l e u g l u l e u v a l a s n c 340
QY 12997 GTAAATTTGACAGTTTCCACANTGAACTCAAAATCTCTCAAAAAGGCTTAAGTTCACTT 13056
Db 340 y s l y s p h e g l y g l n p h e p r o t h r l e u l y s l e u l y s s e r l e u l y a r g l e u t h r p h e t h r s 360
QY 13057 CCAACAAGGTGGGAATGCTTTTTCAGAAGTTGATCTACCAAGGCTTGAGTTTCTAGATC 13116
Db 360 e r e n l y s g l y g l y a s n a l a p h e s e r g l u v a l a s p l e u p r o s e r l e u g l u p h e u a s p l 380
QY 13117 TCAGTAGAAATGGCTTAGATCTGAGCTTCAGATGCTGTCTCAAAAGTATTTGGACAACCA 13176
Db 380 e u s e r a r g a n g l y l e u s e r p h e l y s g l y c y s s e r g l n s e r a s p h e g l y t h r t h r s 400
QY 13177 GCCTAAGTATTTTGAATCTGAGCTTCAGATGCTGTATTAACAGTTCAAACTTCTTG 13236
Db 400 e r l e u l y t y r l e u a s p l e u s e r p h e a s n g l y a l l e t h n e c s e r a s n p h e l e u g 420
QY 13237 GCTTAGAACAACCTAGACATCTGGATTTCCAGATTCCAATTTGAAACAAATGAGTAGT 13296
Db 420 l y l e u g l u g l n l e u g l u h i s l e u a s p h e g l n h i s s e r a s n l e u l y g l n m e s e r l u p 440
QY 13297 TTTTCAGTATTCCTATCTCACTGAAAACCTCATTTACCTTGACATTTCTCATCTCAACA 13356
Db 440 h e s e r v a l p h e l e u s e r l e u a r g a s n l e u l l e t y r l e u a s p l l e s e r h i s t h r i s t h r a 460
QY 13357 GAGTTGCTTTCAGAGCATCTTCAATGGCTTGCTTCAGATCTGAGTCTTGAAAATGGCTG 13416
Db 460 r g v a l a a p h e a s n g l y l e p h e a s n g l y l e u s e r s e r l e u g l u v a l l e u l y s e c l a g 480
QY 13417 GCAATTCCTTTCAGAGAAAACCTTCCTCCAGATATCTTTCACAGAGCTGAGAACTGACT 13476
Db 480 l y a n s e r p h e g l n g l u a s n p h e u p r o a s p l l e p h e t h g l u l e u a r g a s n l e u t h r p 500
QY 13477 TCCTGAACTCTCTCAGTGTCACTGAGAGAGTTGTCTCAACAGCAATTTAACTACTCT 13536
Db 500 h e l e u a s p l e u s e r g l n c y s g l n l e u g l u g l n l e u s e r p r o t h r a l a p h e a s n s e r l e u s 520
QY 13537 CCACTCTTCAGAGTCTAAATATGAGCCACAACAATCTTTTCAATGGATACGTTTCTT 13596
Db 520 e r s e r l e u g l n v a l l e u a s m e t s e r h i s a e n a s n p h e s e r l e u a s p h r p h e p r o t 540
QY 13597 ATAAGTGTGAATCTCCCTCCAGGTTCTTGATTAAGTCTCAATCACTAATGACTTCCA 13656
Db 540 y r l y s c y b l e u a s n s e r l e u g l n v a l l e u a s p y r s e r l e u a s n h i s l e t e t h r s e r l 560
QY 13657 AAAAAACAGAACTACAGCAATTTTCCAGTAGTCTAGCTTTCTTAATCTTACAGAAATG 13716
Db 560 y s l y s g l n g l u l e u g l n h i s p h e p r o s e r s e r l e u a l a p h e l e u a s n l e u t h r g l n a n a 580
QY 13717 ACTTGTCTGTGACTGTTGGAACAACAAGATTTCCCTGCAATGATGATCAAGGAGGAGC 13776
Db 580 s p h e a l a c y s t h r c y s g l n h i s g l n s e r p h e l e u g l n t r p l l e l y s a s p l n i r g l n l 600
QY 13777 TCTTGATGAGAGTTGAAGCAATGGAATGTGCAACAACCTTCAGATTAAGAGGAGCTG 13836
Db 600 e u l e u v a l g l u v a l g l u a r g m e t g l u c y s a l a t h r p r o s e r a s p l y s g l n l y m e t p r o v 620
QY 13837 TGCTGAGTTGAATATCACTGTGAGATGAATTAAGACCATTCATTTGGTGTGCTCTCA 13896
Db 620 a l l e u s e r l e u a s n l e t h r c y s g l n e a s n l y s t h l l e i l e g l y a l s e r v a l l e u s 640
QY 13897 GTGTGCTTGTAGTATCTGTGTAGACAGTTCGTGTCTAATTAATCTTATTTTCACTGATGC 13956
Db 640 e r v a l l e u v a l v a l s e r v a l v a l a l a l e u v a l t y r l y s p h e t y r p h e h i s l e u m e t l 660
QY 13957 TTCTTGCTGCTGCATAAAGTAGTAGAGTGAACCAATCATATGATCCCTTGTATTCT 14016

Db 660 e u l e u a l a g l y c y s l e l y s t y r g l y a r g g l y g l u a s n l l e t y r a e p a l a p h e v a l l e t 680
QY 14017 ACTCAAGCCAGATGTGAGATCTGGGTAAAGAAAGACTACTAATAAGATTAGAAGAGGGG 14076
Db 680 y r s e r s e r g l n a p r g l u a e t r p v a l a r g a s n g l u l e u v a l l y s a s n l e u g l u g l y 700
QY 14077 TGCCCTCAATTCAGCTCTGCTCTTCATCAAGAGACTTAAATCCCGGTGGCCATTCCTG 14136
Db 700 a l p r o p h e g l n l e u c y b l e u h i s t y r a r g a s p h e l l e p r o g l y v a l a l a l e a l a 720
QY 14137 CCAACATCATTCAGTGAAGTTTCCATTAAGCCGAAAGGTGATTTGGTGTGCCAGC 14196
Db 720 l a s n l l e l l e h i s g l u g l y p h e h i l y s e r a r g l y s v a l l e v a l v a l s e r g l n h 740
QY 14197 ACTTCATCCAGACCCCTGCTGTATCTTTGAATAGATGTTGCTGACCTGGCAGTTTC 14256
Db 740 l a p h e l l e g l n s e r a r g t r p c y s l l e p h e g l u t r l u l l e a l a g l n t h r t r p g l n p h e l 760
QY 14257 TGAGCAGTGGTGGTATCATCTTCATTTGCTTCGACAGAAAGTGAGAAACCTGCTCA 14316
Db 760 e u s e r s e r a r g a l a g l y l l e l l e p h e l l e v a l l e u d l n l y s v a l g l u l y s t h r l e u a 780
QY 14317 GGCAGAGGTGAGAGCTGTACCGCTTCTCAGCAGAAACCTTACCTGAGTGGAGAGACA 14376
Db 780 r g l n g l n l v a l g l u l e u t y r a r g l e u s e r a r g a s n t h r t y r l e u g l u t r p g l u a s p s 800
QY 14377 GTGTCTGGGGCGGCACTTTCTTGAGAGAGACTCAAGAAAGCCCTGGAGTGAAT 14436
Db 800 e r v a l l e u g l y a r g h i s l l e p h e t r p a r g t r g l e u a r g l y s a l a l e u l e u a s p g l y l y s s 820
QY 14437 CATGGAATCCAGAGAAACAGTGGGTACAGAGATGCAATTTGGCAGAAACATCTATC 14495
Db 820 e r t t r a n p r o g l u g l y t h r v a l g l y t h r c l y c y a s n t r p a l n g l u a l a t h s e r l e 839

RESULT 4
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN NC02003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002M0-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI: 2003-481990/45.
DR N-PSDB; ADCT8784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327bp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

XX Sequence 839 AA;

Alignment Scores:

Pred. No.:	0	Length:	839
Score:	3905.50	Matches:	773
Percent Similarity:	93.46%	Conservative:	13
Best Local Similarity:	91.91%	Mismatches:	20
Query Match:	11.81%	Indels:	35
		Gaps:	6

US-09-396-985b-47 (1-18989) x ADC78785 (1-839)

```

QY 11992 TGCTTATCATGTAAGCCCTAATGCAAAAAAGACCTATATGTCAGCCAGTATGATAA 12051
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 29 CysValGluValAlaProAsnIleThrTyrGlnCysMetGluLeuAsn----- 44
QY 12052 TACTCAGCTGTGGGGCTTCTTATTTGCTT-----ATTCATCATCATCTGTCTG 12102
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 45 -----PheTyrLysIleProAspAsnLeuProPheSerThrLysAsn 58
QY 12103 CTGATGCTTGTGCTTATGCAACAATCATATGACCA--TCACATCTGTATGAAGAGCTG 12159
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
QY 12160 GATGACTAGATTAATATTCTATTAGTTTCTTATTC---GCAGAAATATTAGATAT 12216
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 12217 CAATGCTTTTATTCTCTAGTGTGTAATCCAGACAACTGAGAGGGGCGATATGCA 12276
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 81 GlnAlaLeuAspLeu--SerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlns 100
QY 12277 GCCTAAGCACTCTCTACTTAAATATTGACAGAAACCCCATCCAGAGTTAGCCCTGG 12336
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 100 erLeuSerHisLeuSerThrIleuThrGlnAsnProIleGlnSerIleuAlaLeuG 120
QY 12337 GAGCCTTTTCTGACATATCAAGATTACAGAGCTGTGTGCTGTGAGACAAATTAGCAT 12396
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 120 LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAla 140
QY 12397 CTCTAGAGAACTTCCCATTTGAGATCTCCAAACTTTGAAAGACTTAATGTGCTACA 12456
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 140 erLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAla 160
QY 12457 ATCTTATCAATCTTCAAAATTACCTGAGTATTTTCTAATCTGACCAATCTAGAGACT 12516
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 160 snLeuIleGlnSerPheLysLeuProGlnLysThrPheSerAsnLeuThrAsnLeuGlnHis 180
QY 12517 TGAACCTTTCCAGAACAAAGATTCAAAATATTATTCAGACAGACTTGGGGTTCTACATC 12576
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 180 euAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisG 200
QY 12577 AAATGCCCTACTCAATCTCTCTTACAGCTGTCCCGGAGACCCATATGCTTTTCAAC 12636
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 200 InMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnHisIleGlnP 220
QY 12637 CAGGTGATTTAAAGAAATTTAGGCTTCATAGCTGATTCATTAAGAAATATTGATAGTT 12696
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 220 roGlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerL 240
QY 12697 TAAATGTATGAAAATTTGATTTCAAGGCTGTGGGTGTTTGAAGTCCATGTTGGTTTC 12756
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 240 euAsnValMetLysThrCysIleGlnGlnLeuAlaGlyLeuGlnValHisArgLeuValL 260
QY 12757 TGGAGAAATTTAGAAAGAAAGAACTTGAAGAAAGTTTGAACAATCTGCTCTAAGAGGCC 12816
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 260 euGlyGlnPheArgAsnGlnIleGlnLeuGlnLysPheAspLysSerAlaLeuGlnIle 280
QY 12817 TGTCAATTTGACATTTGAAGAAATTCGATTAGCATCTTACTACTGCTGATGATA 12876

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Db 280 euCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspI 300
QY 12877 TTAATGACTAATTTAAATTTGTTTGAACAAAGCTTCTTCATTTCCCTGCTAGAGTGACTA 12936
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 300 IleIleAspLeuPheAsnCysLeuThrAsnValIleSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAGAGGTAAAGACTTTTCTTATATATTTCGATGCGAACACTTTAGAAATTTAGTTAACT 12996
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 320 IeGlnValGlyAspPheSerTyrAsnHeGlyTyrGlnHisLeuGlnLeuValAsn 340
QY 12997 GTAAATTTGACAGTTTCCACATGGAACCTCAAAATCTCTCAAAAGGCTTACTTTCACTT 13056
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 340 LysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheHis 360
QY 13057 CCACAAAGGTGGGAAAGCTTTTTCAGAACTTGTATTCACCAAGCTTGAAGTTTCTATATC 13116
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 360 erAsnLysGlyGlnAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspL 380
QY 13117 TCAGTAAAGATGGCTGATGTTTCAAGAGTTGCTGTTCTCAAGATTTTGGGACAACA 13176
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 380 euSerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrHis 400
QY 13177 GCCTAAAGTATTTAGATCTGAGCTTCAATGCTGTATTTACCATGATGATCAACTTCTGG 13236
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 400 erLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420
QY 13237 GCCTAAGCAACTAGAACATCTGATTTCCAGCATTCCTCAAGAGCTTGAAACAAATAGTACGT 13296
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Db 420 LysLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerL 440
QY 13297 TTTCAAGATTCCTATCATCTCAGAAACCTCATTTACCTTGAATTTCTCATCTACACCA 13356
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Db 440 heserValPheLeuSerLeuAsnGlyLeuLysLeuAspIleSerHisThrHisAla 460
QY 13357 GAGTGTCTTCAATGGCATCTTCAATGCTTGTCCAGTCTCGAAGTCTTGAAGATGGCTG 13416
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 460 rGlyAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
QY 13417 GCATTTCTTCCAGAAACCTTCTCTCCAGATATCTTCAAGAGCTTGAGAACTTGACCT 13476
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Db 480 LysAsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrP 500
QY 13477 TCCAGACCTCTCTCAGTGTCACTGGAGAGATTGTCTCAACAGACTTAATACCTACTCT 13536
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Db 500 heLeuAspLeuSerGlnCysGlnLeuGlnLysLeuSerProHisAlaPheAsnSerLeu 520
QY 13537 CCAAGCTTCAAGTACTAATATATGAGCCACAACAACCTTTTCAATGATACGTTTCTT 13596
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Db 520 erSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPhePro 540
QY 13597 ATTAAGTCTGAACTCCCTCCAGGTTCTTGATTAACGTTCAATCACAATATGACTTCCA 13656
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Db 540 YrLysCysLeuAsnSerLeuGlnValLeuAspLysSerLeuAsnHisIleMetThrSerL 560
QY 13657 AAAAAGCAAGAACTACAGCAATTTTCAAGTGTCTAGCTTCTTAATCTTACTACAGATG 13716
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Db 560 LysLysGlnGlnLysGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsn 580
QY 13717 ACTTTGCTGTGACTTTGTAACAACAGATTTCTGCAATGATATCAAGACAGAGGAGC 13776
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 580 sPheHisLacTyrThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnL 600
QY 13777 TCTTGGTGAAGTTGAACGAATGGAATGTGCAACCTTCAATTAAGCAGGGCAATGCTG 13836
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 600 euLeuValGlnValGlnLysArgMetGlnCysAlaThrProSerAspLysGlnGlnMetPro 620
QY 13837 TGTGAGTTTGAATATCACTGTCAGATGAAATTAAGCAATCATTTGGTGTGTGCTGCTCA 13896
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 620 alLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 640
QY 13897 GTGTGCTTGTAGTATCTGTGTGATGAGACTTCTGTGCTAATAGTTCTATTTTCACTGATGC 13956

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Db 640 erValleuValSerValValaValleuValTyRlysPheTyPheHisleulect 660
QY 13957 TTCTTGCTGGCTGATTAAGATGTAGAGGTGAAAACATCTATGAGCCTTGTATCT 14016
Db 660 euNeuAlaGlyCyHisleuTyRglYarGlyGluAenIlleTyRAspAlaPheAlaIleT 680
QY 14017 ACTCAAGCCAGATGAGAGTGGTAAAGATGAGTAAAGATTTAGAGAGAGGG 14076
Db 680 yRserSerGlnAspGluAspTrpValAlarGhengluNeuValYAsnleuGluGluY 700
QY 14077 TGCTTCATTTGAGCTTGCCTTCACTACAGAGACTTATCCGGTGGCCATTCCTG 14136
Db 700 alPProPheGlnleuCyHisleuTyRarGAspPheIleProGlyValAlaIleAla 720
QY 14137 CCAACATCATCCAGATGATTCATTAAGCCGAAAGGTGATTTGGTGGCCAGC 14196
Db 720 laaenIlleHIsleuGlyPheHislySerArGlyValIleValValSerGlnH 740
QY 14197 ACTTCATTCAGAGCCGCTGTGTATCTTGAATATGAGATTTGCTCAGACCTGACGTTTC 14256
Db 740 IsPheIleGlnSerArGTrpCyHislePheGluTyRgluIleAlaGlnThrTrpGlnPhe 760
QY 14257 TGACGAGCTGCTGTGTATCATTTTCATTTCTCTGCGAGAGGTGAGAGACCTGCTCA 14316
Db 760 euSerSerArGAlaGlyIleIlePheIleValleuGlnlyValGluIlyeThrleuNeuA 780
QY 14317 GGCAGAGGTGAGAGCTGTACCCGCTTCTCAGAGAAACACTTACTGAGTGGAGGACA 14376
Db 780 rGlnGlnAlaValGluNeuTyRarGleuNeuSerArGAsnThrTyRleuGluTrpIuAspS 800
QY 14377 GTGTCTGTGGGCGGACATCTTCTGAGACGACTCAGAAAAGCCCTGCGATGATTAAT 14436
Db 800 erValleuGlyArGHisIlePheThrPArGArGleuArGlyAlaIleuNeuAspGlylysS 820
QY 14437 CATGGAATCCAGAGAAACAGTGGGTACAGATGCAATTTGGCAGAAACCAATCTATC 14495
Db 820 erTrpAsnProGluGlyThrValGlyThrGlyCyAsnTrpGlnGluAlaThrSerIle 839

RESULT 5
ADD48826
ID ADD48826 standard; protein, 839 AA.
XX
AC ADD48826;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
WP1; 2003-268312/26.
DR GENBANK; AAF05316.

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page: 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
SQ

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 3905.50 Matches: 773
Percent Similarity: 93.46% Conservative: 13
Best Local Similarity: 91.91% Mismatches: 20
Query Match: 11.81% Indels: 35
DB: Gaps: 6

US-09-396-985B-47 (1-18989) x ADD48826 (1-839)
QY 11992 TGCTTATCATGTATGCTTAACATGACAAAAGAGCTATCATTTGACGCCAGTATGATA 12051
Db 29 GlnValGluValAlaProAenIlleThrTyRGlncyMetGluNeuAsn----- 44
QY 12052 TACTCAGCTGTGGGCTTCTTATTTGCTT-----ATTCATCATCATCTGTGCTG 12102
Db 45 -----PheTyRlySIlleProAspAsnleuProPheSerThrlySAsn 58
QY 12103 CTTGATGCTTTTGCTTATGACACATCATATGACCCA---TCACATCTGTATGAAAGCTG 12159
Db 59 leuAspNeu-----SerPheAsnProleuAsnRghIs----- 68
QY 12160 GATGACTAGGATTAATATTCTAATTTAGTTCCTTATTC---GCAGAAATATTAGATAAT 12216
Db 69 -----LeuGlySerTyRserPhePheSerPheProGluLeu 80
QY 12217 CAATGCTTTTATTTCTCTGAGGTGAATCCAGCAATTTGAAGATGGGAGCATATCAGA 12276
Db 81 GlnValleuAspNeu--SerArGcySerGluIleGlnThrIleGlnuAspGlyAlaTyRlGns 100
QY 12277 GCCTTAAGCCAGCTTCTACCTTAATATTTGACAGAAACCCCATTCAGAGTTAGCCCTGG 12336
Db 100 erleuSerHisleuSerThrleuIleleuThrGlyAsnProIleGlnSerleuAlaleuG 120
QY 12337 GAGCTTTTGTGAGCTATCAAGTTTACAGAGCTGTGGTGTGGAGACAAATCTAGCAT 12396
Db 120 lyAlaPheSerGlyleuSerSerleuGlnlySerleuValAlaValGluThrAsnleuAlas 140

QY 12397 CTGAGAACTCCCACTTGACATCTCAAACTTTGAAAGAACTTAATGTGCTCA 12456
 DB 140 erleuGluaSnPheProIleGlyHisleuYsThrleuYsGluLeuAsnValAlaHisA 160
 QY 12457 ATCTTAATCCATCTTTCAAAATTTACCTGAGTATTTTCTTAATCTGACCAATCTTACGACCT 12516
 DB 160 snleuIleGlnSerPheYsleuProGluYrPheSerAsnleuThrAsnleuGlnHisSL 180
 QY 12517 TGACCTTCCAGAAACAAGATTCAAAGTATTTATTCAGACACTGGGGTCTTACATC 12576
 DB 180 euasPheSerSerAsnYsIleGlnSerIleYrCysThrAspLeuArgValIleuHisG 200
 QY 12577 AAATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAAACCTTATGAACTTTATCCAC 12636
 DB 200 lmetProleuLeuAsnleuSerleuAspLeuSerleuAsnProMetAsnHelleGlnP 220
 QY 12637 CAGGTGCAATTAAGAAATTAAGCTTCAATAGCTGACTTTAAGAAATTAATTTGATGATT 12696
 DB 220 roGlyAlaPheYsGlnIleArgleuHisYsleuThrleuArgAsnAsnHepSerL 240
 QY 12697 TAAATGTAATGAATCTGTATTCAGAGTCTGGCTGTTTGAAGTCCATGTTTGGTTC 12756
 DB 240 euasValMetLysThrCysIleGlnYleuAlaGlyleuGlnValHisArgleuValL 260
 QY 12757 TGAGAGAAATTTAGAAATGAAGAAACTTGAAGAAATTTGACAAATCTGCTTACAGAGGCC 12816
 DB 260 euGlyGluPheArgAsnGlnGlyAsnleuGlnYrPheAspYsSerAlaIleuGlnGlyL 280
 QY 12817 TGTCAATTTGACCAATTTGAGAAATTCGATTAAGCAATTAAGTACTACTCTGATGATA 12876
 DB 280 euCysAsnleuThrIleGlnGluPheArgleuAlaYrleuAspYrTyTyIleuAspAspI 300
 QY 12877 TTATGACTTAATTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGGTGTGACTA 12936
 DB 300 IeIleAspLeuPheAsnCysleuThrAsnValSerSerPheSerleuValSerValThrI 320
 QY 12937 TTGAAGGGTAAAGACTTTTCTTAATATTTCCGATGGCAACTTATTAATTAAGTAACT 12996
 DB 320 IeGluValYsIleAspPheSerYrAsnHepGlyTrpGlnHisIleuGlnleuValAsnC 340
 QY 12997 GTAAATTTGACAGCTTTCCCATTTGAAACTCAATCTCTCAAAAGGCTTACTTCACTT 13056
 DB 340 YsYsPheGlyGlnPheProThrleuYsleuYsSerleuYsArgleuThrPheThrS 360
 QY 13057 CCAACAAAGTGGGAAATGCTTTTTCAGAAATGATCTACCAAGCTTGAGTTTCAATC 13116
 DB 360 eIraenYsGlyGlyAsnAlaPheSerGlnValAspLeuProSerleuGluPheleuAspL 380
 QY 13117 TCAGTAGAAATGGCTTGATTTCAAGGTTGCTGTCCAAGATTTTGGAGCAACA 13176
 DB 380 euSerIraGAsnGlyLeuSerPheYsGlyCysSerGlnSerAspPheGlyThrS 400
 QY 13177 GCCTAAAGTATTTAGATCTGAGCTTCAATGCTTATTAATCCAGATTTCAAACTTCTGG 13236
 DB 400 eIreleuYsYrleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnHelleuG 420
 QY 13237 GCTTGAACAACACTGAAATCTGGAATTTCCAGACTTCCATTTGAAAACAAATGAGTACT 13296
 DB 420 YleuGlnGlnleuGlnHisIleuAspPheGlnHisSerAsnleuYsGlnMetSerGluP 440
 QY 13297 TTTAGATTCCTTCACTCACTGAGAAACCTCAATTTACTGACATTTCTCATCTACACA 13356
 DB 440 heSerValPheLeuSerleuArgAsnleuIleYrleuAspIleSerHisThrHisThrA 460
 QY 13357 GAGTTGCTTTCATGAGATCTTCAATGCTTGTCCAGTCTGAGACTTGTGAAAATGGCTG 13416
 DB 460 rGValAlaPheAsnGlyIlePheAsnGlyleuSerSerleuGlnValleuYsHecIaG 480
 QY 13417 GCATTTCTTTCAGAGAAACTTCTTCCATATCTTCAACAGACTGAGAACTTGACT 13476
 DB 480 YlaenSerPheGlnGlnleuAsnPheleuProAspIlePheThrGlnleuArgAsnleuThrP 500

QY 13477 TCCTGACCTCTCTCACTGTCACCTGAGAGATTTGTCTCAACAGACTTTAACTCACTCT 13536
 DB 500 heIleuAspLeuSerGlnCysGlnleuGlnleuSerProThrAlaPheAsnSerleuS 520
 QY 13537 CCACTTTCAGAGTCTAAATATGAGCCACAAACACTTCTTTTCAATTTGATACGTTCTCT 13596
 DB 520 eIserleuGlnValleuAsnMetSerHisAsnAsnPheSerleuAspThrPheProT 540
 QY 13597 ATAGTCTGACCTCCCTCAGAGTCTTGAATTAACATCACTCAATCATATATGACTTCCA 13656
 DB 540 YrYsCysleuAsnSerleuGlnValleuAspYrSerleuAsnHisIleMetThrSerL 560
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 DB 560 YsYsGlnGlnleuGlnHisPheProSerleuAlaPheleuAsnleuThrGlnAsnA 580
 QY 13717 ACTTGTCTTGTACTTGTGAACACCAAGATTTCTGCAATGATGATCAAGACCAAGGACAC 13776
 DB 580 spPheIaCysThrCysGlnHisGlnSerPheleuGlnTrpIleYsAspGlnArgGlnL 600
 QY 13777 TCTTGTGGAAGTTGAAGCAATGGAATGTCACACCTTGACATTAAGCAGAGGCACTGCTG 13836
 DB 600 euIleuValGlnValGlnArgMetGlnCysAlaThrProSerAspYsGlnGlyMetProV 620
 QY 13837 TGCTGAGTTTGAATATCACCTGTCAGATGAATGAAGACCATCATTTGCTGTGCTCTCA 13896
 DB 620 alIeuserleuAsnIleThrCysGlnMetAsnYsThrIleGlyValSerValIleuS 640
 QY 13897 GTGTGCTTGTGATCTGTGTGAGACGTTCTGCTTAATAGTTCTATTTTCACTGATGC 13956
 DB 640 eValleuValIleSerValValAlaValleuValYrYsPheYrPheHisIleuMetL 660
 QY 13957 TTTCTGTGCTGCTGCTCAATGAATATGATGAGTGAAGAAACATCTATGAGCTTTGTTATCT 14016
 DB 660 euIleuAlaGlyCysIleYsYrGlyArgGlyGlnleuIleYrAspAlaPheValIleT 680
 QY 14017 ACTCAAGCCAGATGAGAGATGAGGATGAAGATGAGTGAAGATTAATTAAGAAAGAGG 14076
 DB 680 YrIserSerGlnAspGlnAspTrpValArgAsnGlnleuValYsAsnleuGlnGlnGlyY 700
 QY 14077 TGCTCCATTTGAGCTCTGCTTCACTACAGAGACTTATTTCCGGTGTGACCTGCTG 14136
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 QY 14137 CCAAGATCAATCAATGAAGTTTCCATTAAGCCGAAAGGATGTTGTGTGCTGCCAGC 14196
 DB 720 IAsnIleIleHisGlnGlyPheHisYsSerArgYsValIleValValSerGlnH 740
 QY 14197 ACTTCATCCAGACCCGCTGTGATCTTGAATATGAGATTTGCTCAGACCTGGCAGTTTC 14256
 DB 740 IspHeIleGlnSerArgTrpCysIlePheGlnYrGlnIleAlaGlnThrTrpGlnPheL 760
 QY 14257 TGAAGCTCGTGTGATCATCTTCAATGCTCTGCAAGAGTGAAGAGACCTGTGCTCA 14316
 DB 760 euSerSerArgAlaGlyIleIlePheIleValleuGlnYsValGlnYrThrleuAsnA 780
 QY 14317 GGCAGAGGTGAGCTGTACCCGCTTCTCAGCAGAAACATTAACCTGAGTGGAGAGACA 14376
 DB 780 rGlnGlnValGlnleuYrArgleuLeuSerArgAsnThrYrleuGlnTrpGlnAspS 800
 QY 14377 GTGTCCGTGGGGGAGCATCTTGTGAGAGAGACTCAAGAAAGCCGTGAGTGGTAAAT 14436
 DB 800 eValleuGlnYsGlnHisIlePheTrpArgArgleuHisGlyAlaIleuLeuAspGlyYsS 820
 QY 14437 CATGGAATCCAGAAAGAAAGTGGGTACAGATGCAATTTGGCAGAGAAACAATCTATC 14495
 DB 820 eTrIraenPProGlnGlnYrThrValGlyThrGlyCysAsnTrpGlnGlnValaThrSerIle 839
 RESULT 6
 AAM86352 standard; protein; 799 AA.
 ID AAM86352
 XX AAM86352;


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Db      451  ILlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln 470
Qy      13509 TTGCTCCAAAGAGATTAACTCACTCCAGCTGCTTGAGTACTAAATATAGACACAC 13568
Db      471  LeuSerProtnAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
Qy      13569 AACTCTTTTCATTGATGATACCTTTCTTATAGTGTCTGAATCCCTCCAGATTCTTGAT 13628
Db      491  AsnHePheSerLeuAspThrPheProTyrIleCysLeuAsnSerLeuGlnValLeuAsp 510
Qy      13629 TACAGTCTCAATCAATATGATGATCTCCAAAAAGAGAACTACAGACATTTTCCAGTATG 13688
Db      511  TyrSerLeuAsnHisIleMetThrSerIleGlnLeuGlnHisPheProSerSer 530
Qy      13689 CTAGCTTTCTTAATCTTACTCAGAAATGACTTTCCTGTTGATTTGAAACACAGATTC 13748
Db      531  LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysTrpCysGlnHisGlnSerPhe 550
Qy      13749 CTGCAATGATCAAGACACAGAGCAGCTCTTGAGTGAAGTTGAACGAATGAATGCA 13808
Db      551  LeuGlnTrpIleIleValAspGlnArgGlnLeuValGlnValGlnArgMetGlnCysAla 570
Qy      13809 ACACCTTCAGATTAAGACAGGAGGATGCTGTGCTGAGTTGAATATCACCTGCAGATGAT 13868
Db      571  ThrProSerAspIleGlnGlyMetProValLeuSerLeuAsnIleTrpCysGlnMetAsn 590
Qy      13869 AAGACATCATTTGCTGTGCTGCTGCTCAAGTGTCTGAGTATGATCTGTTGAGCAGTTCTG 13928
Db      591  LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaValLeu 610
Qy      13929 GTCTATTAAGTCTTATTTTCACTGATGCTTCTGCTGCTCAATTAAGTATGATGATGAT 13988
Db      611  ValTyrIleSerPheTyrPheHisLeuMetLeuAlaGlyCysIleIleTyrGlyArgGly 630
Qy      13989 GAAAAATCTATGATGCTGCTTGTATCTACTCAAGCCAGATGAAGATGAGATGAGTAAAGAT 14048
Db      631  GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsn 650
Qy      14049 GAGCTATTAAGAATTTTGAAGAAGAGGGGCTCCATTTCACTGCTGCTCACTACAGA 14108
Db      651  GluLeuValIleValAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisIleTyrArg 670
Qy      14109 GACTTATTCCTCCGGTGGCCATGCTGCCAATCATCATGATGATGATGATGATGATGATGAT 14168
Db      671  AspPheIleProGlyValAlaAlaIleAlaAsnIleIleHisGlnGlyPheHisIleYser 690
Qy      14169 CGAAAGGTGATTTGTTGCTGCTCCACAGACTTCACTCAAGACCGCTGGTATCTTTGAA 14228
Db      691  ArgIleValIleValValIleValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 710
Qy      14229 TATGAGATTTGCTGACCTGCGACGTTTCTGAGCAGTGTGCTGTGATCATCTTATGTC 14288
Db      711  TyrGlnIleLeuIleGlnTrpGlnPheLeuSerSerArgIleGlyIleIlePheIleVal 730
Qy      14289 CTGCAAGAGGTGAGAGAGACCTGCTCAGGACAGAGGTGAGGAGTACCGCTTCTGAC 14348
Db      731  LeuGlnIleValIleGlnIleValIleValIleValIleValIleValIleValIleVal 750
Qy      14349 AGGAACACTTACCTGAGAGTGGAGAGACAGTGTCTGAGGAGCGGACATCTTCTGAGAGCA 14408
Db      751  ArgAsnThrTyrLeuGlnIleValIleValIleValIleValIleValIleValIleVal 770
Qy      14409 CTGAGAAAAGCCCTGCTGAGATGTAATCATGCAATCCAGAGAGACAGTGGTACAGA 14468
Db      771  LeuArgIleValIleValIleValIleValIleValIleValIleValIleValIleVal 790
Qy      14469 TGCAATTTGGAGAGAGAGACATCTATC 14495
Db      791  CysAsnTrpGlnGlnAlaHisSerIle 799

```

```

ID      AAE16093 standard; protein: 799 AA.
XX
AC      AAE16093;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Human DNAX Toll like receptor (DTRL) 4 #1.
XX
KW      Human; DNAX Toll like receptor; DTRL; therapy; immunological disorder;
XX      interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS      Homo sapiens.
XX
PN      WO200190151-A2.
XX
PD      29-NOV-2001.
XX
PF      23-MAY-2001; 2001WO-US016766.
XX
PR      25-MAY-2000; 2000US-0207558P.
XX
PA      (SCHE ) SCHERING CORP.
XX
PI      Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX      WPI; 2002-083085/11.
XX      DR      N-PSDB; AAD26283.
XX
XX      New DNAX Toll like receptor (DTRL) proteins, useful for treating
XX      conditions exhibiting abnormal expression of the receptors of their
XX      ligands, particularly abnormalities manifested by immunological
XX      disorders.
XX
PS      Claim 1, Page 35; 297pp; English.
XX
XX      The invention relates to mammalian receptor proteins, e.g., primate,
XX      human DNAX Toll like receptor (DTRL) protein and their corresponding
XX      nucleic acids. The DTRL is useful for treating conditions exhibiting
XX      abnormal expression of the receptors of their ligands. Such abnormality
XX      is manifested by immunological disorders. In particular, the DTRL is
XX      useful for treating various disease or disorders associated with abnormal
XX      expression or abnormal triggering of response to a ligand. The DTRL is
XX      also useful as an immunogen for the production of antisera or antibodies
XX      specific, e.g. capable of distinguishing between other interleukin (IL)-1
XX      receptor family members, for the DTRL or its various fragments. The
XX      purified DTRL can be used to screen monoclonal antibodies or antigen-
XX      binding fragments. The antibodies are useful for screening expression
XX      libraries for particular expression products. These are useful for
XX      detecting or diagnosing various immunological conditions related to
XX      expression of DTRL or cells that express it. The present sequence is
XX      human DTRL4 protein. The DTRL4 gene is located on chromosome 9q32-33
XX
SQ      Sequence 799 AA:
XX
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Gaps: 9
DB: 5 Indels: 1

```

Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIly 90
QY 12369 CTGGTGGCTGTGGAGAGCAATCTTAGCATCTCTAGAGAACTTCCCATTTGACATCTTCAA 12428
Db 91 LeuValAlaValAlaGlnThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuIly 110
QY 12429 ACCTTGAAGAAGCTTAAATGAGGCTCACACTTATCCAACTTCAATTAACCTGAGTAT 12488
Db 111 ThrLeuIlySerGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheIlySerProGlnIly 130
QY 12489 TTTTCAATCTGACCAATCTTAGAGCACTTGAACCTTTCCAGCAACAAGATTCAAGTAT 12548
Db 131 PheSerLeuLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnIlySerIle 150
QY 12549 TATTGCGACAGACTTGGGGTTCATCATCAAAATGCCCTTCAATCTCTTTAGACCTG 12608
Db 151 TyrCysThrAsnProLeuAsnValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnPro 170
QY 12609 TCCCTGAACCTTATGAACCTTATTCACACAGGTCATTTAAAGAAATTAGGCTTCATAG 12668
Db 171 SerLeuAsnProMetAsnProIleGlnProGlyAlaPheIlySerGlnIleArgLeuHisIly 190
QY 12669 CTGACTTTAAGAAATATTTTGAATGATTAAATGTAATGAAAACCTTGATTCAGAGCTG 12728
Db 191 LeuThrLeuAsnArgAsnAsnProPheAsnSerLeuAsnValMetIlySerIlySerIleGlnIly 210
QY 12729 GCTGGTTTAAAGTCCATCGTTGGTCTGGAGAAATTTAGAAATGAAGAACTTGGAA 12788
Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGln 230
QY 12789 AAGTTTGAACAATGTGCTCTAGAGGCGCTGCAATTTGACCATTAAGAATTCAGATTA 12848
Db 231 LysPheAsnProMetAlaLeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheAsnPro 250
QY 12849 GCATACTTAAGACTACTACCTCGATGATATTAATGACTTAATTTAATTTGACAAATGT 12908
Db 251 AlaIlyLeuAsnProIlyTyrIlyLeuAsnProIleIleAsnProPheAsnProLeuThrAsnVal 270
QY 12909 TCTTCATTTTCCCTGGAGAGTGATGATCTAGTAAAGGTAAGGCTTTCTTAAATTTTC 12968
Db 271 SerSerPheSerLeuValSerValThrIleGlnArgValIlyAsnProPheSerTyrAsnPro 290
QY 12969 GGAATGGCAACATTTAGATTAAGTAACTGTAATTTGAGCAGTTTCCCACTTAAGACTC 13028
Db 291 GlyTyrGlnHisLeuGlnLeuValAsnProLysPheGlnIlyPheProHisLeuIlySer 310
QY 13029 AAATCTGTCAAAAGGCTTACTTCTTCACTTCCAAACAAGGTGGAAATGCTTTTTCAGAA 13088
Db 311 LysSerLeuIlySerArgLeuThrPheThrSerAsnIlySerGlyAlaAsnAlaPheSerGlnVal 330
QY 13089 GATCTACCAAGCCTTGAAGTTTCTAGATCTCAGTGAAGAAATGGCTTGAAGTTTCAAG 13148
Db 331 AsnLeuProSerLeuGlnPheLeuAsnProLysSerArgAsnGlnIlyLeuSerPheIlyGlyCys 350
QY 13149 TGTCTCAAGAGTATTTTGGGCAACAGCCTTAAGATTTAGATCGAGCTTCAAGT 13208
Db 351 CysSerGlnSerAsnProIlyThrThrSerLeuIlySerIlyLeuAsnProLysPheAsnGly 370
QY 13209 GTTATTTACATGATGATCAAACTTCTTGGGCTTAGAAACAATCAAGAACTTGGATTTTCAG 13268
Db 371 ValIleThrMetSerSerAsnProPheLeuGlnIlyLeuGlnIlyLeuGlnHisLeuAsnProGln 390
QY 13269 CATTCCAATTTGAAAACAATAGAGTATTTCAAGTATCTTATCACTCAGAACTCAT 13328
Db 391 HisSerAsnLeuIlySerGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle 410
QY 13329 TACCTTGAATTTCTGATACCTCAGACCAAGGTTGCTTCAATGGAGTCTTCAATAGGCTTG 13388
Db 411 TyrLeuAsnProIleSerHisThrHisThrArgValAlaPheAsnGlnIlyIlePheAsnGlyLeu 430
QY 13389 TCCAGTCTGAAAGTCTTGAAGAAATGGCTGGCAATTTCTTCCAGAAACCTTCTTCAGAT 13448

Db 431 SerSerLeuGlnValLeuIlySerMetAlaGlyAsnSerPheGlnIlyAsnProPheLeuProAsn 450
QY 13449 ATCTTCAGAGCTGGAGAAACCTTGACCTTCTGAGACCTTCTCAGTGTCAATGAGAGCAG 13508
Db 451 IlePheThrGlnLeuAsnProMetLeuThrPheLeuAsnProLysSerGlnCysGlnLeuGlnIly 470
QY 13509 TTGTCTCAACAGCAATTTAACTCACTTCCAGTCTTTCAGGTACTAAATATGAGCCACAAC 13568
Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTTTTCTTTCATGGAATCGTTTCTTAAAGTGTCTGAACCTTCCAGGTTCTTGAT 13628
Db 491 AsnPhePheSerLeuAsnProThrPheProIlyLysCysLeuAsnSerLeuGlnValLeuAsn 510
QY 13629 TACAGTCTCAATCACTAATGACTTCCAAAAACAGAACTACAGCAATTTTCCAAAGTAT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerIlySerGlnIlyLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTATTTGTAACACACAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAsnProPheAlaCysThrCysGlnHisGlnSerPhe 550
QY 13749 CTGCAATGATCAAGACACAGAGGCACTTGTGTGGAAGTTGAACGAATGAAATGTGCA 13808
Db 551 LeuGlnIlyProIleLysAsnProGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 570
QY 13809 ACACCTTCAGATTAAGAGGAGCAATGCTGTGCTGAGTTGAATATCACTGTCAAGATGAAT 13868
Db 571 ThrProSerAsnProLysGlnIlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
QY 13869 AAGACCATCATTTGGTGTGTGTGTCTCAGTGTGCTTGTAGATCTGTTGAGAGATTTCTG 13928
Db 591 LysThrIleIleGlyAlaSerValLeuSerValLeuValSerValAlaAlaValLeu 610
QY 13929 GTCTTAAGTTCATTTTTCACCTGATGCTTCTTGGCTGTGCTGCTTAAGTATGATAGCT 13988
Db 611 ValIlyLysPheThrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyAsnGly 630
QY 13989 GAAAACATCATGATGCTTGTATCTACTCAAGCCAGAGATGAGCACTGGTGAAGAAAT 14048
Db 631 GlnAsnIleTyrAsnAlaPheValIleTyrSerSerGlnAsnProLysProValAlaAsn 650
QY 14049 GAGCTAGTAAAGATTTAGAAAGAGGGGCTCCATTTCAAGCTGTGCTTCACTACAGA 14108
Db 651 GlnLeuValLysAsnLeuGlnIlyAlaProProPheGlnLeuCysLeuHisTyrArg 670
QY 14109 GACTTAATTTCCGGTGTGGCAATGCTGCTGCCAACAATCATCAAGAAAGTTTCCATAAAGC 14168
Db 671 AspPheIleProGlyAlaAlaIleAlaAlaAsnIleIleHisGlnIlyPheHisLysSer 690
QY 14169 CGAAGGTGATTTGTTGGTGTGCCAGCACTTCAATCCAGAGCCGCTGTATCTTGAAG 14228
Db 691 ArgIlyValAlaIleValAlaValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
QY 14229 TATGAGATTTGCTGAGCCTTGGCAGTTTCTGAGCAGTGTGCTGTATCATCTTCAATGTC 14288
Db 711 TyrGlnIleHisGlnHisThrProGlnPheLeuSerSerArgHisGlyIleIlePheIleVal 730
QY 14289 CTGCAAGAGGTGAGAAAGACCTTGTCTCAGCAGCAGAGGTGAGCTGTACCGCTTCTCAGC 14348
Db 731 LeuGlnIlyValAlaGlnIlySerThrLeuLeuArgGlnIlyValGlnIlySerIlyAsnLeuSer 750
QY 14349 AGGAACACTTAACCTGAGAGTGGAGGACAGGTGCTTGGAGGAGGACATCTTCTGAGAGCA 14408
Db 751 ArgAsnThrTyrLeuGlnIlyProGlnAsnSerValLeuGlnIlyArgHisIlePheThrPArgArg 770
QY 14409 CTCAGAAAAGCCTGTGCTGATGTTAATCATGGAATCCAGAAAGAAACAGTGGGTACAGCA 14468
Db 771 LeuArgIlyAlaLeuLeuAsnProLysSerTyrAsnProGlnIlyHisThrValGlnIlyThrGly 790
QY 14469 TGCATTTGGCAGAGAACACATCTTATC 14495
Db 791 CysAsnThrProGlnIlyAlaThrSerIle 799

RESULT 8
AB83162
ID AB83162 standard; protein; 799 AA.
AC AB83162;
XX
XX 09-AUG-2002 (first entry)
XX
XX Human Toll-like receptor-4, Tlr4.
DE
XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
KM cytosolic; immunostimulatory; scavenger receptor; Toll receptor;
KW respiratory tract infection; Toll-like receptor; Tlr4.
XX
XX Homo sapiens.
OS
FN WO200235236-A1.
XX
XX 02-MAY-2002.
XX
XX 26-OCT-2001; 2001WO-FR003352.
XX
XX 27-OCT-2000; 2000FR-00013883.
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX
XX Jemnin P, Magistrelli G, Herbault N, Bonnefoy J;
XX WPI; 2002-383586/41.
DR N-PSDB; ABN83318.
XX
XX Identifying agent that binds to scavenger receptors and signals through a
PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
PT cytotoxic T cell response.
XX
XX
XX Disclosure; Page 58-60; 71pp; French.
XX
XX The present invention relates to a method for identifying new therapeutic
CC compounds (I) by selecting molecules that bind to scavenger receptors and
CC signal through a Toll receptor. The present sequence is the protein
CC sequence for human Toll-like receptor-4, Tlr4, which was used to
CC illustrate the method of the invention. (I) are useful as carriers and/or
CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC tumor cell, especially a pathogen that causes respiratory tract
CC infection, also more generally for inducing an immune response. (I) can
CC also be used for specific targeting of active agents (antigens etc.) to
CC antigen-presenting cells (especially immature dendritic cells), for
CC subsequent internalisation by these cells
XX
XX Sequence 799 AA;
SQ
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 5 Gaps: 1
US-09-396-985b-47 (1-18989) x AB83162 (1-799)
QY 12216 TCATGCTCTTTATTC-----TGTAGGTGAATC 12248
Db 31 SerTyserPhePheSerPheProGluLeuGlnValIleuAspLeuSerArgCysGluIle 50
QY 12249 CAGACATTTGAAGATGGGCGATATCAGAGCTTACCTTACCTTAATTTGACA 12308
Db 51 GlnThrIleGluAspGlyAlaIleArgIleSerIleuSerHisIleuSerThrIleLeuThr 70
QY 12309 GGAAGCCCATCCAGAGTTTACCCCTGGAGCCCTTTCTGAGACTATCAGTTTACAGAG 12368
Db 12309 GGAAGCCCATCCAGAGTTTACCCCTGGAGCCCTTTCTGAGACTATCAGTTTACAGAG 12368

Db 71 GlyAsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerIleuGlnIle 90
QY 12369 CTGGTGGCTGTGAGAGAAATCTTAGCATCTCTTAGAGAACTTCCCATTTGACATCTCAA 12428
Db 91 LeuValAlaValGlnThrAsnLeuAlaSerIleuGlnAsnPheProIleGlyHisIleuLys 110
QY 12429 ACTTTGAAGAACTTAATGTGGCTCAGACATCTTATCCATCTTCAATTAACGAGATAT 12488
Db 111 ThrIleuGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheIleuProGluIle 130
QY 12489 TTTTCAATCTGACCAATCTAGAGCACTTGACCTTTCAGCAACAAGATTCAGATAT 12548
Db 131 PheSerAsnLeuThrAsnLeuGlnHisIleuAspLeuSerSerIleuGlnIle 150
QY 12549 TATTGCAACACTTGGCGGCTTCTACATCAATGCCCCCTACTCAATCTCTCTTAGACTG 12608
Db 151 TyrCysThrAspLeuArgValIleuHisGlnMetProIleuAsnLeuSerIleuAspLeu 170
QY 12609 TCCCTGAACCTTATGAACTTATTCACACAGGTGATTTAAAGAAATTTAGGCTTCATAG 12668
Db 171 SerIleuAsnProIleAsnPheIleGlnProGlyAlaPheIleuGlnIleHisIleuLys 190
QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAATGTAATGAAACTTGATTCAGAGTCTG 12728
Db 191 LeuThrIleuArgAsnAsnPheAspSerIleuAsnValMetIleuThrCysIleGlnGlyLeu 210
QY 12729 GCTGGTTTAAAGTCCATCGTTGTTGCTTGGGAGAAATTTGAATGAGAAACTTGAA 12788
Db 211 AlaGlyLeuGlnValHisArgLeuValIleuGlyGluPheArgAsnGlnGlyAsnLeuGln 230
QY 12789 AGTTTGACAAATCTGCTCAGAGGGCTGCAATTTGACCAATTTGAGAAATTCAGATTA 12848
Db 231 LysPheAspLysSerIleuAlaLeuGlnGlyLeuCysAsnMetThrIleGlnGluPheArgLeu 250
QY 12849 GCATACTTAGACTACTGATGATGATATTTAGTATTTATTTGATTTGACAAATGTT 12908
Db 251 AlaTyrIleuAspLysTyrTyrIleuAspAspIleIleAspLeuPheAsnGlySerIleuThrAsnVal 270
QY 12909 TCTTCATTTTCCCTGGTGGATGCTGATCTATTTGAAAGGTTAAAGATTTTCTTATATTC 12968
Db 271 SerSerPheSerIleuValSerValThrIleGlnArgValLysAspSerTyrAsnPhe 290
QY 12969 GATGGCAATTTTAGAATAGTTAACTGTAATTTGACAGTTTCCCATGAGAACTC 13028
Db 291 GlyTyrGlnHisIleuGlnLeuValAsnCysLysPheGlyGlnPheProIleuLysLeu 310
QY 13029 AAATCTCTCAAAAGGCTTACTTCACTTCCACAAAGGTGGAGATGCTTTTTCAGAGATT 13088
Db 311 LysSerIleuLysArgLeuThrPheThrIleSerAsnLysGlyGlyAsnAlaPheSerGluVal 330
QY 13089 GATCTACCAAGCCTTGAGTTTCTAGATCTCAGTGAAGAATGGCTTGAGTTCAAGGTTC 13148
Db 331 AspLeuProSerIleuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 350
QY 13149 TGTTCCTCAAGGATTTTGGGACAACACAGCTTAAGATTTAGTCTGAGCTTCAATGCT 13208
Db 351 CysSerGlnSerAspPheGlnTyrIleuSerIleuLysTyrIleuAspLeuSerPheAsnGly 370
QY 13209 GTTATTACATGATTCAAACTTCTTGAGGCTTGAACAATCAGACATCTGATTTTCAG 13268
Db 371 ValIleThrMetSerSerAsnPheLeuGlnIleuGlnIleuGlnIleuAspPheGln 390
QY 13269 CATTCAATTTGAAACAATAGAGTGTTCAGATTTCTCATCTCAGAAACTTCATT 13328
Db 391 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerIleuArgAsnLeuIle 410
QY 13329 TACCTGCAATTTCTCATCTCAGACACAGAGTGTTCCTCAATGGCACTTCAATGCTTG 13388
Db 411 TyrLeuAspLysSerHisIleuThrIleArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
QY 13389 TCCAGTCTCGAAGTCTTGAAGATGCTGCAATCTTCTCAGAGAAACTCTCTTCAGAGAT 13448
Db 431 SerSerIleuGlnValIleuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 450


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QY 13449 ATCTTCACAGAGCTGAGAACTTGAACCTTCTGACCTCTCTGAGTCAACTGAGACAG 13508
DB 451 TLebheThrGluLeuAArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
QY 13509 TTGCTCCACAGACTTAACTCACTCCAGCTTCCAGGACTTAATATGAGCCAAAC 13568
DB 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTCATTGATGATACGTTTCTTAAAGTGTGTGAACCTCCCTCCAGGTTCTTGAT 13628
DB 491 AsnPheSerSerLeuAspThrPheProTyrCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCAATCACTCAATGACCTTCCAAAAAAGAGACATACAGCACTTTTCCAGTACT 13688
DB 511 TysSerLeuAsnHisIleMetThrSerLysLysGlnGluLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTAACCTGACAAATGACTTTGCTGTGACTTGTGAAACACAGAGTTTC 13748
DB 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisLeuGlnSerPhe 550
QY 13749 CTGCAATGATCAAGACACAGAGGACGCTTGGTGAAGTTGAACGAATGAAATGTGCA 13808
DB 551 LeuGlnTrpIleLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 570
QY 13809 ACACCTTCAGATTAAGCAGGAGGACGCTGCTGCTGAGTTGAATATACCTGTCAGATGAAT 13868
DB 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsp 590
QY 13869 AAGACATCATATGGTGTGTGCTGAGCTCAAGTGTGCTGATGATCTGTGTGAGCACTTGTG 13928
DB 591 LysThrIleIleGlyValSerValLeuSerValValSerValValAlaValLeu 610
QY 13929 GTCTAATAAGTTCTAATTTTCACTGATGCTTGTGCTGCTGCTGCAATAAGTATGATGAGT 13988
DB 611 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
QY 13989 GAAACATCTATGATGCTTGTGCTTGTATCTCAAGCCAGACATGAGATGAGGATGAGGAT 14048
DB 631 GlnAsnIleTyrAspAlaPheValIleLysIserSerGlnAspGlnAspTrpValArgAsn 650
QY 14049 GAGCTAGTAAGAATTATGAGAGAGGGGCTCCATTCAGTCTGCTGCTGCTCACTAGACA 14108
DB 651 GlnLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
QY 14109 GACTTATTCCTGGGTGGCCATGCTGCTGCAACATCATCAATGAAGTTTCCATAAAGC 14168
DB 671 AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSer 690
QY 14169 CGAAGGATGATTTGTTGGTGTGCTCCAGACTTCAAGCCAGGCTGATCCGCTGATCTTGA 14228
DB 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheHis 710
QY 14229 TATGAGATTGCTGACCTGCGACGTTTCTGACAGCTCTGCTGATCATCTTCAATGTC 14288
DB 711 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
QY 14289 CTGCAAGAGGTGAGAGAGACCTGCTCAGGCAAGCTGAGCTGATCCGCTTCTCAAC 14348
DB 731 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
QY 14349 AGGAACAATTACCTGAGAGTGGAGAGACGTCCTGGGGGGGCGACATTTCTGGAGACGA 14408
DB 751 ArgAsnThrTyrLeuGlnTrpGlnAspSerValLeuGlyArgHisIlePheTrpArgArg 770
QY 14409 CTCGAAAGAGCCCTGCTGATGTAATCATGGAATCCAGAGAAACAGTGGTACAGA 14468
DB 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrCly 790
QY 14469 TGCATTTGGCAGAGAAACAATCTATC 14495
DB 791 CysAsnTrpGlnGlnAlaThrSerIle 799
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RESULT 9
ABR42963
ID ABR42963 standard; protein; 799 AA.
XX
AC ABR42963;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human Toll-like receptor 4.
XX
KW Human; Toll-like receptor 4; receptor; antiinflammatory; immunomodulator.
XX
OS Homo sapiens.
XX
PN M02003044163-A2.
XX
PD 30-MAY-2003.
XX
PF 14-NOV-2002; 2002MO-US036390.
XX
PR 19-NOV-2001; 2001US-00001863.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Karas JG, Koller E;
XX
DR WPI; 2003-468766/44.
DR N-PSDB; ACC83601.
XX
PT New antisense oligonucleotides for modulating Toll-like receptor 4 gene
PT expression, particularly useful for preventing, delaying or treating e.g.
PT inflammatory disorders, or conditions involving Th1 or Th2 immune
PT responses.
XX
PS Example 14; Page 100-104; 110pp; English.
XX
CC The present sequence is the protein sequence human Toll-like receptor 4.
CC The invention provides chimeric phosphorothioate oligonucleotides (see
CC ACC8381-98) targeted to human Toll-like receptor 4 mRNA. Such antisense
CC oligonucleotides inhibit the expression of human Toll-like receptor 4 and
CC are useful for treating or preventing a disease or condition associated
CC with Toll-like receptor 4, e.g. an inflammatory disorder or a condition
CC involving an immune response, particularly Th1 or Th2 responses
XX
SQ Sequence 799 AA;
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 6 Gaps: 1
US-09-396-985b-47 (1-18989) x ABR42963 (1-799)
QY 12216 TCAATGCTTTTATATCC-----TGTAGTGTGAATC 12248
DB 31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
QY 12249 CAGCAATTGAGATGGGAGCATATCAGAGCCTTCTTCACTTAATATTTGACA 12308
DB 51 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisIleSerThrLeuIleThr 70
QY 12309 GGAACCCCATCCAGACTTTAGCCCTGGAGCCCTTTTCTGACTATCAAGTTTACAGAG 12368
DB 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 90
QY 12369 CTGATGCTGTGGAGAGCAAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAA 12428
DB 91 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLys 110
QY 12429 ACTTGAAAGAACTTAATGTGGCTCAACAATCTTATCCAAATCTTGAATGATAT 12488
```

Db 111 ThrLeuysGIuLeuAsnValAlAhIsAsnLeuIleGInSerPheLyLeuProGIuLyx 130
 Qy 12489 TTTTCTATCTGACCAATCTGAGACCTTGAGACCTTTCACAGCAACAAGATTCAAGTAT 12548
 Db 131 PheSerAsnLeuThrAsnLeuGIuHIsLeuAspLeuSerSerAsnLySileGIInSerIle 150
 Qy 12549 TATTGACAGACTTGCGGGTCTACATCAATGCCCCCTACATCTCTCTTGAAGCTG 12608
 Db 151 TyrCysThrAspLeuArgValLeuHIsGInMetProLeuLeuAsnLeuSerLeuAspLeu 170
 Qy 12609 TCCCTGAACCTTATGAACTTTATCCACAGGTGCAATTTAAGAAATTAAGGCTTCAAG 12668
 Db 171 SerLeuAsnProMetAsnPheIleGInProGIuAlaPheLySGIuIleArgLeuHIsLyS 190
 Qy 12669 CTGACTTTAAGAAATTAATTTGATAGTTAAATGTAAGAAACTTGATTCAGAGTCTG 12728
 Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetLySThrCysIleGIInGIuLeu 210
 Qy 12729 GCTGGTTTAGAAGTCCATCGTTTGGTCTGGAGAGATTAGAAATGAAGAACTTGAA 12788
 Db 211 AlaGIuLeuGIuValHIsArgLeuValLeuGIuGIuPheArgAsnGIuGIuAsnLeuGIu 230
 Qy 12789 AAGTTTGAACAATCTGCTCTGAGAGGCGCTGCAATTTGACCAATTTGAAGAAATTCGATTA 12848
 Db 231 LysPheAspLySserAlaLeuGIuGIuGIuLeuGIuGIuLeuGIuGIuLeuGIuGIuLeu 250
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 Db 251 AlaLyxLeuAspLyxTyrTyrLeuAspAspIleIleAspLeuPheAsnCySLeuThrAsnVal 270
 Qy 12909 TCTTCATTTTCCCTGGAGAGTGTGACTATTGAAAGGGTAAAGACTTTCTTATTAATTC 12968
 Db 271 SerSerPheSerLeuValSerValIThrIleGIuArgValLySAspPheSerTyrAsnPhe 290
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 Qy 13089 GATTCACCAAGCTTGAAGTTTCTAGATCTCAGTAAGAAATGGCTTGAAGTTCAAGTTC 13148
 Db 331 AspLeuProSerLeuGIuPheLeuAspLeuSerArgAsnGIuLySLeuPheLySLeu 350
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 Qy 13209 GTTATTACATGATTAACACTTTTGGGCTTGAACAACATTAACAATCTTGATTTCCAG 13268
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 Db 411 TyrLeuAspIleSerHIsThrHIsThrArgValAlaIlePheAsnGIuGIuLeu 430
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 Qy 13989 GAAAAACATCATGATGCTTGTATTAATCTACTCAAGCAGAGATGAGCACTGGTAAAGAT 14048
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 Qy 14049 GAGCTAGTAAGAATTTAGAAAGAGGCGCTTCCATTTGAGCTTGCCTTCACTACAGA 14108
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 Db 671 AspPheIleProGIuValAlaIleAlaIleAlaAsnIleIleHIsGIuGIuPheHIsLySser 690
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 Qy 14229 TATGAGATTGCTCAGACTGCGAGTTTCTGAGCAATGCTGCTGATCATCTTCAATGCT 14288
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 Qy 14289 CTGCAAGAGGTGAGAAAGACCTGCTCAGGCAAGAGGTGAGCTGTACCGCTTCTCAGC 14348
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 Qy 14409 CTGAGAAAGCCCTGCTGATGTGTAATCATGATTCAGAAAGAAAGAGTGGTACAGCA 14468
 Db 771 LeuArgLySAlaLeuLeuAspGIuLySsetTArgAsnProGIuGIuGIuThrValGIuGIuGIu 790
 Qy 14469 TGCATTTGGCAGAGCAACATTTATC 14495
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 RESULT 10
 ADB39121 standard; protein; 799 AA.
 ID ADB39121
 XX
 AC ADB39121;
 XX
 DT 04-DEC-2003 (first entry)

XX Human toll-like receptor (TLR) -4 protein amino acid sequence.
 DE
 XX
 KM vascular disease; Toll-like receptor-4 inhibitor; TLR-4 inhibitor;
 KM atherosclerosis; restenosis; inflammation; vasotrophic;
 KM antiatherosclerotic; thrombolytic; cardiatic; antiinflammatory;
 KM antiense therapy; gene therapy; transplant atherosclerosis;
 KM vein-graft atherosclerosis; thrombosis; stent restenosis;
 KM angioplasty restenosis; heart disease; human.
 XX Homo sapiens.
 OS
 XX
 PN US2003077279-A1.
 PD
 XX
 PD 24-Apr-2003.
 XX
 PF 23-APR-2002; 2002US-00128166.
 XX
 PR 24-OCT-2001; 2001US-0315637P.
 PR 17-DEC-2001; 2001US-0341359P.
 XX
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX
 PI Arditi M, Rajavashisth T, Shah PK;
 XX
 DR WPI: 2003-615986/58.
 DR N-PSDB; ADB39120.
 XX
 PT Treating a vascular disease, particularly atherosclerosis, thrombosis,
 PT restenosis, stent restenosis or angioplasty restenosis, by administering
 PT a Toll-like receptor-4 (TLR-4) inhibitor to a mammal.
 XX
 PS Disclosure; Page 13-15; 21pp; English.
 XX
 CC This invention relates to a novel method for the treatment of a vascular
 CC disease through the administration of a Toll-like receptor-4 (TLR-4)
 CC inhibitor to a mammal. The TLR-4 protein has been linked to several
 CC disease such as atherosclerosis, restenosis, inflammation and other
 CC vascular diseases. Compounds which inhibit the activity of TLR-4, through
 CC the inhibition of its receptor, may have vasotropic,
 CC antiatherosclerotic, thrombolytic, cardiatic and antiinflammatory
 CC activities. This may also be achieved through antisense therapy or gene
 CC therapy. The method or the system of the invention may therefore be
 CC useful for inhibiting or treating a vascular disease, for example
 CC atherosclerosis, transplant atherosclerosis, vein-graft atherosclerosis,
 CC thrombosis, restenosis, stent restenosis, angioplasty restenosis, or
 CC inflammation and other heart disease. The present sequence is the amino
 CC acid sequence of the human TLR-4 protein which was the target receptor
 CC for inhibitory compounds in the method of the invention.
 CC
 XX
 SQ Sequence 799 AA:
 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 7 Gaps: 1
 US-09-396-985B-47 (1-18989) x ADB39121 (1-799)
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 DB 31 SerYrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 50
 QY 12249 CAGCAATTGAAGATGGGCGATATCAGAGCCTTCTACCTTATATTGACA 12308
 DB 51 GlnHrIleGluAspGlyAlaIleTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
 QY 12309 GGAAGCCCATCCAGAGTTTGAAGCCCTGGAGCCTTTTCTGACATCAATCAAGTTTGAAG 12368
 DB 71 GlyenProIleGlnSerIleuAlaIleuGlyAlaPheSerGlyLeuSerSerIleuGlnIlys 90

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 QY 12429 ACTTTGAAGAACTTAAATGTGGCTGCAAACTTTATCCAACTTTTCAAAATTTACTGGTAT 12488
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 QY 12609 TCCCTGAACCTTATGAACTTTATCCAAACGAGTGCAATTTAAGAAATTAAGCTTCATAG 12668
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 DB 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 210
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 DB 391 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAspAsnLeuIle 410
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 QY 13389 TCCAGTTCGACAGCTTGAAGAAATGGCTGGCAATTTCTTCCAGAGAAACCTTCCAGAT 13448
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 Db 451 ILePheThrgIuLeuAArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
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 Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAspMetSerHisAsn 490
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 Db 491 AsnPhePheSerLeuAspThrPheProTyrIuScyLeuAsnSerLeuGlnValLeuAsp 510
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 QY 13869 AAGACATCATTTGCTGTGCTGCTCTCAAGTGTGCTGTGATGATCTGTGTGACAGTTCTG 13928
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 Db 631 GluLeuIleTyrAlaPheAlaPheValIleTyrSerSerGlnAspGlnuAspThrValArgAsn 650
 QY 14049 GAGCTAGTAAAGATTTAAGAAAGAGGGGTGCTTCCATTTACGCTGTGCTTCACTACAGA 14108
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 QY 14109 GACTTTTCCCGGTGGCCATGCTGCGCAACATCATTCATGAAGTTTCCATAAAGC 14168
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 QY 14169 CGAAAGGTGATTTGTGTGTGTCCACAGACTTCATCCAGAGCCGCTGATCTTGA 14228
 Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
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 Db 711 TyrcIuIleAlaGlnThrTyrGlnPheLeuSerSerArgAlaGlnIleIlePheIleVal 730
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 QY 14409 CTGAGAAAGCCCTGCTGATGTGTAATTCATGGAATCCAGAAAGAGACAGTGGGTACAGA 14468
 Db 771 LeuArgLysAlaLeuLeuAspGlnLysSerThrAsnProGlnGlnIuThrValGlnThrGln 790
 QY 14469 TGCAATTGGAGAGAGACATCTATC 14495
 Db 791 CysAsnThrPnglnAlaIuAsnSerIle 799

RESULT 11

ADP5656
 ID ADP5656 standard; protein; 799 AA.
 XX
 AC ADP5656;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human Toll-like receptor (TLR)-related protein - SEQ ID 8.
 XX
 KW expression system; Toll-like receptor; TLR; immune response modifier;
 KW IRK; cancer; gene therapy; human; receptor.
 XX
 OS Homo sapiens.
 XX
 PN MO2004053057-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 31-OCT-2003; 2003MO-US034563.
 XX
 PR 11-DEC-2002; 2002US-0432651P.
 XX
 PA (MINN) 3M INNOVATIVE PROPERTIES CO.
 XX
 PI Gupta SK, Ghosh TK, Fink JR,
 XX
 DR WPI; 2004-468833/44.
 DR N-PSDB; ADP56655.
 XX
 PT New expression system comprising a first nucleic acid sequence that
 PT encodes a Toll-like receptor (TLR), useful for preparing a composition
 PT comprising TLR agonist for treating e.g., cancer.
 XX
 PS Claim 4; SEQ ID NO 8; 699p; English.
 XX
 CC The invention relates to a novel expression system comprising a first
 CC nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
 CC linked to a first expression control sequence and a second nucleic acid
 CC sequence that encodes a reporter. TLRs are immune response modifiers
 CC (IRMs). The expression system of the invention may be useful for
 CC preparing a composition comprising the TLR agonist for treating cancer,
 CC possibly via gene therapy. The current sequence is that of the human Toll
 CC -like receptor (TLR)-related protein (SEQ ID 8) of the invention.
 XX
 SQ Sequence 799 AA.
 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 8 Gaps: 1
 US-09-396-985b-47 (1-18989) x ADP5656 (1-799)
 QY 12216 TCATGCTTTTATTC-----TGTAGTGTGAATC 12248
 Db 31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
 QY 12249 CAGACATTAAGATGAGGGGATATCAGAGCCTTAAGCACCTCTCACTTAATATTGACA 12308
 Db 51 GlnThrIleGlnuAspGlnAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
 QY 12309 GGAACCCCATCCAGATTAGCCCTGGAGACCTTTTCTGACTATCAAGTTTACAGAG 12368
 Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlnAlaPheSerGlnLeuSerSerLeuGlnLys 90
 QY 12369 CTGGTGGCTGTGAGAGCAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAA 12428
 Db 91 LeuValAlaValaGlnThrAsnLeuAlaSerLeuGlnuAsnPheProIleGlnHisLeuLys 110
 QY 12429 ACTTGAAGAAGCTTAATGTGGCTCAACATCTTATCCAAATTAATTAATTAATTAAT 12488

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Db 111 ThrLeuysglLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluLys 130
QY 12489 TTTTCTAATCGACCAATCTAGACACTTGGACCTTCCAGCAACAAGATTCAAAAGATT 12548
Db 131 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 150
QY 12549 TATGCAAGACTTGGGGTCTACATCAAAATGCCCTACTCAATCTCTTTAGACTG 12608
Db 151 TyrCysThrAspLeuAlaGluValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
QY 12609 TCCCTGAACCTTATGAACCTTATTCACACAGCTGCATTTAAAGAAATTTAGGCTTCATAG 12668
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QY 12669 CTGACTTTAAGAAATATTTTGTATGATTTAAATGTAATAAATTTGATTTCAAGCTG 12728
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QY 12729 GCTGGTTTAGAAGTCCATCGTTTGTTCTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
Db 211 AlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGlu 230
QY 12789 AAGTTTACAAGATGTGCTCTAGAGGGCTGTGCATTTGACCATTTGAAGAAATTCGAGTTA 12848
Db 231 LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGlnGluPheArgLeu 250
QY 12849 GCATCTTAGACTCTACCTCCGATGATATTATGACTTATTTATTTGAGCAAAATGTT 12908
Db 251 AlaTyrLeuAspLysTyrTyrLeuAspAspLysIleAspLeuPheAsnCysLeuThrAsnVal 270
QY 12909 TCTTCATTTCCCTGCTGAGTGTGACTATTGAAGGGTAAAGACTTTCTTATATATTC 12968
Db 271 SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 290
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QY 13029 AAATCTCTCAAAAGGCTTACTTCACTTCCACAAAGGTGGAGATGCTTTTTCAGAGTT 13088
Db 311 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyLysAlaAlaPheSerGluVal 330
QY 13089 GATCTACCAAGCTTGAAGTTCTAGATCTAGATGAAGAAATGCTTGAAGTTCAAGTTGC 13148
Db 331 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 350
QY 13149 TGTCTCAAGATGATTTTGGACAACAGCCTAAAGATTTTGAATCTGAGCTTCAATGCT 13208
Db 351 CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 370
QY 13209 GTTATTACAGAGATTCAACTTCTGGCTTGAACAACATGAACATTCGATTTCCAG 13268
Db 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHisLeuAspPheGln 390
QY 13269 CATTCATTTGAACAAATAGAGTGTTCAGATTCCTATGACTCAGAAACCTCAT 13328
Db 391 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAlaGlnLeuIle 410
QY 13329 TACCTTGACATTTCTCATCTCACAACAGAGTTGCTTCAATGGCATTTCAATGGCTTG 13388
Db 411 TyrLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
QY 13389 TCCAGTCTCGAAGCTTGAAGAAATGCTGGCAATTTCTCCAGAAATTTCTCCAGAT 13448
Db 431 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 450
QY 13449 ATCTTCAAGAGCTGAGAAATTTGACTTCTTGACCTCTCAGTGTCAACTGGAAGAG 13508
Db 451 IlePheThrGluLeuAlaGlnAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
QY 13509 TTGTTCTCAAGCAATTTAACTCACTCCAGTCTTCAGGTACTAAATATAGCCACAAC 13568
|||||

Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTTCATTTGATAGCTTTCTTAAATGTCTGAACCTCCAGAGTTCTTGAT 13628
Db 491 AsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCAATCACAATTAATGACTTCCAAAACAGAACTACAGCATTTTCCAGTAGT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerLysLysGlnGluLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTCTCAGATGACTTTTGCTGTGATCTTGTAACACAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGluHisGlnSerPhe 550
QY 13749 CTGCAATGATCAAGAGCAGAGAGCAGCTCTTGTTGGAAGTTGAAGAAATGATGCA 13808
Db 551 LeuGlnThrLysAspArgIleArgIleLeuLeuValGluValGluArgMetGluCysAla 570
QY 13809 ACACTTTCAGATTAAGAGGAGATGCTGTGCTGAGTTTGAATATCACTGTCAAGATGAT 13868
Db 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
QY 13869 AAGACCATCATTTGGTGTGTCGCTCAGAGTGTGATGATCTGTGATGAGAGTTTC 13928
Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaAlaValLeu 610
QY 13929 GTCTATAGTTCTAATTTTCACTGATGCTTCTTGCTGCTGATGAAGTATGATGATGAT 13988
Db 611 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
QY 13989 GAAAACATCTAGATGCTTTGTTATCTACTCAAGCCAGATGAGACATGGGTAAAGAT 14048
Db 631 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAsn 650
QY 14049 GACCTAGTAAAGAAATTTAGAAAGAGGGGCTCCATTTCACTGCTCCACTCAGAC 14108
Db 651 GluLeuValLysAsnLeuGluGluGlyValProPheGlnLeuCysLeuHisTyrArg 670
QY 14109 GACTTATTTCCGGTGTGGCCATTTGCTGCCACATCATCATGAAGTTTCCATAAAGC 14168
Db 671 AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGluGlyPheHisLysSer 690
QY 14169 CGAAGGTGATTTGTGTGTGCTCCAGACCTTCAATCCAGACCGCTGTGTATCTTGA 14228
Db 691 ArgLysValAlleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlu 710
QY 14229 TATGAGATTTCTCAGACCTGGCAGTTTCTGACGACGCTGCTGATCATCTTCAATGTC 14288
Db 711 TyrGluIleAlaGlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
QY 14289 CTGCAAGAGGTGGAAGAACCTGTGCTCAGGACAGCAGGTGAGCTGTACCGCTTCTCAGC 14348
Db 731 LeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 750
QY 14349 AGGAACACTTACCTGAGTGGAGAGACAGTGTCTGGGGCGGCAATTTTGGAGACGA 14408
Db 751 ArgAsnThrTyrLeuGluTyrGluAspSerValLeuGlyArgHisIlePheTyrArgArg 770
QY 14409 CTCAGAAAACCTGTCTGATGTGTAAATCATGTGAATCCAAAGAACAGTGGGTACAGCA 14468
Db 771 LeuAlaGlyAlaLeuLeuAspGlyLysSerTyrAsnProGluGluThrValGlyThrGly 790
QY 14469 TGCATATGCGAGGAGCAACATCTATC 14495
Db 791 CysAsnTyrPheGlnAlaThrSerIle 799

RESULT 12
ADP48597
ID ADP48597 standard; protein; 799 AA.
XX AC ADP48597;
XX DT 09-SBP-2004 (first entry)

Db 451 IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlu 470
QY 13509 TTGCTCCAAAGAGATTAACTGACTCCAGTCTTGAGGACTTAATATGAGCACAAC 13568
Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTCATTGATAGAGTTCCTTATTAAGTGTGAACTCCCTCAGAGTTCCTGAT 13628
Db 491 AsnPheSerSerLeuAspThrPheProTyrIleCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCAATCACAATAGACTTCCAAAAAGAGAACTACAGCACTTTTCCAGTATG 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerIleGlnGlnLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAATCTTACAGAAATGACTTCTGTGCTGTGTAACCCAGAGTTCC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
QY 13749 CTGCATATGATCAAGACACAGAGCAGCTCTTGAGTGAAGTTGAACGAATGAAATGTGA 13808
Db 551 LeuGlnTrpIleIleuAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 570
QY 13809 ACACCTTCAGATAAGCAGGGGACCTCTGTGCTGAGTTGAATATCAGCTTCAGATGAAT 13868
Db 571 ThrProSerAspIleGlnGlnIleMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
QY 13869 AAGACCATCATGTTGGTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13928
Db 591 LysThrIleIleGlnValSerValLeuSerValLeuValSerValAlaValAlaValLeu 610
QY 13929 GTCTATAAGTTCCTATTTTCACTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13988
Db 611 ValIleTyrIlePheIleTyrPheHisIleMetLeuLeuAlaGlyCysIleIleTyrGlnArgGly 630
QY 13989 GAAAAACATCTATGATGCTTGTATCTACTCAAGCCAGAGTGAAGACTGGGTGAAGAAAT 14048
Db 631 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspIleTyrValArgAsn 650
QY 14049 GAGCTAGTAAGATTTTAAAGAAAGGGGCTCCATTCAGCTGCTGCTGCTGCTGCTGCTGCTG 14108
Db 651 GluLeuValIleAsnLeuGlnGlnGlnIleValProProPheGlnLeuCysValHisIleTyrArg 670
QY 14109 GACTTTATTCCTGGGCTGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14168
Db 671 AspPheIleProGlnValAlaIleAlaHisAsnIleIleHisGlnGlnIlePheHisIleSer 690
QY 14169 CGAAAGGTGATGTTG 14228
Db 691 ArgIleValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 710
QY 14229 TATGAGATGCTGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14288
Db 711 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
QY 14289 CTGCAGAAAGGTGAGAGAACCTGCTCAGCAGCAGCTGAGCTGATCCGCTTCTCAGC 14348
Db 731 LeuGlnIleValIleGlnIleValIleValIleValIleValIleValIleValIleValIleVal 750
QY 14349 AGGAACACTTACCTGAGCTGAGAGAGCAGTGTCTGTGGGCGGCAATCTTGTGAGAGCA 14408
Db 751 ArgAsnThrTyrLeuGlnIleTrpGlnAspSerValLeuGlnArgHisIlePheThrArgArg 770
QY 14409 CTCGAAAAAGCCCTGCTGAGTGTATCATGGAATCCAGAAAGAAACAGTGGGTATCAGCA 14468
Db 771 LeuArgIleValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 790
QY 14469 TGCATTGGCAGAGAAACATCTATC 14495
Db 791 CysAsnTrpGlnGlnAlaThrSerIle 799

RESULT 13
AAW86361
ID AAW86361 standard; protein; 837 AA.

XX AC AAW86361;
XX 15-MAR-1999 (first entry)
DT 15-MAR-1999 (first entry)
XX DE Human DNAX toll-like receptor DTLR4.
XX DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
XX interleukin 1 receptor; phosphate metabolism; innate immunity response;
XX modulate inflammatory function; morphological effect;
XX immunological disorder.
XX OS Homo sapiens.
XX PN WO9850547-A2.
XX PD 12-NOV-1998.
XX PF 07-MAY-1998; 98WO-US008979.
XX PR 07-MAY-1997; 97US-0044293P.
XX PR 22-JAN-1998; 98US-0072212P.
XX PR 05-MAR-1998; 98US-0076947P.
XX PA (SCHE) SCHERING CORP.
XX PI Hardiman GT, Rock FL, Bazan JF, Kaetzelin RA;
XX WPI; 1999-059670/05.
XX DR N-PSDB; AAW8675.
XX XX
XX PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
XX metabolism, modulate inflammatory function or innate immunity responses.
XX PS Claim 3; Page 147-149; 171pp; English.
XX CC The present invention specifically describes human DNAX toll-like
XX receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
XX in the present invention. Also described are: (1) a fusion protein
XX comprising a DTLR protein or peptide; (2) a binding compound, preferably
XX an antibody or antibody fragment which specifically binds to a DTLR
XX protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
XX; (4) an expression vector comprising the nucleic acid of (3); and (5) a
XX host cell comprising the vector of (4). The host cell of (5) can be used
XX to produce the DTLR proteins. The DTLR proteins can be used to alter
XX phosphate metabolism, to modulate inflammatory function, innate immunity
XX responses or morphological effects. The DTLR proteins can be used in the
XX treatment of conditions exhibiting abnormal expression of the receptors
XX of their ligands. These abnormalities are typically manifested by
XX immunological disorders
XX CC
XX SQ Sequence 837 AA;
XX SO
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 837
XX Score: 3903.50 Matches: 757
XX Percent Similarity: 98.57% Conservative: 1
XX Best Local Similarity: 98.44% Mismatches: 2
XX Query Match: 11.81% Indels: 9
XX DB: 2 Gaps: 1
XX
XX US-09-396-985b-47 (1-18989) x AAW86361 (1-837)
XX
XX QY 12216 TCAATGCTTTTATTC-----TGTAGTGTGAATC 12248
XX Db 69 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 88
XX QY 12249 CAGCAATTAAGATGGGATATCAGAGCTTACCTTAAATATTGACA 12308
XX Db 89 GlnThrIleGlnAspGlnAlaTyrGlnSerSerHisLeuSerThrLeuIleLeuThr 108
XX QY 12309 GAAACCCCATCAGAGATTAGCCCTGGAGACCTTTTCTGAGCTATCAGATTACAGAG 12368

Db 109 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuLys 128
 QY 12369 CTGGTGGCTGTGGAGACAATCTAGCATCTAGAGAACTTCCCATGGACATCTCAAA 12428
 Db 129 LeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuLys 148
 QY 12429 ACTTGAAGAAGAACTTAATGTGGCTCACAACTTATCCAACTTTGCAATTAACCTGATAT 12488
 Db 149 ThrLeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheGlyLeuProGluTyr 168
 QY 12489 TTTTCTAATCTGACCAATCTGAGAGACCTTGGACCTTCCAGACAACAATTCAGATAT 12548
 Db 169 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 188
 QY 12549 TATTGACAGACTTGGGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
 Db 189 TyrCysThrAspLeuAspValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
 QY 12609 TCCCTGAACCCCTAGAACCTTTATCCAACCAAGGCTGATTTAAAGAAATTAAGGCTTCATAG 12668
 Db 209 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
 QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAATGTAAATGAAATCTGTATTCAGGCTGTG 12728
 Db 229 LeuThrLeuAspLeuAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
 QY 12729 GCTGGTTTGAAGTCCATCGTTGGTCTGGGAGAAATTTAGAAATGAAGAACTTGAA 12788
 Db 249 AlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGlu 268
 QY 12789 AAGTTTGAACAATCTGCTCTAGAGAGGCTGTGCAATTTGACATTGAAGAATTCGATTA 12848
 Db 269 LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 288
 QY 12849 GCATCACTTAGACTCTACTGATGATGATATTTGACTTATTTAATGTTTGAACAATGTT 12908
 Db 289 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 308
 QY 12909 TCTTCATTTTCCCTGGTGAAGTGTGACTTATGAAGGGTAAAGACTTTCTTATTAATTC 12968
 Db 309 SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 328
 QY 12969 GGATGGCAACATTAGAAATTAGTTAACTGTAAATTTGGACAGTTTCCCAATTGAAATC 13028
 Db 329 GlyTyrGlnHisLeuGluLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 348
 QY 13029 AAATCTCCAAAAGGCTTACTTCACTTCCACAAGAGTGGAAATGCTTTTTCGAAGTT 13088
 Db 349 LysSerLeuLysAspLeuThrPheThrSerAsnLysGlyAlaAsnAlaPheSerGluVal 368
 QY 13089 GATCTACCAAGCTTGAAGTTCTAGATCTAGTGAAGATGGCTGAGTTCAAAAGTTGC 13148
 Db 369 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 388
 QY 13149 TGTTCCTCAAGATTTTGGAGACAACAGCTTAAGATTTAGATCTGAGCTTCATATGT 13208
 Db 389 CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 408
 QY 13209 GTTATTTACATGATTTCAAACTTTGGGGCTTAACAACAATGAAATCTGAGATTTCCAG 13268
 Db 409 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGlnHisLeuAspPheGln 428
 QY 13269 CATTCCAATTTGAACAATAAGTAGAGTTTCAATATTCATCACTCAGAACTCATAT 13328
 Db 429 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAspLeuIle 448
 QY 13329 TACCTGACATTTCTCACTACTCACACAGAGTTCTTTCAATGACATCTTCAATGCTGTG 13388
 Db 449 TyrLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
 QY 13389 TCCAGTCTCAAGCTTGAAGAAATGGCTGGCAATCTTTCCAGGAAATCTCTCCAGAT 13448
 Db 469 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 488
 QY 13449 ATCTTCACAGAGCTGAGAAATTTGACCTTCCGTGACCTTCTCAGTGTCAACTGAGACAG 13508
 Db 489 IlePheThrGluLeuAspLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 508
 QY 13509 TTGTCTCCAAACAGCATTTAACTCACTCTCCAGTCTTCAGGATCTAAATATGAGCCACAAC 13568
 Db 509 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
 QY 13569 AACTCTTTTCACTTGAATAGGTTTCTTATTAAGTGTCTGAATCTCCCTCAGGTTCTTGAT 13628
 Db 529 AsnPheSerSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 548
 QY 13629 TACAGTCCATATCAATTAAGACTTCCAAAAACAGAACTACAGCAATTTCCAAATGT 13688
 Db 549 TyrSerLeuAsnHisIleMetThrSerLysGlnGluLeuGlnHisPheProSerSer 568
 QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTCTGTACTGTGTGAACACAGAGTTTC 13748
 Db 569 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGluHisGlnSerPhe 588
 QY 13749 CTGCAATGATCAAGAACCCAGAGGACCTTTGGTGAAGTTGAACGAATGGAAATGGCA 13808
 Db 589 LeuGlnThrPheLysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 608
 QY 13809 ACACTTCAGATTAAGCAGGAGGATGCTGTGCTGAGTTGTAATATCACCTGTCAAGTGAAT 13868
 Db 609 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
 QY 13869 AAGACATCATGATGGTGTGTGCTCTCAGTGTCTGTAGTATCTGTTTGAAGAGTTCTG 13928
 Db 629 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 648
 QY 13929 GTCTATTAAGTTCTATTTTCACTGATGCTTTCTGCTGCAATTAAGTATGCTGAGGT 13988
 Db 649 ValTyrLysPheTyrPheHisLeuMetLeuAlaGlyCysIleLysTyrGlyArgGly 668
 QY 13989 GAAAAACATCATGATGCTTGTATATCTATCAAGCAGAGATGAGGCTGGTAAAGGAAT 14048
 Db 669 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspLysProValAlaArgAsn 688
 QY 14049 GAGCTAGTAAAGATTTAGAAAGAGGGTCCCTCCATTTCCAGTCTGCTTCACTACAGA 14108
 Db 689 GluLeuValLysAsnLeuGlnGluGlyValProProPheGlnLeuCysLeuHisTyrArg 708
 QY 14109 GACTTATTTCCCGGTGGTGGCAATGCTGCCAATCATCATGAAGTTTCCATTAAGC 14168
 Db 709 AspPheIleProGlyAlaAlaIleAlaAsnIleIleHisGluGlyPheHisLysSer 728
 QY 14169 CGAAGGTGATTTGTGGGTGCCAGCACTTCAATCAGAGCGGCTGTATCTTTGAA 14228
 Db 729 ArgLysValIleValAlaValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlu 748
 QY 14229 TATGAGATGCTCAGACTGGCAGTTTCTGAGCAGTGTGCTGTATCATCTTCAATGTC 14288
 Db 749 TyrGluIleIleGlnThrProGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
 QY 14289 CTGCAAGAGGTGAGAAAGACCTGCTCAGGACAGAGGTGAGCTGTACCGCTTTCAGC 14348
 Db 769 LeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 788
 QY 14349 AGGAACACTTACTCTGAGTGGAGGAGCAGGTGCTGGGGGGGAGCAATCTTGGAGAACGA 14408
 Db 789 ArgAsnThrTyrLeuGlnLysProGluAspSerValLeuGlyArgHisIlePheTyrArgAsn 808
 QY 14409 CTCAGAAAAGCCCTGTGATGAGTAAATCATGGAATCCAGAAAGAAACAGTGGGTACAGGA 14468
 Db 809 LeuArgLysAlaLeuLeuAspGlyLysSerTyrAsnProGlnGlyThrValGlyThrGly 828
 QY 14469 TCGAATTTGGCAGAGAACCAATCTATC 14495
 Db 829 CysAsnTrpGlnGluAlaThrSerIle 837

RESULT 14
AAE16102
ID AAE16102 standard; protein; 837 AA.
XX
AC AAE16102;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #2.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN M0200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
XX
DR N-PSDB; AAD26292.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 3; Page 41; 297p; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other Interleukin (IL)-1
CC receptor members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC sequence shown in page 240-243 (AAE16116). However these sequences differ
CC at several locations
XX
SQ Sequence 837 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
Gaps: 1
US-09-396-985B-47 (1-18989) x AAE16102 (1-837)
QY 12216 TCAATGCTTTTATTC-----TGAGGTGCAATTC 12248
DB 69 SerTySerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGlnIle 88

QY 12249 CAGACAATTGAGATGGGCGATATCAGAGCCTAAGCCATCTCTAATTAATTGACA 12308
DB 89 GlnThrIleGlnuSpGlyAlaTyrlnSerLeuSerHisLeuSerThrIleuThr 108
QY 12309 GGAAGCCCATCCAGAGTTTAGCCCTGGAGCCTTTCTGGATATTCAGAGAG 12368
DB 109 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
QY 12369 CTGGGCTGGTGGAGCAAAATCTAGCATCTCTAGAGAACTCCCATTTGACATCTCAAA 12428
DB 129 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnuSpPheProIleGlyHisLeuLys 148
QY 12429 ACTTGAAAGACTTAATGAGCTCACAATCTTAATCAATCTTCAATTAATCTAGATAT 12488
DB 149 ThrLeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyx 168
QY 12489 TTTTCTAATCTGACCAATCTAGAGCACTTGAGACCTTTCCAGCAACAAGATTCAAGATAT 12548
DB 169 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 188
QY 12549 TATTGACAGACTTGGGGGTTCTTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
DB 189 TyCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
QY 12609 TCCCTGAACCCCTATGAACTTATCCAAACGAGTGCAATTTAAGAAATTAGGCTTCATAG 12668
DB 209 SerLeuAsnProMetLeuAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAATGTAATGAAGAACTGTATTCAGAGCTCTG 12728
DB 229 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
QY 12729 GCTGGTTTAAAGTCATCGTTGGTCTGAGGAATTTGAATGAAGAACTTGAA 12788
DB 249 AlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluLysAsnLeuGlu 268
QY 12789 AAGTTGACAAATCTGCTCTAGAGGGCTGTGCAATTTGACATTTGAAGAAATTCAGATTA 12848
DB 269 LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 288
QY 12849 GCATACTTAAAGTACTACCTCGATGATATTATTGACTTAATTATTGTTGACAAATGTT 12908
DB 289 AlaTyLeuAspTyTyTyTyLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 308
QY 12909 TCTTCATTTTCCCTGGAGTGTGAGTGAATTAAGAAAGCTTAAGCTTTCTTAATATTC 12968
DB 309 SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyAsnPhe 328
QY 12969 GGAATGCAAACTTGAATTAAGTAACTGTAAATTTGACAGTTTCCCATTTGAAATCTC 13028
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QY 13029 AAATCTCTGAAAGGCTTACTTTTCACTTCCAAACAAGGTGGGAATGCTTTTTCGAAAGTT 13088
DB 349 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluVal 368
QY 13089 GATCTACCAAGCCTTGAGTTTCTAGATCTAGTGAAGAAAGCTTGAGTTTCAAGAGTTGC 13148
DB 369 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnLysLeuSerPheLysGlyCys 388
QY 13149 TGTTCCTGAAGTATTTGGGACAAACGAGCTAAAGTATTAGTCTGAGCTTCAATGCT 13208
DB 389 CysSerIleAsnArgPheGlyThrThrSerLeuLysTyTyLeuAspLeuSerPheAsnGly 408
QY 13209 GTTATTACATGAGTTCAAACTTCTGGGCTTTAGAACATCTAGAACATCTGGATTTCCAG 13268
DB 409 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGlnHisLeuAspPheGln 428
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Qy      13449 ATCTTCAGAGCTGAGAACTTGACCTTCCGACCTCTGACCTCTGACCTGTCACATGAGCAG 13508
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Qy      14049 GAGCTAGTAAGAAATTTAGAAAGGAGGCTGCTCCATTTCACTCTGCTGCTTCACTACAGA 14108
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Qy      14109 GACTTTATCCCGGTGGCCATGCTGCTGCCAATCATCATGAAAGTTTCCATAAAGC 14168
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Qy      14289 CTGAGAAAGGTGAGAAAGACCTCTGCTCAGGAGCAGAGTGGAGCTGACCGCTTCTCAGC 14348
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XX
DE  29-JAN-2003 (first entry)
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DE  Human expressed protein tag (EPT) #1442.
XX
KW  Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW  protease; protease inhibitor; transporter; cytoskeletal protein;
KW  receptor; transcription factor; cancer; MHC;
KW  major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW  adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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OS  Homo sapiens.
XX
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XX
PD  10-OCT-2002.
XX
PE  28-MAR-2002; 2002W0-US009671.
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PR  04-DEC-2001; 2001US-0336780P.
PR  20-FEB-2002; 2002US-0358985P.
XX
PA  (ZYCO-) ZYCOS INC.
XX
PI  Chicz RM, Tomlinson AJ, Urban RG;
XX
DR  WPI; 2003-040607/03.
XX
PT  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT  cytoskeletal proteins, receptors or transcription factors), useful for
PT  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT  leukemia.
XX
PS  Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC  The invention describes a purified polypeptide, which comprises a
CC  fragment of a kinase, phosphatase, protease, protease inhibitor,
CC  transporter, cytoskeletal protein, receptor or transcription factor. The
CC  polypeptide is useful as an immunogenic composition for eliciting in a
CC  mammal an immunogenic response directed against any of the purified
CC  polypeptide. The purified polypeptide, or the antibody that binds to this
CC  polypeptide, is useful for treating cancer. The polypeptide is also
CC  useful for identifying compounds that binds to a naturally processed
CC  class I or class II MHC-binding polypeptide. The polypeptides and
CC  polynucleotides are particularly useful for treating or preventing
CC  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC  lymphoma or leukaemia. These are also useful for screening agents for
CC  treating the above mentioned diseases. This sequence represents an
CC  expressed protein tag (EPT) isolated from human tissue for translational
CC  profiling. Note: This sequence does not appear in the printed
CC  specification but was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SO  Sequence 837 AA.

Alignment Scores:
Pred. No.: 0 Length: 837
Score: 3903.50 Matches: 757

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Best Local Similarity: 98.44% Mismatches: 2
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QY 12309 GGAAGCCCATCCAGATTTAGCCCTGGAGCCCTTTCTGACATCAAGTTTACAGAG 12368
DB 109 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
QY 12369 CTGGTGGCTGGAGCAATCTGACATCTTGAAGAACTTCCCATTTGACATCTGAAA 12428
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DB 149 ThrIleuysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyr 168
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 153 Seconds
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SUMMARIES

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3	529	1.6	661	1	US-08-514-014-4
4	529	1.6	661	1	US-08-833-823-4
5	497	1.5	775	4	US-09-949-016-8799
6	287.5	0.9	1112	3	US-09-353-585-3
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8	267.5	0.8	863	2	US-08-666-271-2
9	267	0.8	605	3	US-09-063-950-5
10	267	0.8	1874	4	US-09-331-403-2
11	263.5	0.8	1166	4	US-10-101-464A-900
12	262.5	0.8	907	4	US-09-170-496D-264

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14	258	0.8	605	1	US-08-190-802A-49	Sequence 49, Appl
15	258	0.8	605	3	US-08-477-346-49	Sequence 49, Appl
16	258	0.8	605	3	US-08-473-089-49	Sequence 49, Appl
17	258	0.8	605	4	US-08-467-072A-49	Sequence 49, Appl
18	258	0.8	605	4	US-09-538-092-1087	Sequence 1087, App
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27	246	0.7	391	4	US-09-270-767-43901	Sequence 43901, A
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ALIGNMENTS

RESULT 1
US-09-949-016-9438
Sequence 9438, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9438
LENGTH: 844
TYPE: PRT
ORGANISM: Human
US-09-949-016-9438
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Score: 3903.50
Percent Similarity: 98.57%
Best Local Similarity: 98.44%
Query Match: 11.81%
DB: 4
Gaps: 1
US-09-396-985B-47 (1-18989) x US-09-949-016-9438 (1-844)
12216 TCAATGCTTTTATTC-----TGTAAGTGAATC 12248

|||||
Db SerIysSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 95
12249 CAGCAATTTGAAGTGGGGCATATCAGAGCTTAAGCCACTCTTACTTAAATTGACA 12308
Db GlnThrIleGluAapGlyAlaTyrgInSerLeuSerHisLeuSerThrIleLeuThr 115
12309 GGAAGCCCAATCCAGAGTTTACCCCTGGAGCCTTTTCTGGACATATGAAGTTTACAGAG 12368
Db GlnAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIys 135
12369 CTGGTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAA 12428
Db LeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuIys 155
12429 ACTTTGAAGAATTTAATGTGGCTCAATCTTATCCAACTTTTCAAAATTACCTGATAT 12488
Db ThrLeuIysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIysLeuProGluTyx 175
12489 TTTTCTAATCTGACCAATCTAGACACTTGGACCTTTCACAGCAAGATTCAAGTAT 12548
Db PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnIysIleGlnSerIle 195
12549 TATTGACAGACTTGGGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
Db TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 215
12609 TCCCTGAACCTTAGAACTTTATTCACACAGAGTGCATTTAAAGAAATTAGCTTCATAG 12668
Db SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuHisIlys 235
12669 CTGACTTAAAGAAATTAATTTGATAGTTAATGAATGAAGAACTTGATTCAGAGTCTG 12728
Db LeuThrLeuAspGlnAsnPheAspSerLeuAsnValMetCysThrCysIleGlnGlyLeu 255
12729 GCTGATTTGAAGTCCATCGTTGGTTCTGGAGAAATTTAGAAAAGAACTTGGAA 12788
Db AlaGlyLeuGlnValHisArgLeuValLeuGlyGluPheArgAsnGlnGlyAsnLeuGln 275
12789 AAGTTTGACAATTCGCTCTAGAGGGCTTGACAAATTTGACATTTGAAGAATTCGATTA 12848
Db LysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeu 295
12849 GCATACTAGACTACTACTGAGATGATTTATGACTTATTAATTTGTTGACAAATGTT 12908
Db AlaTyrlsLeuAspTyrlTyrlsLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 315
12909 TCTTCATTTCCCTGGTGGTGGTGTGACTATTTGAAAAGGTTAAAGACTTTTCTTAATATTC 12968
Db SerSerPheSerLeuValSerValThrIleGluArgValIysAspPheSerTyrlAsnPhe 335
12969 GGATGGCAACATTTAGAAATTAATTAATTTGACAGAGTTTCCCAATGAAACTC 13028
Db GlnTyrlPrgGlnHisLeuGlnLeuValAsnCysLysPheGlnPrgInProThrLeuIysLeu 355
13029 AAATTCCTCAAAAGCTTACTTTCCTCCAAAGAGGTGGAAATGCTTTTTCAGAGTT 13088
Db LysSerLeuLysAspGluThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluVal 375
13089 GATCTACCAAGCTTGAAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAGGTTGC 13148
Db AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheIysGlyCys 395
13149 TGTTCGAAAGTATTTGGGCAACACAGCTTAAGATTTTGAATCTGAGCTTCATGCT 13208
Db CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrlsLeuAspLeuSerPheAsnIly 415
13209 GTTATTACAGAGTTTCAAACTTCTGGGCTTGAACAACATAAGCATCTGGATTTCCAG 13268
Db ValIleThrMetSerSerAsnPheLeuGlnLeuGlnGlnLeuGlnHisLeuAspPheGln 435
13269 CATTCCAATTTGAACAATGAGTGAAGTTTTCAGATTCCTATCACTAGAAACCTCAAT 13328

Db HisSerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIle 455
13329 TACCTTGACATTTCTGATATCTCACACAGAGTTGCTTTCAATGCAATGCAATGCGCTTG 13388
Db TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 475
13389 TCCAGTCTCGAAGCTTGAAGAAATGGCTGGCAATCTTCTTCAGAGAAACTTCTTCAGAT 13448
Db SerSerLeuGlnValLeuIysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 495
13449 ATTTTGACAGAGCTTGAGAACTTGAACCTTCTGGAGCTCTCTCAAGTGTCAATGGAGCG 13508
Db IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln 515
13509 TTGCTCCCAACAGACTTTAATCTCACTCCAGCTTCAGGCTTCAAGTAAATATGAGCCAAAC 13568
Db LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 535
13569 AACTCTTTTCATTTGATACGTTTCTTATTAAGTGTCTGAATCCCTCCAGGTTCTTGAT 13628
Db AsnPheSerLeuAsnThrPheProTyrlsCysLeuAsnSerLeuGlnValLeuAsp 555
13629 TACAGTCTCAATACATPATGACTTCCAAAAACAGAACTTACAGCAATTTCCAGTACT 13688
Db TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 575
13689 CTAGCTTTCTTAATCTTACTCAAGATGACTTTGCTTGTACTTGTGTAACACAGAGTTTC 13748
Db LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 595
13749 CTGCATGATCAAGACACAGAGGACGCTTGTGGAGATTTGAACGAATGAATGTGCA 13808
Db LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 615
13809 ACACCTTCAGATTAACAGAGGCAATGCTGTGCTGAGATTGAATATCACCTTCAGATGAAT 13868
Db ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 635
13869 AAGACCATCATGTGTGTGTGCGCTCCAGTGTGCTGTAGTATCTGTGTGAGAGGTTCTG 13928
Db LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaAlaValLeu 655
13929 GTCTATAGTTCTAATTTTCACTGATGCTTCTTGTGGCTGCAATAAGTATGGTAGAGT 13988
Db ValTyrlsPheTyrlPheHisIleMetLeuLeuAlaGlyCysIleLysTyrgIysGly 675
13989 GAAAACATCTATGATGCTTGTATATCTACTCAAGCCAGATGAGATCGGATGAAGAT 14048
Db GluAsnIleTyrlAspAlaPheValIleTyrlSerSerGlnAspGluAspTyrlValArgAsn 695
14049 GAGCTACTAAGAAATTTAGAAAGAGGAGTGCCTCCATTTGAGCTTGCCTTCACTACAGA 14108
Db GlnLeuValIysAsnLeuGlnGlnGlyValaProProPheGlnLeuCysLeuHisTyrlArg 715
14109 GACTTATTCCTCGGTGGCCATTTGCTGCCAATCATTCATGAAGGTTTCCATAAAGC 14168
Db AspPheIleProGlyValAlaIleAlaHisAsnIleHisGlnGluPheHisIysSer 735
14169 GAAAAGTGAATGTTGTGTGTGTCCAGCACTTCAACAGCCGCTGTGTATCTTTGAA 14228
Db ArgIysValIleValAlaValaIserGlnHisPheIleGlnSerArgTyrlCysIlePheGln 755
14229 TATGAGATTCCTGACACTGGCACTTCTGAGCAGTGTGCTGGTATCATCTTCATGTC 14288
Db TyrlGlnIleAlaGlnThrTyrlPrgGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 775
14289 CTGCAGAGGTGAGAGAACCTTGTCAAGCAGAGGCTGAGCTGTATCCGCTTTCAGC 14348
Db LeuGlnIysValaGluTyrlThrLeuLeuArgGlnGlnAlaGluLeuTyrlArgLeuLeuSer 795
14349 AGAACAATTAACCTGAGAGTGGAGAGACAGTGTCTGGGGGCGGCAATCTTTCGAGACGA 14408
Db ArgAsnThrTyrlsLeuGlnIuTyrlPrgIuAspSerValLeuGlyArgHisIlePheTyrlArg 815

QY	14409	CTCGAAAAAGCCCTGCGTAGATGTAATTCATGGATATCAGAACAGGAGGCTAACAGG	14466
Db	816	LeuargylsalaleuLeuLeuApeGlyLysSerTrpAsnProGluGlyThrValGlymrgly	835
QY	14469	TGCAATTGCGAGAGCAACATCTATC	14495
Db	836	CysantrpGinginiuaIatThrSerIle	844
RESULT 2			
US-09-982-308B-23			
/ Sequence 23, Application US/09982308B			
/ Patent No. 6531290			
/ GENERAL INFORMATION:			
APPLICANT: Dalié, Barbara			
APPLICANT: Fan, Xuedong			
APPLICANT: Lundell, Daniel			
APPLICANT: Lunn, Charles A.			
APPLICANT: Tan, Jimmy C.			
APPLICANT: Zavadny, Paul J.			
TITLE OF INVENTION: Mammalian TNF-alpha Convertases			
FILE REFERENCE: JB0601QC			
CURRENT APPLICATION NUMBER: US/09/982,308B			
CURRENT FILING DATE: 2001-10-17			
PRIOR APPLICATION NUMBER: 09/156,163			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 08/889,909			
PRIOR FILING DATE: 1997-07-10			
PRIOR APPLICATION NUMBER: 60/021,710			
PRIOR FILING DATE: 1996-07-12			
NUMBER OF SEQ ID NOS: 23			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 23			
LENGTH: 784			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-982-308B-23			
Alignment Scores:			
Pred. No.: 3,64e-52 Length: 784			
Score: 557.50 Matches: 220			
Percent Similarity: 41.59% Conservative: 121			
Best Local Similarity: 26.83% Mismatch: 260			
Query Match: 1.69% Indels: 219			
DB: 4 Gaps: 38			
US-09-396-985B-47 (1-18989) x US-09-982-308B-23 (1-784)			
QY	12246	ATCCAGACAATTTGAAGATGGGGCATATCAAGGCTTACGACCTCTCTAATTATATTTG	12305
Db	88	IlleanthrrillegingluuApsSerPheSerSerIleuGlyuhHsleuApleu	107
QY	12306	ACAGAAAACCCCATCCAGAGATTTAGCCCTGGAGACCTTTTCTGGACTATCAAGTTTACG	12365
Db	108	SerlyrAsnTryleuSerAsnleuSerSerSerTrpPheAsProleuSerSerIleuThr	127
QY	12366	AAGCTG-----GTGGGTGGAGACAAT	12389
Db	128	PheleuSenleuLeuGlyAsnProTrylrlyThrIleuGlyluThrSerleuPheSerHis	147
QY	12390	CTAGACATCTTAGAGAACTTCCCATTTGACATCTCAAACT-----	12431
Db	148	LeuThrlyrleuGlnIleleuArgValGlyAsnMetaphrThrPheThrlyrIleGlnArg	167
QY	12432	-----TTGAAAGAACTTATATGTGGCTACAACTTTATCCAA	12467
Db	168	LysAspPheAlaGlyLeuThrPheLeuGlnGluLeuGluIleAspAlaSerPheLeuGln	187
QY	12468	TCCTTCAAATTAATCCTGAGTATTTTCTAATCTGACCACTTAGAGCACTTGACCTTCC	12527
Db	188	SerlyrGlu---ProlyrSerleuLysSerIleGlnAsnValSerHisleuIleuHis	206
QY	12528	AGCAACAG-----ATCAAGATATTATTTGC	12554

Dd	207	MetIleuGlnIleLeuLeuLeuGluIlePheValAspValThrsSerSerValGluCys	226
Qy	12555	ACAGACTGGGGGTTCTACATCAAAATGCCCTACAAATCTCTTTAAGCACTGCCCTCG	12614
Dd	227	LeuGluLeuArg-----AspThrAspLeu	234
Qy	12615	AACCTTATGAACCTTT-----ATCCAAACGAGTGCAATTAAAGAAATTAGGCTTCATAG	12666
Dd	235	AspThrPheHisPheSerGluLeuSerThrGlnIleuThrAsnSerLeu---IleIleCys	253
Qy	12669	CTGACTTAAGAAAT-----AATTGTAACGTTT---AATTATATGAATAACTTGT	12716
Dd	254	PheThrPheArgAsnValIysIleThrAspGluSerLeuPheGlnValMetCysLeuLeu	273
Qy	12717	-----ATTCAAGGTCTGGCTGGTTTAGAAGTCATCGTTGGTTTG-----GGA	12765
Dd	274	AsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly	293
Qy	12762	GAATTTGAATGAAATGAGAAACTTGAAAGTTTGACAAATCTGCTCTAGAGGCTGTGC	12821
Dd	294	AsnPheArgIaSerAspAsnAspArgValIleAspProGlyLeuValGlu-----	310
Qy	12822	AATTGACCTATGAGAAATCCGATTAGCA-----TACTTACACTACTACCTCGATGAT	12875
Dd	311	ThrIleuThrIleArgArgLeuHisIleProArgPheCysLeuPheCys-----Asp	327
Qy	12876	ATTATGACTATTTATTTATTTGTTGACAAATGTTTCTTCATTTTCCCTGGAGAGTGACT	12935
Dd	328	LeuSerThrIleuArgSerLeuThrGluArgValLys-----ArgIleThr	342
Qy	12936	ATTGAAAGGGTAAAGAAGCTTTCTTTATTAATTTCGATGCGACATTAGAAATTAGTTAAC	12995
Dd	343	ValGluAsnSerIleValPhe-----LeuValPro	352
Qy	12996	TGTTAAATTGAGACAGTTTCCCAATGAAACTCAATCTCTCAAAAGGCTTACTTTCACT	13055
Dd	353	CysLeuLeuSerGln-----	357
Qy	13056	TCCAAACAAGGTGGGAATGCTTTTTCAGAAAGTGATCTACCAAGCTTAGAGTTTCTAGAT	13115
Dd	358	-----HisLeuLysSerLeuGluIleuAsp	366
Qy	13116	CTCAGTAGAAAT-----GGCTTGAGTTTCAAAAGTTCGTTCTCAAACT	13160
Dd	367	LeuSerGluAsnLeuMetValGluGluIleuArgAsnSerIaCys-----	382
Qy	13161	GATTTTGGGCAACCAAGCTTAAGTATTAGATCTGAGCTCAATGCTGTTATTACCAAG	13220
Dd	383	GluAspIaIleThrProSerLeuGlnThrIleIleLeuArgGluAsn-----	397
Qy	13221	AGTTCAAAATCTTTGGGCTTAGAACAACATGAAATCTGAGATTTTCAGACTTCAAAATTG	13280
Dd	398	-----HisLeu-----AlaSerLeu	402
Qy	13281	AAACAATGAGTAGATTTCAGATTCTTATCTATCTACAGAAACCTCAATTACCTTGACAT	13340
Dd	403	GluArgThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIleAspIle	420
Qy	13341	TCTCATACTCAACACCAAGAGTTGCTTCAATGCAATCTTCAATGGCTTGTCACAGTCCGA	13400
Dd	421	SerLys-----	422
Qy	13401	GTCCTGAAAATGGCTGGCAATCTTTCACAGAAAATCTCTCCAGATATCTTACACAGAG	13460
Dd	423	-----AsnSerPheHisSer-----MetProGluThrCysGlnThr	434
Qy	13461	CTGAGAAATGACCTTCTCTGACACTCTCTCAAGTTCACATGAGACAGTTGCT-----	13514
Dd	435	ProGluLysMetLysIleuLeuAsnLeuSerThrArgIleHisSerIaIleThrGlyCys	454
Qy	13515	---CCAACAGACTTTAACTACCTCTCAGCTTTCAGGTACTTAATATGAGCCCAAC---	13568

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Db      455  llepro-----LysThrLeuGluIleLeuAspValSerAsnAsn 468
QY      13569  ---AAGCTCTTTGATTTGAT-----
Db      469  LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrIleSerArgAsnLys 488
QY      13587  -----ACGTTTCTCT--TAAAGTGTCTGAACCTCCAGGAGTCTTGAATTACAGTCTC 13637
Db      489  LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValIleSerArg 508
QY      13638  AATCACAATAATGACTTCCAAAAACAGAACTACAGCAATTTCCAGTAGCTTTC 13697
Db      509  AsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe--HisThrLysThr 527
QY      13698  TTTAAATCTTACTGAGATGACTTGTGTTGACTTGTGAACCCAGAGTCTTCTGCATGG 13757
Db      528  LeuGlnIaIaGlyGlnAsnAsnPheIleCysSerCysGluPheLeuSerPheThrGln-- 546
QY      13758  ATCAGAGACGACGAGCCTCTGTGTGAAGTT-----GAACGAATGGAA 13802
Db      547  -----GluGlnGlnIaIaLeuAlaLysValIleuIleAspTrpProIaAsnTyrLeu 563
QY      13803  TGTGCAACACCTTGCAGATTAAGCAGGCAATGCTGTGCTGAGTTGAATATCAC-- 13856
Db      564  CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLysSerValSer 583
QY      13857  ---TGTCAGATGAATTAAGACATATGCTGTGTCGCTGCTCCTCAATGCTTGTAGTACT 13913
Db      584  GluCysHisArgIleAlaLeuValSerGlyMetCysCysAlaLeuPheLeuIleu 603
QY      13914  GTTGTAGCAGTTTGTGCTTAATGATTTCTAT-----TTTCCATGATGCTTCTGTGAGC 13967
Db      604  LeuThrGlyValIleCysHisArgPheHisGlyLeuTyrPheLysMetMetTrpAla 623
QY      13968  TGCATAAAGTATGTGTAGA-----GCTGAAAATCT--TATGATGCC 14006
Db      624  TrpLeuGlnIaLysArgLysProArgLysAlaProSerArgAsnIleCysTyrAspAla 643
QY      14007  TTTGTTATCTATCTCAAGCCAGATGAGACCTGGGTGAAGATGAGCTAGTAAATTTA 14066
Db      644  PheValSerLysArgLysArgAspAlaLysTrpValGlnAsnLeuMetValGlnGluLeu 663
QY      14067  GAAAGAGGGGTGCTCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14126
Db      664  GluAsnPheAsnProProPheLysLeuCysLeuHisLysArgAspPheIleProGlyLys 683
QY      14127  GCCATGTGTCGCAATCATCATCATGATGAAGGTTTCCATAAAGCCGAAAGGTGATTTGTG 14186
Db      684  TrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisLysThrValPheVal 702
QY      14187  GTGTCCAGCACTTCATCCAGACCGCTGTGTATCTTTGAATATGATGATTCCTCAGACC 14246
Db      703  LeuSerGluAsnPheValLysSerGluTyrCysLysTyrGlnLeuAspPheSerHisPhe 722
QY      14247  TGGAGATTCTGAGACGTCGTGTGTATCTTTCACTTTCTGCTGCAAGAGTGAAGAG 14306
Db      723  ArgLeuPheAspGlnAsnAsnAspAlaIaIleLeuIleLeuGlnProIleGlnLys 742
QY      14307  ACCCTGCTCAGCAGCAG--GTGAGCTGTACCGCTTTCACAGAGAACATTACTGTG 14363
Db      743  LysAlaIleProGlnArgPheCysIleLeuArgLysIleMetAsnThrLysThrTyrLeu 762
QY      14364  GAGTGGAGGAGACAGTCTCTGGGGGAGCAATCTTCTGAGACGACTCAGAAAAAGCTGTG 14423
Db      763  GluTrpProMetAspGlnAlaGlnArgGlnGlyPheTrpValAsnLeuArgAlaIaIle 782

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; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 488-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-514-014-4
;
Alignment Scores:
Pred. No.: 5e-49 Length: 661
Score: 529.00 Matches: 183
Percent Similarity: 44.83% Conservative: 103
Best Local Similarity: 28.68% Mismatches: 254
Query Match: 1.60% Indels: 98
Gaps: 26
US-09-396-985b-47 (1-18989) x US-08-514-014-4 (1-661)
QY      12171  TTAATATCTAATTTTGAAGTTCTTA-----TTGACGAGAAATATT 12209
Db      58  LeuGluPheSerPheAsnPheLeuProThrIleHisAsnArgThrPheSerArgLeuMet 77
QY      12210  AGATTAATCAATGCTTTTATTTC--TGAAGTGTGAATCCAGACAAATTGAAGATGG 12266
Db      78  -----AsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrpIleHisGluAsp 95
QY      12267  GCATATCAGAGCCTTAAGCCACTCTTACCTTAATATTGACAGAAACCCATCCAGAGT 12326
Db      96  ThrPheGlnSerHisHisGlnLeuSerThrLeuValLeuThrGlyAsnProLeuIlePhe 115
QY      12327  TTAGCCCTGGAGCCTTTTGTGACTATACAGATTACAGAACTGTGCTGTGAGACA 12386
Db      116  MetAlaGlnThrSerLeuAsnGlyProLysSerLeuLysHisLeuPheLeuIleGlnThr 135
QY      12387  AATTAGACATCTCTAGGAACCTTCCCATGTGACATCTCAAACTTTGAAGAATTAAAT 12446
Db      136  GlyIleSerAsnLeuGluPheIleProValHisAsnLeuLysLeuGluSerLeuTyr 155
QY      12447  GTGCTCACAATCTTATCCATCTTTCAATATTAAGTATTTCTAATCTGACCAAT 12506
Db      156  LeuGlySerAsnHisIleSerSerIleLysPheProLysAspPhePro--AlaArgAsn 174
QY      12507  CTAGAGCACTTGACCTTTCCAGACACAGAAATTCAAAGTATTAATTGACACAGCTTCGG 12566
Db      175  LeuLysValLeuAspPheGlnAsnAsnAlaIleHisTyrIleSerArgGluAspMetArg 194

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QY 12567 GTTTCACATAAGCCCTTACTCAATCTCTTTAGACCTGCTCCATGACCTATGAC 12626
 DB 195 SerLeuGlnGln-----AlaIleAsnLeuSerLeuAsnPhenAlaSerLeuValys 212
 QY 12627 TTTATCCACACAGGTGATTTAAAGAAATTAGCTTCATAGCTGACTTTAAGAAATAT 12686
 DB 213 GlyIleGluLeuGlyAlaPheAspSerThrValPheGlnSerLeu-----Asn 228
 QY 12687 TTGATGATTTAAATGTAATGAAAACTGTATTCAGAGCTGCGCTGTTAGAGTCAT 12746
 DB 229 PheGlyGlyThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsnSerThrThrGln 248
 QY 12747 CGTTGGTCTGGAGAAATTGAAATGAGAAAATTGAGAAAATTGACAAATCTGCT 12806
 DB 249 SerLeuThrLeuGlyThrPheGlnAspIleAspAsp---GluAspIleSerSerAlaMet 267
 QY 12807 CTAGAGGCTGTGCAATTTGACCATTTGAGAAATTCGATTTGACATTTAGACTACTAC 12866
 DB 268 LeuIysGlyLeuCysGluMetSerValGluSerLeuAsnLeuGln-----GluHisArg 285
 QY 12867 CTCATGATATTTATGAC---TTATTTAATGTTTGAAGAAATGTTTCTCATTTTCTCT 12923
 DB 286 PheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGlnIleAspLeu 305
 QY 12924 GTGAGTGTGACTATTGAAAGGTAAGACCTTTCTTATTAATTCGATGCGCAACTTTA 12983
 DB 306 ThrIaIthrHisIleuIysGlyLeuProSer-----GlyMetIysGlyLeu 320
 QY 12984 GAATTAGTTAAC-----TGTAATTT--- 13004
 DB 321 AsnLeuLeuIysIysLeuValLeuSerValAsnHisPheAspGlnLeuCysGlnIleSer 340
 QY 13005 ---GGACAGTTCCCACTTG-----AACTGAAATCTCTCAA 13040
 DB 341 AlaIleAsnPheProSerLeuThrHisIleuTyrlleArgIysAsnValIysLeuHis 360
 QY 13041 AGCGTACTTTCACCTTCAACAAAGGTGGAATGTTTTCAGAAAGTTGATCTACCAAC 13100
 DB 361 LeuGlyValGlyCysLeuGlnIleuGlyAsn----- 371
 QY 13101 CTGAGTTTCTAGATCTCAGTAGAAATGCTGAGTTTCAAGGTTGCTGTTCTCAAGT 13160
 DB 372 LeuGlnThrIleAsnLeuSerHisAsnAspIleGluAlaSerAspCysCysSerLeuGln 391
 QY 13161 GATTTGGGACACACCGCTTAAAGTATTAGATCTGAGCTTCAATGGTATTATTCATG 13220
 DB 392 LeuIysAsnLeuSerHisIleuGlnThrIleAsnLeuSerHisAsnGluProLeuGlyLeu 411
 QY 13221 AGTTCAAC---TTCTGGGCTTAGAACACTAGAACATCTGGAATTCACG----- 13268
 DB 412 GlnSerGlnAlaPheIysGlyCysProGlnLeuGlnLeuAspLeuAlaPheThrArg 431
 QY 13269 ---CATTCGAATTTGAAACAAATGATGAGTTTCA-----GTATTCCTATCTCACTG 13319
 DB 432 LeuHisIleAsnAlaProGln---SerProPheGlnAsnLeuHisPheLeuGlnValLeu 450
 QY 13320 AACTCATTTAC-----CTTGAATTTCTCATCTACACACGATTTGCTTCAATGCGC 13373
 DB 451 AsnLeuThrTyrcysPheLeuAspThrSerAsnGlnHis----- 463
 QY 13374 ATCTTCATGCGCTGTGCAAGCTGCAAGCTTGAAGAAAGGCTGCAATTTCTTCAGAGA 13433
 DB 464 LeuLeuAlaGlyLeuProValLeuArgHisIleuAsnLeuIysGlyAsnHisPheGlnAsp 483
 QY 13434 AACTTCTCT-----CCAGATATCTTCCACAGCTGAGAAATCTGACCTTCTGAGACCTC 13487
 DB 484 GlyThrIleThrIysThrAsnLeuGlnThrValGlySerLeuGlnValLeuIleLeu 503
 QY 13488 TCTCAAGTCTCACTGAGACAGTGTCTCAACAGCATTTAACTCATCTCTCCAGTCTTCA 13547
 DB 504 SerSerCysGlyLeuLeuSerIleAspGlnGlnAlaPheHisSerLeuGlyLysMetSer 523

QY 13548 GTACTAAATATGACCAACAACACTCTTT-----TCATTTGATAGCTTTCTTAT--- 13598
 DB 524 HisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSerLeuSerHisIleu 543
 QY 13599 -----AACTGTCAACTCTCCACAGTCTTGATTTAGTCTCAT 13640
 DB 544 LysGlyIleTyrlleuAsnLeuAlaAlaAsnSerIleAsnIleIleSerProArgLeuLeu 563
 QY 13641 CACATATGACTTCCAAAAACAGAACTACAGATTTTCCAGATGCTGATCTTCTCTTA 13700
 DB 564 ProIleLeu-----SerGlnGlnSerThrIle 572
 QY 13701 AATCTTACAGAAATGACTTTGCTTGTGATCTTGACACAGAGTTTCTGCAATGATC 13760
 DB 573 AsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPheLeuThrTyrPyr 592
 QY 13761 AAGACACAGAGCAGCTCTTGTTGTTGAAAGTTGAACGAATGGAATGCAACCTTCAGAT 13820
 DB 593 LysGluAsnLeuHisIysLeuGlnGlySerGlnGluThrThrCysAlaAsnProSer 612
 QY 13821 AAGCAGGCAATGCTGCTGAGTTGATTAATATCACTGTGACAGAAATTAAGACCATCAT 13880
 DB 613 LeuArgGlyValIysLeuSerAspValIysLeuSerCysGlyIle-----ThrAlaIle 630
 QY 13881 GTGTGTGCTGCTCTCAGTGTCTTGTGATATCTGTTGAGCAAGTTCTGTCTAT 13934
 DB 631 GlyIlePhePheLeuIleValPheLeuLeu-----LeuLeuAlaIleLeuPhe 647
 RESULT 4
 US-08-833-823-4
 ; Sequence 4, Application US/08833823
 ; Patent No. 5969093
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McKenough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; TITLE OF INVENTION: ENCODED THEREBY
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,823
 ; FILING DATE: 10-APR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/514,014
 ; FILING DATE: 11-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-833-823-4


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: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ. ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ. ID NO: 8799
: LENGTH: 775
: TYPE: PRT
: ORGANISM: Human
: US-09-949-016-8799

Alignment Scores:
Pred. No.: 2,22e-45 Length: 775
Score: 497.00 Matches: 205
Percent Similarity: 40.87% Conservative: 113
Best Local Similarity: 26.35% Mismatches: 242
Query Match: 1.50% Indels: 218
DB: 4 Gaps: 37

US-09-396-985b-47 (1-18989) x US-09-949-016-8799 (1-775)

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DB 143 Serlyrhantryleuseranleusersertertrpheyysproleuserserleuhr 162
QY 12366 AAGCTG-----GTGGCTGTGGAGACAAT 12389
DB 163 PheleuhsenleuengllyanProtyrlythrleuglygluthrserleuPheSerHis 182
QY 12390 CTAGCATCTTAGAAGAACTTCCCATTTGACATCTCAAACT----- 12431
DB 183 leuhrlyrleuglnlleuargValglyanMetAspThrPhehrlyslleGlnArg 202
QY 12432 -----TTGAAGAAGTAATATGCGCTCAACATCTTATCA 12467
DB 203 LysAspPhealaglyleuThrPheleuglnleugluileaspalasAspPheugln 222
QY 12468 TCCTTCAAAATTAACCTGAGATTTTCTTAATCTGACCAATAGACATTTGACCTTCC 12527
DB 223 Serlyrleu---ProlyserleuLysSerlleGlnsnValSerHisleuileuHis 241
QY 12528 AGCAACAG-----ATTCAAGTATTTATTC 12554
DB 242 MetlyseGlnHisleuLeuLeuGluilePheValAspValThrSerSerValGlyCys 261
QY 12555 ACAGACTGGGGGTTCATCAATCAATGCCCTACTCATCTCTTTAGACCTCCCTG 12614
DB 262 LeuGlnleuArg-----AspThrAspLeu 269
QY 12615 AACCTTATGACTTT-----ATCCAACAGGTGCATTTAAAGAAATTAAGCTTCATAG 12668
DB 270 AspThrPheHisPheSerGlnleuSerThrcllygluthrAsnSerleu---llelylys 288
QY 12669 CTGACTTAAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAAACTTGT 12716
DB 289 PhehrthearAsnVallyslleThrAspGlnSerleuPheGlnValMetlyLeuLeu 308
QY 12717 -----ATTCAAGGTCTGGCGTGTGTAAGTCATGGTTGTTCTG-----GGA 12761
DB 309 AsnGlnlleSerGlyleuLeuGlnleuPheAspCysThrleuAsnGlyValGly 328
QY 12762 GAATTTAGAAATGAGAAACTTGGAAAAAGTTTGACAAATCTGCTTAGAGGGGCTGTGC 12821

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DB 329 AsnPheArgAlaSerAspAsnAspArgValilleAspProGlylyValGlu----- 345
QY 12822 AATTGACCAATGGAAGAAATCCGATAGCA-----TACTAGACTCTACTCGATGAT 12875
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QY 12876 ATTATGACTTAATTAATGTTTGAACAATGTTTCTTCAATTTCCCTGAGTGTGACT 12935
DB 363 leuSerThrleuTyrsSerleuThrleuGluArgValys-----Argllehr 377
QY 12936 ATTGAAGAGGTAAAGACTTTTCTTAATTAATTTGGAATGGCAATTTAGAAATGTTAAC 12995
DB 378 ValGlnleuSerlyrValPhe-----LeuValPro 387
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QY 13056 TCCAACAAAGGTGGAAATGCTTTTTCAGAGTTGATCTCAACAGCTTGAATTTCTAGAT 13115
DB 393 -----HisleuysSerleuGluTyrlleuAsp 401
QY 13116 CTCAGTAGAAAT-----GGCTGAGTTTCAAAAGGTGCTGTTCATTAAGT 13160
DB 402 leuSerGlnleuLeuMetValGluGluTyrlleuLysAsnSerAlaCys----- 417
QY 13161 GATTTGGGACACACACCTTAAGATTTAGATCTGAGCTTCAATGATGTTATTAACATG 13220
DB 418 GlnAspAlaTrpProSerleuGlnThrleuileuLysArgGlnsn----- 432
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DB 433 -----Hisleu-----AlaSerleu 437
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DB 456 Serlys----- 457
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QY 13461 CTGAGAAACTTGACCTTCTCTGACCTCTCTCAAGTGTCACTGAGAGAGTGTCT----- 13514
DB 470 ProGlnlyserMetlyrlyrleuAsnleuSerSerThrArglleHisSerValThrcllyCys 489
QY 13515 ---CCACAGCAATTTAACTCACTCTCCAGTCTTCAGTCTCACTAATATATGAGCCACAC-- 13568
DB 490 llePro-----LysThrleuGlnlleuAspValSerAsnAsn 503
QY 13569 ---AAGTCTTTCATTTGAT----- 13586
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QY 13587 -----ACGTTTCTCT---TATAAGTGTGTAAGCTCCCTCAGAGCTTCTTGAATACGTC 13637
DB 524 leuMetThrleuProAspAlaSerleuLeuPheMetleuLeuValleuLyslleSerArg 543
QY 13638 AATCACTAATATGACTTCCAAAAGAGAACTACAGACTTTTCCAACTAGTCTTTC 13697
DB 544 AsnAlalleThrThrPheSerlyrGlnGlnleuAspSerPhe---HisThrleuLysThr 562
QY 13698 TTAATCTTACTCAGATGACTTGTCTGTGATCTTGGAACAACAGAGTTTCCGCAATGG 13757
DB 563 leuGlnAlaGlyllysnAsnPheilleCysSerCysGlnPheleuSerPheThrGln--- 581
QY 13758 ATCAAGACCAAGAGAGCTCTTGAGTAAGTT-----GAACGAATGAA 13802

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Db      599 CysAserPerPsoSerHisValArgGLyGINgInIvalGlInArValArgLysenValSer 618
Qy      13857 ---TGTCAGATGAATAAGCAACATTCGTGTGTGGTCCGTACTAGTGTGCTTGTAGATTC 13913
Db      619 GlucYshIsarGThrAlaLeuValSerGIyMeCySeValAleuDeuLeuIleu 638
Qy      13914 GTTGTACAGTTCGTGCTGTATTGTTAT-----TTTCACTGATGCCTTCCTGCTGC 13967
Db      639 LeuthrGlyValLeuCyShIsarGPhenIGLyLeuTrpTyrmetylmethetrrAla 658
Qy      13968 TGCATAAAGTAGTAGTACA-----GGTGAACAATC---TATGATGCC 14006
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Qy      14007 TTGTGTATCTACTAACACAGATGAGGACTGGGTAAAGAATAGCTAGTAAAGATTTA 14066
Db      679 PheValSerTySergIuarGyaPaLaTyrtTryValGIuSbnLeuMetValGingluEn 698
Qy      14067 GAAGAAGGGGTCCTTCATTTCAGCTGTGCCTTCACTACAGACATTTATCCCGGTGG 14126
Db      699 GIuSnArPheaNPorFoprhelySLCySeuHISyArGysPheIleProGLyLys 718
Qy      14127 GCCATGCTGCGCAACATCATCATGAGGTTTCCATTAAGCCGAAGGTGATTTGTGG 14186
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Qy      14187 GTGTCCAGACCTTCATCCAGAGCCGTGTGTATCTTTGAATATAGATGCTCAGACC 14246
Db      738 LeuSerGIuAnPheValyLSerGIuTrpCySLySerytGIuLeuAsPheSerHisPhe 757
Qy      14247 TGGCAGTTTCAGACAGTCGCGTGTATCATCTTCATTCCTCGCAGGAAGTG 14300
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RESULT 6
US-09-353-585-3
? Sequence 3, Application US/09353585
? Patent No. 6287865
? GENERAL INFORMATION:
? APPLICANT: Dixon, Mark S
? Jones, David A
? Jones, Jonathan DG
? TITLE OF INVENTION: Plant pathogen resistance genes and uses
? thereof
? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Nixon & Vanderhye PC
? STREET: 8th Floor, 1100 No. 6287865th Giebe Road
? CITY: Arlington
? STATE: Virginia
? COUNTRY: United States of America
? ZIP: 22201-4714
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/353,585
? FILING DATE: 15-Jul-1999
? CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
? 1/68
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/930,277
? FILING DATE: 27-OCT-1997
? APPLICATION NUMBER: PCT/GB96/00785
? FILING DATE: 01-APR-1996
? APPLICATION NUMBER: GB 9506658.5
? FILING DATE: 31-MAR-1995

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: ATTORNEY/AGENT INFORMATION:
: NAME: Ms Mary J Wilson
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 620-69
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1112 amino acids
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: YES
: ORIGINAL SOURCE:
: ORGANISM: Tomato
: STRAIN: Cf2
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3
:
Alignment Scores:
Pred. No.: 9.61e-22 Length: 1112
Score: 287.50 Matches: 132
Percent Similarity: 42.17% Conservative: 78
Best Local Similarity: 26.51% Mismatch: 159
Query Match: 0.87% Indels: 89
DB: Gaps: 20
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QY 12339 GCCTTTCTGAGATCAAGATTACAGAAAGCTGGCTGGTGGAGACAATCTAGCATCT 12398
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QY 12519 GACCTTCCAGCAACAAGATTCAAAAGTATTATTGACACAGACTGGGGTCTCAATCA 12578
DB 509 AsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIleGlyTyrLeuArgSer 528
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DB 545 AlaSerPheGlyAsnLeu-----AsnAsnLeuSerArgLeu 556
QY 12699 AATGTATAGAAAACCTTATATCAAGGCTGCGCTGTTGAAGTGCATGCTTTGGTCTCG 12758
DB 557 AsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIle----- 571
QY 12759 GGAGAAATTTAGAAATGAAGAAACTTGGAGAAATTTGACAAATCTGCTTAGAGGCG-- 12815
DB 572 GlyTyrLeuArgSerLeuAsnAspLeu--GlyLeuSerGluAsnAlaLeuAsnGlySer 590
QY 12816 -----CTGTGCAATTGACACCTTGAAGAAATTCGATTAGCAATCTTAGACTTAC 12863
DB 591 IleProAlaSerLeuGlyAsnLeuValAsnAsnLeuSerMetLeuTyrLeuTyrIleAsnGln 610
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Db      611 LeuSerGlySerIleProGluGluIleGlyTyrLeuSerSerLeuThrTyrLeuSerLeu 630
QY      12924 GTGAGTGTGACTATGAAAGGTAAGAAGCTTTCTTATATATTCGATGGCAACATTTA 12983
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Db      631 GlyAsnAsnSerLeuAsn----- 636
QY      12984 GAATTAAGTAACTGTAATTTGACAGTTTCCACATTGAAATCTCAATCTTCAAAAGG 13043
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Db      637 GlyLeuIleProAlaSerPheGly-----AsnMetArgAsnLeuGlnAla 651
QY      13044 CTTCCTTCACTTCCACAAAGGTGGGAATCTTTTTCAGAAAGT----- 13088
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Db      652 LeuIleLeuAsnAspAsn-----AsnLeuIleGlyGluIleProSerSerValCys 668
QY      13089 GATCTACCAAGCTTGTAGTTCTTCAATCTCAGTAAATGCTTCAAGTTTCAAGGTTGC 13148
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Db      669 AsnLeuThrSerLeuGlnValLeuTyrMetProArgAsnAsnLeu-----LysGlyLys 686
QY      13149 TGTTCCTCAAGTGAATTTTGGGACCAAGCTTAAAGTATTTAGATCTGAGCTTCAATGT 13208
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Db      687 ValProGlnCysLeuGlyAsnIleSerAsnLeuGlnValLeuSerMetSerSerAsnSer 706
QY      13209 GTTATT---ACGATGAGTTCAACTTCTTGAGCTTAGAACAACACTAGAACATCTGATTTT 13265
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Db      707 PheSerGlyGluLeuProSerSerIleSerAsnLeuThrSerLeuGlnIleLeuAspPhe 726
QY      13266 CAGCATTCGAATTTGAAACAATAGAGAGTTTTCAGATTTCCATATCCTAGAAACCTC 13325
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Db      727 GlyArgAsnAsnLeuGly----- 733
QY      13326 ATTACCTTGACATTTCTCATCTACACAGAGTGTCTTCAATGGCATCTTCATAGGC 13385
        |||
Db      734 -----AlaIleProGlnCysPheGlyAsn 741
QY      13386 TTGTCCAGTCTCGAAGTCTTGAATAATGGCTGGCAATCTTTCAGAAATCTCTTCCA 13445
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Db      742 IleSerSerLeuGlnValPheAspMetGlnAsnAsnLysLeu---SerGlyThrLeuPro 760
QY      13446 GATATCTTCCACAGAGCTGAGAAACTTGACCTTCTGAGACCTCTCTCACTGATCGACAG 13505
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QY      13506 CAGTTGTCTCCACAGAGCTTAACTCACTCCAGTCTTCACTTAAATATGAGCCAC 13565
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Db      781 AspGlnIleProArgSerLeuAspAsnCysLysLysLeuGlnValLeuAspLeuGlyAsp 800
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Db      801 AsnGlnLeu-----AsnAspThrPheProMetTyrLeuGlyThrLeuProGlnLeuArg 818
QY      13620 GTTCTGATTACAGTCTCAATCAGATA-----ATGACTTCCAAAMAAACAGAACTA 13670
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Db      819 ValLeuArgLeuThrSerAsnLysLeuIleGlyProIleArgSerSerArgAlaGlnIle 838
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STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: CF2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2
Alignment Scores:
Pred. No.: 3,5e-21 Length: 1112
Score: 282.50 Matches: 137
Percent Similarity: 40.04% Conservative: 68
Best Local Similarity: 26.76% Mismatches: 208
Query Match: 0.85% Indels: 99
DB: Gaps: 20
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QY      12276 AGCTTAAGCCACTCTCTTCAATTAATTAATGACAGAAACCCATCCAGATTAGCCCTG 12335
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Db      381 AsnLeuAsnAsnLeuSerMetLeuTyrLeuTyrAsnAsnGlnLeuSerGlySerIlePro 400
QY      12336 GGAAGCTTTTGTGACTATCAAGATTACAGAAAGCTGTGCTGTGAGAGCAAAATCTAGCA 12395
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Db      401 AlaSerLeuGlyAsnLeuAsnAsnLeuSerArgLeuTyrLeuTyrAsnAsnGlnLeuSer 420
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Db      441 AsnSerIleAsnGlyPhe---IleProAlaSerPheGlyAsnMetSerAsnLeuAlaPhe 459
QY      12516 TTGAGACTTTCCAGCAACAAGATTCAAGATTATTTGACACAGCTTGGGGTTCTACAT 12575
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Db      460 LeuPheLeuTyrGlnLysGlnLeuAlaSerSerValProGlnGluIleGlyTyrLeuArg 479
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480 Ser-----LeuAsnVal---LeuAspLeuSerGluAsnAlaLeuAsnGlySerIle 495
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QY 12696 TTAATATTAATGAAGAACTTGATTCAGGCTGGCTGGTTTGAAGTCCATCGTTGGTT 12755
DB 508 LeuAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIle----- 523
QY 12756 CTGGGAGAAATTTAGAAATGAAGAACTTGAGAAAGTTTGCATTCGTCTAGAGGCG 12815
DB 524 ---GlyIyrLeuArgSerLeu---AsnValLeuAspLeuSerGlnAlaLeuAsnGly 541
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DB 561 -----Asn 561
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DB 562 GlnLeuSerGlySerIleProGluGluIleGlyIyrLeuArgSerLeuAsnAspLeuGly 581
QY 13050 TTCACTTCCAAC-----AAAGTGGGAATCTTTTCAGAAAGTTGATCTACCAAGCCTT 13103
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QY 13104 GAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAGTGTCTTCAAAAGTGAT 13163
DB 602 SerMetLeuIyrLeuIyrAsnAsnGlnLeuSer-----GlySerIleProGluGluIle 619
QY 13164 TTGGGACAAACAGCCTTAATATTTAGTCTG-----AGTTCAATGGGTATTT 13214
DB 620 GlyIyrLeuSerSerLeuThrIyrLeuSerLeuGluAsnAsnSerLeuAsnGlyLeuIle 639
QY 13215 ACCATGAGTTCAAACTTCTGGGCTTAGAAACAATCAACATTCGATTTCCACATTTCC 13274
DB 640 ProAlaSer-----PheAlaAsnMetArgAsnLeuGlnAlaLeuIleLeuAsnAspAsn 657
QY 13275 AATTGAAACAATGAGTGAAGTTT---TCAGTATTCCTATCACTCAGAAACCTCATTTAC 13331
DB 658 AsnLeu-----IleGlyGluIleProSerSerValCysAsnLeuThrSerLeuGluVal 675
QY 13332 CTTCGACATTTCTCATCTCACACCAAGAGTTGCTTTCATGGCATCTTCAATGGCTGTCC 13391
DB 676 LeuIyrMetProArgAsnAsnLeuIyrGlyValProGlnCysLeuGlyAsnIleSer 695
QY 13392 AGTCCGAGATCTTGAATAGGCTGGAGATTTCTTCCAGAAACTTCTCCAGATATC 13451
DB 696 AsnLeuGlnValLeuSerMetSerSerAsnSerPheSerGlyGlu---LeuProSerSer 714
QY 13452 TTCACAGAGCTGAGAAACTTGAACCTTCTGACCTCTCTCAGGTGCACTGAGAGCAGTTG 13511
DB 715 IleSerAsnLeuThrSerLeuGlnIleLeuAspPheGlyArgAsnAsnLeuGluGluVal 734
QY 13512 TCTCCAAAGCATTTTAATCACTCTCCAGCTCTTCAGGTAATTAATAGCAACAAC 13571
DB 735 IleProGlnCysPheGlyAsnIleSerSerLeuGluValPheAspMetGlnAsnAsnGly 754
QY 13572 TTC-----TTTCATG----- 13583
DB 755 LeuSerGlyThrLeuProThrAsnPheSerIleGlyCysSerLeuIleSerLeuAsnLeu 774
QY 13584 -----GATACGTTTCTTATTAAGTCTTGAAAC-----TCCCTCGAG 13619
DB 775 HisGlyAsnGluLeuGluAspGluIleProArgSerLeuAspAsnCysLeuIyrLeuGln 794

QY 13620 GTCTTGATTAACAGTCTCAATCATATATGACTTCCAAAAACAGGAAGCTACAGCATTTT 13679
DB 795 ValLeuAspLeuGluIyrAspAsnGlnLeuAsnAspThrPheProMetIyrLeuGlyThrLeu 814
QY 13680 CCAAGTAGTCTAGCTTTCTTAAATCTTACTCAGAAAT 13715
DB 815 Pro---GluLeuArgValLeuArgLeuThrSerAsn 825

RESULT 8
US-08-666-271-2
; Sequence 2, Application US/08666271
; Patent No. 5920000
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN D
; APPLICANT: HAMMOND-KOSACK, KIM E
; APPLICANT: THOMAS, COLMTR M
; APPLICANT: JONES, DAVID A
; TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,271
; FILING DATE: 19-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02812
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326428.1
; FILING DATE: 24-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409363.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-666-271-2

Alignment Scores:
Pred. No.: 1,37e-19 Length: 863
Score: 267.50 Matches: 193
Percent Similarity: 37.32% Conservative: 122
Best Local Similarity: 22.87% Mismatches: 309
Query Match: 0.81% Indels: 220
DB: 2 Gaps: 37

US-09-396-985B-47 (1-18989) x US-08-666-271-2 (1-863)
QY 12047 GATAAATCACTAGCTGTGGGCTTCTTATTTGCTTATTCATCATCATCTGCTGCTTG 12106
DB 12047 GATAAATCACTAGCTGTGGGCTTCTTATTTGCTTATTCATCATCATCTGCTGCTTG 12106

Db 2 AspCysValIysLeuValPheLeuMetLeuYThrPheLeuCysGlnLeuAlaLeuSer 21
 QY 12107 ATGTCTTGGCCATGACATCATATGACCCATCATCTGTATGAAAGCTGATGACT 12166
 Db 22 SerSerLeuPro-----HisLeuCysProGlnAspGlnAla-Le 34
 QY 12167 AGATTAATATTTATTTTATTTAGTCTTATTCAGCAAAATATTAATATTAATGCTTTT 12226
 Db 34 userLeuLeu---GlnPheYAsnMetPheThrIleAsnProGlnAlaSerAspTyr-Cy 53
 QY 12227 TTATTCCTGTAGTGTGAATTCAGACAAATTAAGATGGGCAATTCAGACCTTAAGCA 12286
 Db 53 sTy-----AspIleArgThrTyrValAsp-----IleGlnSerTyr-ProAr 67
 QY 12287 CCTCTCACTTAATATGACAGAAACCCCATCCAGAGTTTATGCGCTGGAGCCTTTTC 12346
 Db 67 g-----ThrLeuSerTyrAsn-----LysSerThrSerCysCysSerTyrAs 81
 QY 12347 TGAATA-----TCAGATTTCAGAAAGCTGGTGGCTGTGAGACAAATCTAGATC 12397
 Db 81 pGlyValHisCysAspGlnThrThrGlyGlnValIleAlaLeuAspLeuArgCysSerG 101
 QY 12398 TCTAGAG-----AACTCCCATTTGACATCTCAAACTTTGAAAGAACT 12442
 Db 101 nLeuGlnGlyLysPheHisSerAsnSerSerLeuPheGlnLeuSerAsnLeuLysArgLe 121
 QY 12443 TAATGTGGCTCACTTATTCATCCATCTTTCAATACCTGATTTTCTTAATCTGAC 12502
 Db 121 uAspLeuSerPheAsnAsnPheThrGlySerLeuIleSerProLysPheGlyGlnPheSe 141
 QY 12503 CAATCTAGACACTTGAACCTTTCCAGACAAAGATTCAAATATTTATTTGACAGACT 12562
 Db 141 rAsnLeuThrHisLeuAsnLeuSerHisSerSerPheThrGlyLeuIleProSerGlnI 161
 QY 12563 GCGGCTTACATCAATGCCCTTACTCATCTC-----TCTTAAAGCTTGTCCCTGAA 12616
 Db 161 eCysHisLeuSerLeuHisSvalLeuArgIleCysAspGlnTyrGlyLeuSerLeuVa 181
 QY 12617 CCTGTAGACTTATTCACACAGTGATTTAAAGAAATTTAGGCTTCAATAGCTGAC- 12674
 Db 181 lProLysAsnPhe-----GlnLeuLeuLeuLysAsnLeuThrG 194
 QY 12675 -TTAAGAAAT--AATTTGATAGTTTAAATGTAATGAATACTTATTTCAAGT- 12725
 Db 194 nLeuArgIleuAsnLeuGlnSerValAsnIleSerSerThrIleProSerAsnPheSe 214
 QY 12726 -----CTGCGTGTATTAGAACTCCATCGTTGGTTCTGGAGAA 12763
 Db 214 rSerHisLeuThrThrLeuGlnLeuSerGlyThrGlnLeuHisGlyIleLeuProGlnAr 234
 QY 12764 ATTTGAATGAGAAATCTTGAA----- 12788
 Db 234 gValPheHisLeuSerAsnLeuGlnSerLeuHisLeuSerValAsnProGlnLeuThrVa 254
 QY 12789 -----AAGTTTGAACAATCTGCT----- 12806
 Db 254 lArgPheProThrThrLysTyrPheAsnSerSerHisLeuSerMetThrLeuTyrValAspSe 274
 QY 12806 ----- 12806
 Db 274 rValAsnIleAlaAspArgIleProLysSerPheSerHisLeuThrSerLeuHisGlyIle 294
 QY 12807 -CTAGAGGCGCTGTGCATTTTGAC-----ATTGAAGA 12838
 Db 294 uTyrMetGlyArgCysAsnLeuSerGlyProIleProLysProLeuTyrPheAsnLeuThrAs 314
 QY 12839 ATTCCGATTAGCATCTTA--GACTACTACCTCCAGATATATTTAGCTTATTAATG 12895
 Db 314 nIleValPheLeuHisLeuGlyAspAsnHisLeuGlnGlyProIleSerHisPheThrI 334
 QY 12896 TTTCGAAATGTTTCTTCAATTTTCCCTGGTGAAGTGTGACTATTAAGAGGATTAAGACT 12955
 Db 334 ePheGlnLysLeuLysArgLeuSerLeuValAsnAsnAsnPheAspGlyGlyLeuGlnLuph 354

QY 12956 T-----TCTTAATATTTCCGANTGGCAACATTAGAAATTA--CTTACTGTAATTTGACA 13009
 Db 354 eLeuSerPheAsnThrGlnLeuGlnArgLeuAspLeuSerSerAsnSerLeuThrGlyPr 374
 QY 13010 GTTTCACCA-----TTGAATCTCAAAATCTCTCAAAAGCTTACTTTCACCTCCAAACA 13063
 Db 374 oIleProSerAsnIleSerGlyLeuGlnAsnLeuGlnCysLeuTyrLeuSerSerAsnHis 394
 QY 13064 A---GCTGGAAATGCTTTTTCAGAAAGT---GATCTACCAAGCCTTGAGTTTCTGATCT 13117
 Db 394 sLeuAsnGlySerIleProSerTyrPhePheSerLeuProSerLeuValGlnLeuAspLe 414
 QY 13118 CAGTGAAGAATGCTTGACT----- 13136
 Db 414 uSerHisAsnThrPheSerGlyLysIleGlnGlnPheLysSerLysThrLeuSerAlaVa 434
 QY 13137 -----TTCAAGCTTGTGTCTCAAAAGTGAATTTGGACAAACAG 13177
 Db 434 lThrLeuGlnGlnAsnLysLeuLysGlyArgIleProAsnSerLeuLeuAsnGlnLysAs 454
 QY 13178 CTTAAAGTATTTAGATCTGACCTTCAATAGGTGTTAT--ACCAAGACTGCAACTTCTT 13234
 Db 454 nLeuGlnLeuLeuLeuSerHisAsnAsnIleSerGlyHisIleSerSerAlaIleCy 474
 QY 13235 GGGCTTGAACAACACTAGAAACATCTGAGATTTCCAGACTCCAAATTTGAACAATGAGTGA 13294
 Db 474 sAsnLeuLysThrLeuIleLeuLeuAspLeuGlySerHisAsnLeuGlnGlyThrIlePr 494
 QY 13295 GTTTTCAGTATTTCTATCATCTCAGAAACCTCATTTTACCTTGACATTTCTCATCTCACAC 13354
 Db 494 oGlnCysValValGlnArgAsnGlnTyrLeuSerHisLeuAspLeuSerLysAsnArgLe 514
 QY 13355 CAGAGTTCCTTCAATGAGCATCTTCATAGGCTTGCCAGTCCGAAAGCTTGAAGATGCG 13414
 Db 514 uSerGlyThrIleAsnThrThrPheSerValGlyAsnIleLeuArgValIleSerLeuHis 534
 QY 13415 TGGCAATCTCTTCCAGAAACCTTCAGATATCTTCAACAGAGCTGAGAACTTGAC 13474
 Db 534 sGlyAsnLysLeuThrGlyLys---ValProArgSerMetIleAsnCyLysTyrLeuThr 553
 QY 13475 CTTCCTGGACCTCTCTCAAGTGTCAACTGGACAGTGTCTCCAACAGACATTTACTCATCT 13534
 Db 553 rLeuLeuAspLeuGlyAsnAsnMetLeuAsnAspThrPheProAsnTyrLeuGlyTyrIle 573
 QY 13535 CTCAAGTCTTCAAGTACTAAATATGAGCCACAACAACATCTTTTCAATGATGATCTTCC 13594
 Db 573 uPheGlnLeuLysIleLeuSerLeuArgSerAsnLysLeuHisGly-----Pr 589
 QY 13595 TTATPAGTGTCAAGCTC-----CTCAGAGTTCCTTGATTAAGT- 13634
 Db 589 oIleLysSerSerGlyAsnThrAsnLeuPheMetGlyLeuGlnIleLeuAspLeuSerSe 609
 QY 13635 -----CTCAATCAATTAATGACTTCCAAAA 13660
 Db 609 rAsnGlyPheSerGlyAsnLeuProGlnArgIleLeuGlnLysAsnLeuGlnThrMetLysG 629
 QY 13661 A---CAGGACTTACAGACTTTTCCAGTGAAGTCTGACT----- 13694
 Db 629 uIleAspGlnSerThrGlyPheProGlnTyrIleSerAspProTyrAspIleTyrTyrAs 649
 QY 13694 ----- 13694
 Db 649 nTyrLeuThrThrIleSerThrLysGlyGlnAspTyrAspSerValArgIleLeuAspSe 669
 QY 13695 -----TTCTTAATCTTACTCAGAAATGACTTGTCTGTACTTGTAACAC--CAGAG 13744
 Db 669 rAsnMetIleIleAsnLeuSerLysAsnArgPheGln-----GlyHisIleProSe 686
 QY 13745 TTTCCTGCAATGATCAAGACACAGAGCAGCTCTTGCTGGAAGTGAACCAATGCAATG 13804
 Db 686 rIleIleGlyAspLeuValGlyLeuArgThrLeuAsnLeuSerHisAsnValLeuGlnG 706

OY	13805	TGCAACACCTTTCAGATTAACAAGGGCATGCTGTGCCTG-----AGTTT	13846
		::: :::	
Db	706	yHieIleProAlaserPheGlnAsnLeuSerValIleGluSerLeuAspLeuSerSerAs	726
OY	13847	GAAATTCACCTCGTCAGATTGAATAAAGAACCATCATTGGTGTCGGCTCCAGATGCTTGT	13906
		::: ::: ::: ::: ::: :::	
Db	726	nLYseIleSeTdYcIUileProGInGlnLeuAlaserLeuThrPheLeuGlnValLeuAs	746
OY	13907	AGATTCTGTTGTGTAGCACATTCTGCTCTTAAGTTCTAATTTTCACCTAGCTTCTTGCTGG	13966
		::: ::: ::: ::: ::: ::: :::	
Db	746	nLeuSer-----HisAsnHisLeuVal-----GI	754
OY	13967	CTGCATTAAGTAGTGTAGAGGTGAAGAACAATCTATGTATGATGCTTGTGTTACTACTCAAGCCA	14026
		::: ::: ::: ::: ::: :::	
Db	754	yCYsIIeProIySeIlyysGln-----PheAspSerPheGlyAsnThrSerTyrl	771
OY	14027	GGATGAGAGCTGGGTAAAGAAATGAGCTTAGTAAAGAAATTTTGAAGAAGGGGTGCTTCANTT	14086
		::: ::: ::: ::: ::: :::	
Db	771	nGlyAsnAspIlyLeuArg-----GlyPheProIySeu	782
OY	14087	TCACGCTGCC	14096
		:::	
Db	782	rLyIySeuCyS	785

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RESULT 9
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papilio hamadryas
US-09-063-950-5

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Alignment Scores:	
Pred. No.:	1,17e-19
Score:	267.00
Percent Similarity:	39.47%
Best Local Similarity:	24.60%
Query Match:	0.81%
DB:	3
Gaps:	22
length:	605
Matches:	139
Conservative:	84
Mismatches:	216
Indels:	22
Gaps:	22

US-09-396-985B-47 (1-18989) x US-09-063-950-5 (1-605)

OY	12237	AGGCTGTGAATCCAGACAATTGGAAATGGGGCATATCAGAAGCCTTAAGCACCTCTCTAC	12236
		:::::	:::::
Db	131	ArgsnsgintleuAargserleuAlaValgIlyThphneAlaTyThrProAlaleuAlaleu	150
		:::::	:::::
OY	12297	TTAATATTTGACAGCAAAACCACATCAGAGTTTAgGCCCTGGAGCCTTTTCGACTATCA	12356
		:::::	:::::
Db	151	LeugIylenuserianamamarglensearIrglenGlunspGIyleuhheglugIylenGLy	170
		:::::	:::::
OY	12357	AGTTTACGAAGCTGTGGCTGTGCGAGACAATACTTAGCATCTCTAGAGAACCTTCCCATT	12416
		:::::	:::::
Db	171	AasnleutrpAspleuAenleuGIYTrpasnserleuAlaValleuProaspAlalaAphe	190
		:::::	:::::
OY	12417	GGAACATCTCAAAACCTTTGAAAAGAACTTAATTAAGTGCTACACATCTTATCCAATCTTCANA	12476
		:::::	:::::
Db	191	ArgelIylenugIyglIyleuarGluIeuValIeualadIyasnrgIeu---AlatryIleu	209
		:::::	:::::
OY	12477	TTACCTGAGIATTTTTCTTAATCTGCACCAATCTAGAGCATTTGCAGCAACAG	12536
		:::::	:::::
Db	210	GlnProlaleuPneserGIyleuAlaglIleuNrgIyleuNspIenuserIaraganAla	229
		:::::	:::::

[illegible]

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Db      519 ArgThrPheThrProGln-----524:
Qy      13644 ATATGACTTCCAAAAAAGAGAACTACAGCATTTTCCAGTAGCTAGCTTTCTTAAT 13703
Db      525 -----ProProGlyLeuGluArgLeuTrp 532
Qy      13704 CTTACTCAGAAATGACTTTGTTGACTTGTGACACAGAGT-----13745
Db      533 LeuGluGlyAenProTrpAspCysSerCysProLeuLysAlaLeuArgAspPheAlaLeu 552
Qy      13746 -----TTCTGCAATGATC-----AAGCACCAGAG 13772
Db      553 GlnAenProSerAlaValProArgPheValGlnAlaIleCysGluGlyAspAspCysGln 572
Qy      13773 CAGCTCTTGCTGGAAGTGAAGATGGAATGTGCAACACTTTCAGATTAACAGAGGCAATG 13832
Db      573 ProProValIlyrThrTyraAenAenIleThrcysAlaSerProProGluValAlaGlyLeu 592
Qy      13833 CCTGTGCTGAGTTTG 13847
Db      593 AspleuArgAspleu 597

RESULT 10
US-09-331-403-2
; Sequence 2, Application US/09331403
; Patent No. 6489147
;
GENERAL INFORMATION:
; APPLICANT: ALTMANN-JOHL, Regula, PHILIPPSEN, Peter, ALTHOPFER,
; Henning; SEULBERGER, Harald.
; TITLE OF INVENTION: Adenylate cyclase gene, and its use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, Pentium III processor
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect version 6.1
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/331,403
; FILING DATE: 21-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/07309
; FILING DATE: 29-DEC-1997
; INFORMATION FOR SEQ ID NO: 2:
;
SEQUENCE CHARACTERISTICS:
; LENGTH: 1874 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-331-403-2

Alignment Scores:
Pred. No.: 2,92e-19 Length: 1874
Score: 267.00 Matches: 187
Percent Similarity: 37.74% Conservative: 124
Best Local Similarity: 22.69% Mismatches: 286
Query Match: 0.81% Indels: 228
DB: 4 Gaps: 36

US-09-396-985B-47 (1-18989) x US-09-331-403-2 (1-1874)
Qy      11552 ACTGCGTCTATCACTGTGTACAGCATTTACTGTGATTAACAGAACTTTCAAATATCT 11711
Db      462 ThrsrSerIleHtIsAlaGlnGluLeuGluAenAenAepIleGluAspAspLysLeuGln 481

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Qy      11712 AGTGTCAATGACACTTTTTCATTAACATTTAAAGATATCTGTGACACTTATGTGTAATG 11771
Db      482 His---HisLeuGluLysIlyrTyraAenHis-----490
Qy      11772 TTTGATCTCTGAAATGATATTATTTACAGTCAATT-----ATCTGGCTACCAAC 11822
Db      491 -----PheSerAepIleAepIlyrHisIleLysIleTyrrHisIleArgIlePheAenThrAsp 508
Qy      11823 TTAACATCTCAATTTATCTGTACCAATGATGTATTAATCAACAATTTTGTGTGAC---11879
Db      509 AspThrPheThrThrLeuSerCysArgProGluThrThrValLysGluMetIleProGln 528
Qy      11880 ---AGAAATGGCTAAATGATCAAGGCTATTAATC-----11912
Db      529 IleValArgLysPheAenValProProGluAenTyrrGlnValSerLeuLysValGlyLys 548
Qy      11913 -----ATGCTTATTAACGTGCACAAATCTTAT 11939
Db      549 LeuSerLysValLeuArgProThrAlaLysProIleLeuIleGlnIle-----564
Qy      11940 ATATGCAATATTTGATCTTTAATCTGATTTCT-----11972
Db      565 -----ArgLeuLeuLeuPheAenGlyTyrrLysLysThrsAspArgLeuAenIleMetGly 582
Qy      11973 -----TTTATGATTTTCTCCTGCTTATCATGATATGCC 12008
Db      583 IleGluAspleuSerPheValPheSerPheValPheHisProValIleThrSerGlnLeu 602
Qy      12009 TAAATGACAAAAAAGAGCCTATGATTCAGCCAGTATGATATATCACTAGTGTGGGCG 12068
Db      603 ThrTyrrGluGlnGluGlnArgLeuSerLysGlyLysPheValHisValAspLeuArgAsn 622
Qy      12069 TTTCTATTGCTTATTCATCATCATCATCTGCTGCTGATGCTTGTGCTTATGACAAATC 12128
Db      623 Met-AspleuThrIlePro-----628
Qy      12129 ATATGACCCATCATCTGTATGAAAGAGCTGATGACTAGATTAATATTATTTTAG 12188
Db      629 -----ProIleIlePheTyrrGlnHisThrSerAspIleGlu-----640
Qy      12189 TTTCTATTGACAGAAATATTAATCAATGCTTTTATTTCTGTAGT-----12240
Db      641 -----SerLeuAspValSerAenAenAlaAenIlePheLeuProLeuAspPheIleG 658
Qy      12241 -----GTGAATCCAGACAATTGAAGATGGGCAATATCAGACCTTA-----12281
Db      658 uSerValIleLysLeuSerSerLeuArgMetValAenIleArgLaseThrArgPheProse 678
Qy      12282 -----AGCACCCTCTACCTTAATATTGACAGAAACCCATCCAGAG 12325
Db      678 rAsnIleCysGluAlaThrLysLeuIleThrLeuAspLeuGluArgAsnPheIleLysPhe 698
Qy      12326 TTTAGCCCTGGAGCCTTTTCTGACATCAATGATTTACAGAAAGCTGTGGCTGTGAGAC 12385
Db      698 gValPro-----AspGlnMetSerLysLeuThrAsnLeuThrIleLeuAenLe 714
Qy      12386 AAATTCAGATCTCTAGAGAACTTCCCATTTGA-----CATTCAAACTTTGAAGA 12439
Db      714 uArgCysAenGluLeuAspArgLeuProArgGlyPheLysAspLeuLysSerLeuGlnLe 734
Qy      12440 ACTTAATGAGGCTCACATCTTATCCATCTTTCAATTTCCGAGATTTTCTATATCT 12499
Db      734 uLeuAspIleSerSerAsnLysPheAenIleTyrr-----ProGluValIleAenSerCy 752
Qy      12500 GACCAATCTAGAGCACTTGACCTTTCCAGACAACAAGTTCAAGTATTTATTGACAGAGA 12559
Db      752 sThrAsnLeuLeuGlnLeuAspLeuSerTyrrAsnLysIleArgSerLeu---ProAspse 771
Qy      12560 CTTCGGGTTCTTACATCAAAATGCCCTACTCAATCTCT-----12599
Db      771 rMetAsnGlnLeuGlnLysLeuAlaLysIleAenLeuSerAsnAenArgIleThrHisVala 791

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Qy 12600 -----TTAGACCTGCTGCGAACCCTATGAA 12625
Db 791 laenapleuserlysmethrserleuargthleuaspheuhargtryrasmargileg1 811
Qy 12626 CTTTATCCACAGAGCTGATTTAAGAAATTTAGGCTTCATTAAGCTGACCTTAAAGAAATTA 12685
Db 811 userilelys-----CysargValProasleuGlinsanleuPheluthrGluAs 828
Qy 12686 T-----TTTGATAGTTTAAATGTAATGTAATAAACTTGATTTCAAGCTCGGCTGG 12733
Db 828 nargyleuthrmerpheaspparpparglnleumel-----Leuargth 842
Qy 12734 TTTAGAGCTCATGCTTTGGTTCTGGGAGAAATTTAGAAATGAGAAACTTGAGAAAGTT 12793
Db 842 rleugluleuGlN-----ArgasnProleuserileleuthrle 855
Qy 12794 TGACAAATTCGCTGTAGAGGCGCTGTGCATTTGCAATTTGACATTTGAGAAATTCGATTAAGCA 12853
Db 855 ulysasnasptryrleuGlunhlsleuthrserleuserilseerlysalysleuAlava 875
Qy 12854 CTTAGACTACTACTCGATGATATATTATGACTTTATTAATTTGTTGCAAAATGTTCTTC 12913
Db 875 lleuprogln-----SerleuLeuarghargyleuproglyleuGlnly 889
Qy 12914 ATTTCCCTGGTGAAGTGAAGTGAAGGTAAGGTAAGAACTTTCTTATATATTTCGAGATG 12973
Db 889 sleugluleusergluanserleuthrvalleupro----- 901
Qy 12974 GCACATTTAGAAATTAAGTTAACTGTAAATTTGACAGCTTTCCACATTTGAAA---CTCAA 13030
Db 902 -----ProasrlyleuShlsleuLy 908
Qy 13031 ATCTCTCAAAAGCTTACTTTCATTTCCAAAGAGTGGAAATGCTTTTCAGAGAT-- 13088
Db 908 slvsleuvalhlsleuserValAlalyasnlyseuGluserleuproasrGlnulleAl 928
Qy 13089 -GATCTACCAAGCTTGTGATTTCTAGATCTCAGTAGAATAATGGCTTTGAGTTTCAAGGTTG 13147
Db 928 aserleuLyasnleuusermetleuAsrleuHlsCysasnlnleuethrleu----- 946
Qy 13148 CTGTTCTCAAAAGTATTTGGACACACGCTTAAAGTATTTAGATTTGACCTTCAATGG 13207
Db 947 -----ProAlaleuserThrleuserleuthrPhe----- 957
Qy 13208 TGTATTATACATGAGTTCAAACTTTGGGCTTAGAACAACATCAAGATCTGCAATTGCA 13267
Db 958 ----ValasnllseerSerAsnMetleuserGlyHlsHlsGlnleuYrargthrPheG1 976
Qy 13268 G---CATTCGAATTTGAAACAAATGAGTAGAGTTTTCAGTATTCCTATCACTCAAGAACT 13324
Db 976 nglYthrserasnle-----AlalysSerle 985
Qy 13325 CATTACCTTGACATTTCTCATPACTCACACAGAGTTGCTTTCAATGACATCTTCATGG 13384
Db 985 umelrPheluserAlaAlaAsrPasnGlnmelGlyAsrlyspheTrpGlnllePheAsnTh 1005
Qy 13385 CTTGTCAGCTGTCAAGCTTGAAGAAATGGCTGGCAATCTTTCCAGAGAAATCTTCCTCC 13444
Db 1005 rPhelysrThrleuYsVallleuAsnleuserYrasmnDnPhemela-----Leupr 1023
Qy 13445 AGATATCTTCACAGAGCTGAGAACTTGAACCTTCTGAGACCTCTCTCAGTGTCACTGGA 13504
Db 1023 oglnleu-----GlnmelrGlnleuThrGlnleuYrleuserGlyAsnHlsleuth 1041
Qy 13505 GCAGTTGTCTCCACAGCAATTTAATCACTCTCCAGTCTTCAAGTACTAAATATGAGCCA 13564
Db 1041 rThrleuserGlyGlnAlaPheleuYsleuYsSerleuargValleuMetleuAsnAl 1061
Qy 13565 CAACAACCTTTCTTTTATGATGATGCTTTCTTATAGTGTCTGAACCTCCCTCCAGTCT 13624
Db 1061 aasnlnleuGlnleuProAla-----GlnlleseerGlnleuserGlnleuSerValIl 1080
Qy 13625 TGATTACAGTCTCAATCAATTAAGACTTCCAAAAAACAGAACTACAGCATTTT----- 13679

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Db 1080 eaerValglyserAsnGlnleu-----lystrAsnllseerAsnlyrHlsry 1096
Qy 13680 -----CCAAGTAGTCTAGCTTTCTTAAATCTTACTACAGAAAT----- 13715
Db 1096 raerTrPasnTrParglnAsnThrGlnleuYsryrleuAsnPheserGlyAsnThrAr 1116
Qy 13716 -----GACTTGTCTGTACTTGTGAAACACAGAGTTTCTGTCA 13753
Db 1116 grPheGlnlleYserSerlameGlnlyrGly-----ThrAsnMetHlsleuserAsrleuth 1135
Qy 13754 ATGATTCAGAGACCAAGAGCAAGCTC---TTGCTGGAAGTTGAACGAATGGAATGCGAAC 13810
Db 1135 rValleuYsGlnleuargValleuGlnlyleuMetAsrValThrleuAsnThrSerArGva 1155
Qy 13811 ACCTTCAGAT 13820
Db 1155 lProasrPasp 1158

RESULT 11
US-10-101-464A-900
; Sequence 900, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their use in the modification of plant cell signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 900
; LENGTH: 1166
; TYPE: PRF
; ORGANISM: Pinus radiata
; US-10-101-464A-900

Alignment Scores:
Pred. No.: 4,93e-19 Length: 1166
Score: 263.50 Matches: 179
Percent Similarity: 35.83% Conservative: 113
Best Local Similarity: 21.96% Mismatches: 262
Query Match: 0.80% Indels: 262
DB: 4 Gaps: 37

US-09-396-985b-47 (1-18989) x US-10-101-464A-900 (1-1166)
Qy 12103 CTTGATGCTTTGGCTTATGCAATCATATGACCCATCAATCTGTATGAAAGCTGGAT 12162
Db 12103 ----- 12162
Qy 44 leuGlnAlaPheYsAlaSerleuthrTyAsrProserHlsAlaLeuAlaAsnTrpAsp 63
Db 44 ----- 63
Qy 12163 GACTAGATTAATTTGTATTTAGTTCCTTATTCACAGAAATATTAATTAATCAATGT 12222
Db 12163 -----PheValAlaAsnHlsValCys 70
Qy 64 ----- 70
Qy 12223 CTTTATTTCTGTAGTGTGAAATTCAGCAATTTGAGAGTGGGCAATATGAGCTTA 12281
Db 12223 ----- 12281
Qy 71 AsnTrpHrGlyValThrCysAsnProHlsYsleuKrgValserAlaLeuAsnleuthr 90
Db 71 ----- 90
Qy 12282 -----AGCCACCTCTTCACTTAAATTAATTAATGACAGAAAC 12314
Db 12282 ----- 12314
Qy 91 AsnMetSerleuGlnGlnlyThrIleProPheHlsleuGlnYasnllseerPhelueGly--- 109

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QY 12315 CCCATCCAGATTAGCCCTGGAGCCTTTCTGACATA----- 12353
 Db 110 ---ValleuAenleuThrluAenSerPheSerGlylleleProAenGluLeuGlyAs 128
 QY 12353 ----- 12353
 Db 129 LeuAArgLeuLysArgLeuSerLeuYsglnAenGlnLeuIleSerSerlleProGlu 148
 QY 12354 -----TCAAGTTTACAGAGCTGGGCTGGAGACAAATCTAGCAGCT 12398
 Db 149 AlaLeuLysAerCystrSerLeuArgLeuAenAenLeuSerHisAasnAenLeuThrlY 168
 QY 12399 CTAGAGAACCTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAATGGCTGACACAT 12458
 Db 169 ThrIleProSerGlyLeuGlyGlnLeuGlnAenGlnAenLeuSerLeuSerPheAen 188
 QY 12459 CTATCCAACTTTCAAAATTAACCTGAGTAATTTTCTAATCTGACCAATCTAGACACTTG 12518
 Db 189 GlyLeuThrlY---LysValProGlnThrlPheGlyAenCySerAlaLeuGlnlleu 207
 QY 12519 GACCTTCCAGCAAC----- 12533
 Db 208 GlyLeuGlySerAasnPheLeuSerGlyThrlleProSerHisLeuGlyMetLeuAlaArg 227
 QY 12534 ---AGATTCAAGT-----ATT 12548
 Db 228 IleYsrIleLeuSerLeuGlyArgAasnGlnLeuSerGlyGlylleProProSerLeu 247
 QY 12549 TATTCACACAGCTTGGGGTTCAT-----CAATGCC 12584
 Db 248 AasnCystrGlnLeuArgGlyLeuYsrLeuYsrGlnAenArgLeuThrlYGlnllePro 267
 QY 12584 ----- 12584
 Db 268 TrpGlnlleGlyAlaLysLeuSerLyslleGlnThrlLeuSerLeuGlyLysGlnleu 287
 QY 12585 -----CTACTCAATCTCT-----TTAGCCCTGCC 12611
 Db 288 SerGlyGlylleProProSerLeuAenAenCystrGlnLeuSerGlnLeuAenLeuYr 307
 QY 12612 CTGAACCTTATGAACCTTATCAACA-----GGTGCATTTAAGAAATTAAGCTT 12662
 Db 308 GlnAenArgLeuThrlYGlnlleProTrpGlnlleGlyAla---LysLeuSerLyslle 326
 QY 12663 CATAGCTGACTTTAAGAAATAT----- 12686
 Db 327 GlnThrlLeuSerLeuGlyLysGlnleuSerGlylleProProSerLeuAen 346
 QY 12687 -----TTGATAGTTTAAGTAATGAATACTGTATTCAAGCTGCCGCTTTA 12737
 Db 347 CysThrlGlnLeuSerGlnLeuAenAenLeuYrGlnAenArgLeuThrlYlleProTrp 366
 QY 12738 GAA-----GTCCATCGTTTGGTTCGGAGAAATTAAGAAATGA 12776
 Db 367 GlnlleGlyAlaLysLeuSerLyslleGlnThrlLeuSerLeuGlyLysGlnleuSer 386
 QY 12777 GGAACCTTGAA-----AAGTTGACAA 12800
 Db 387 GlylleProProSerLeuAenAenCystrGlnLeuSerGlnLeuAenAenAen 406
 QY 12801 TCTGCTGAGAGGCTGTGCAATTTGACATGAAGAAATCCGATTAAGCATAC----- 12854
 Db 407 AasnSerLeuThrlYlleProGlnGlnlleGlyLysLeuArglleLeuGlnAenMet 426
 QY 12855 ---TTAGAC-----TACTACCTGATGATTAATTAATTTAATTTGATTAATTTGATTA 12902
 Db 427 AsnLeuAasnAenAenHisLeuYsrSerGlnleuSerlleSerPheGlyAlaLeuSer 446
 QY 12903 AATGTTCTCATTTTCCCTGGAGTGTGACTATTGAAGGGTAAAGAC----- 12953
 Db 447 AasnCystrAenLeuGlnMetLeuSerLeuSerAasnAenLeuYsglyAenLeuPro 466

QY 12954 -----TTTCTTAATAATTCGATGAGCAACATTTAGATTAGTAATCTGT 12998
 Db 467 GlySerlleAenAenArgLeuSerGlnAenLeu-----LeuYsrLeuYsrLeuGlyLys 484
 QY 12999 AAATTT---GGACAGTTTCCC-----ACATTGAAACTCAAACTCTCAAAAGCTTACT 13049
 Db 485 ArgPheThrlYLyslleProGlnGlnMetSerAenLeuThrlYlleLeuAenAen 504
 QY 13050 TTCACTTCCAAC-----AAGGTGGGAATCTTTTCAGAAATGATCTCAACAGCTT 13103
 Db 505 LeuAasnAenLeuLeuSerGlylleuProSerAlaLeuGlyArgLeuSerlleAen 524
 QY 13104 GAGTTTCTAGATCTCAGTAGAATGGCTTG----- 13133
 Db 525 GlnlleAenAenLeuSerAenArgAasnAenLeuGlnleuAenlleProCyGlnPheSerGln 544
 QY 13134 -----AGTTTCAAAAGTTGCTGTTCTCA 13157
 Db 545 LeuLysArgLeuYsrAlaLeuGlnleuYsrGlnAenAlaPheSerGlyGlnlleGln 564
 QY 13158 AGTATTTTGGAGACACAGCTTAAGTATTATGATCTGAGCTTCATGCTGTTATTT--- 13214
 Db 565 ValPheAlaSerleuGlnleuAenArgLeuAenAenLeuYsrLysLysPheSerGly 584
 QY 13215 ACCATGAGTTCAAACTTCTGGGC---TTAGAACACTAGAACATCTGATTTCCAGCAT 13271
 Db 585 AasnleProAasnAenAenlleGlyAasnCySerAenleuGlnleuAenAenLeuYr 604
 QY 13272 TCCAAATTTGAAACAAATGAGTGAATTTCAATATCTTCAATCTCAAGAACTTC---ATT 13328
 Db 605 AasnGlnleuSerGlyLeuMetSerTrpLysAl---AlaSerleuHisAenleuGlnPhe 623
 QY 13329 TACCTTCAACATTTCTACTACTACACACAGAGTCTTCAATGACATCTCAAGGCTTG 13388
 Db 624 TyrIleAenValSerHisAenAlaLeuThrlYArgValProAlaGlnleuGlyMet 643
 QY 13389 TCCAGTCTCGAAGCTTGAATAATGCTGGCAATCTTCCAGAAACTCTTCCAGAT 13448
 Db 644 HisMetValGlnAlaIleAenAenAenAenAenAenAenAenAenAenAenAenAen 662
 QY 13449 ATCTTCAACAGAGCTGAGAACTTGAACCTTCTGAGCTCTCTCAAGTCAACGAGCAG 13508
 Db 663 GlnleuValAasnCyValaGlnleuAenAenAenAenAenAenAenAenAenAenAen 682
 QY 13509 TTGCTTCAACAGAGATTTAACTACTCTCCAGTCTTCAAGTCAATTAATGAGCAACAC 13568
 Db 683 ThrIleProThrlSerlleAenGlnValaGlyLeuGlnAenAenAenAenAenAenAen 702
 QY 13569 AACTTCTTTCA---TTGATAGCTTCTTATTAAGTGTGAACTGCCCTCCAGGTTCTT 13625
 Db 703 LysLeuSerGlyProLeuProThr-----SerlleGlnLysleu 715
 QY 13626 GATTACAGTCTCAATCAATATGATCTTCCAAAAACAGAACTACAGCATTTTCCAAGT 13685
 Db 716 Gln---LysleuThrlHisLeuAenLeuSerTrpAasnAenPheThrlYGlnValProSer 734
 QY 13686 AGCTTACCTTTC---TTAATCTTATCTCAGAAATGACTTTGCTTACTTGTGAACAC 13739
 Db 735 SerGlyAlaPheArgLysLeuAenLeuThr----- 744
 QY 13740 CAGAGTTTCTG---CAATGATCAAGACACAGAGCAGCTC 13778
 Db 745 ---SerPheLeuGlyAenSerGlyLeuCyGlyArgTrpLysleu----- 757
 QY 13779 TTGGTGAAGTTGAACAGATGATGCAAC-----CCTTCAAGTAAGCAGAGC 13829
 Db 758 -----GlnleuProHisCyLysleuThrlThrlArgHisHisAenAenAenAenAenAen 775
 QY 13830 ATGCTGTGCTGAGTTTGAATATCACTGTCAAGATGAATGAACCATATGCTGTGTGTC 13889
 Db 776 ValVallleleuAla-----ThrlSerValleuThrl 786
 QY 13890 GTCCCTAGTGTGCTTGAATGATCTGTTGACAGTTCGTCTAT 13934

[illegible]

```

: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Daria
: APPLICANT: Ron, Dorit
: TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
: TITLE OF INVENTION: Thereof
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: P.O. Box 60850
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306-0850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/06/190,802A
: FILING DATE: 01-FEB-1994
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Fabian, Gary R.
: REGISTRATION NUMBER: 33,875
: REFERENCE/DOCKET NUMBER: 8600-0139
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 605 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Insulin-like growth factor binding
: INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Alignment Scores:
Pred. No.: 1.2e-18 Length: 605
Score: 258.00 Matches: 139
Percent Similarity: 39.16% Conservative: 85
Best local Similarity: 24.30% Mismatches: 220
Query Match: 0.78% Indels: 138
DB: 1 Gaps: 23

US-09-396-985B-47 (1-18989) x US-08-190-802A-49 (1-605)
QY AGGNTGAATTCACAGCAATTGAAATGGGCATATCAGAGCCCTTACTACC 122368
Dbb ||| :::::::::::::::::::: ||| ::: ||::||| |::|::|
131 ATgaaagcgcgtatcgcttgaaccccatccagaatttgaccctggagcccttttcgactatga 150
QY 122397 TTAATATTGACAGAAAACCCCATCCAGAATTGACCCCTGGAGCCCTTTTCGACTATGA 123566
Dbb ||| |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
151 leucglyleuhserrshnshndarglseuserrarglseugluaspglyleuhhegiuglyleugly 170
QY 123577 AGTTTACAGAAAGCTCGTGCGCTGTGGAGACAAATCTTGACATCTCTAGAGAACTTCCCATT 124166
Dbb ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
171 SerleuhertrapshpsleuhsnleuglytyrPasnserleualvalleuProksp1aalaphe 190
QY 124177 GGACATCTCAAACCTTTGAAAGAACCTTAATGTGGCCACCAATCTTAATCCAATCTTTCAAA 124767
Dbb ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
191 ArgcglyleucliyserleueuarggluleuvalleualaglYAsnhargleu--Alatyrlieu 209
QY 124777 TTACCTGAGTATTTTCTAATCTGACCAACTCTAGAGCACTTGGACCTTTCCAGACAAG 125366
Dbb ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
210 GlmProhlaaleuhsesrrglyleuualagluleuarggluleuhspsleuhserrargshna1a 229
QY 125377 ATTCAAGATATTAATGACAGACTTGGCGGGTTCTACATCAAAATGCCCTACTCAATCTTC 125966

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Db      230 LeuArgAlaIle-----LysAlaAsnValPheValGlnLeuProArgLeuGln--- 245
Oy      12597 TCCTTAGACCTGTCCCTGACACCCATGAACTTTATCCAAACGAGGATTTAAAGAAATT 12656
Db      246 LysLeuTyrLeuAspArgAsnLeuLeuAlaValAlaProGlyAlaPheLeuGlyLeu 265
Oy      12657 AGG---CTTCATTAAGCTGACTTTAAGAAATATTTGATGATTTAAATGATGAAGAACT 12713
Db      266 LysAlaLeuArgTyrPheAspLeuSerHisAsn---ArgValAlaGlyLeuLeuGlnAsp 284
Oy      12714 TGTATTCAAGCTGTGGCTGTTTGAAGATCCATGCTTTGGTTCGGAGAAATTGAAGAAAT 12773
Db      285 ThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeu----- 297
Oy      12774 GAAGAAACTTGAAAAAGTTGACAAATCTGCTAGAGGGCTGTGCATTTGACCAT 12833
Db      298 -----SerHisAsnAlaIleAlaSerLeuArgProArgThrPhe 310
Oy      12834 GAAGAAATTCGATTAGCATACTAGTACTGATCTGATGATATTTGACTTTAT 12893
Db      311 LysAspLeu-----HisPheLeuGlnGlnLeu----- 319
Oy      12894 TGTTTGACAAATGTTTCTTCAATTTCCCTGTGAGTGTGACTATTTGAAAGGTAAAGAC 12953
Db      320 -----GlnLeuGlyHisAsnArgGlyLeuGlnLeuAlaGln 331
Oy      12954 TTTTCTTATATTTCCGATGCGAACATTTAGATTAAGTATTAATTTGGACAGTTT 13013
Db      332 ArgSerPheGln---GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeu 350
Oy      13014 CCCCATTTGAAGTCAATCTCTCAAAAGGCTTACTTTCATCTTCC-----AACAAAGT 13067
Db      351 GlnGlnVallysalaglyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSer 370
Oy      13068 GGGAAATGCTTTTCAAGAAATGATCTACCAAGCCTTGATTTAGATCTCAGTAGA--- 13124
Db      371 GlyAsnCysLeuArg---AsnLeuProGlnGlnValPheArgGlyLeuGlyLeuLeu 388
Oy      13125 AATGCTTGAATTCAAAGTGTGCTG-----TCTCAAAGTATTTGGG 13169
Db      389 HisSerLeuHisLeuGlyGlySerCysLeuGlyArgIleArgProHisPheThrGly 408
Oy      13170 ACAACGACCCTAAGTATTTGATCTGAGTTCATGATGATGATTTATTCATGATTTCAAC 13229
Db      409 LeuSerGlyLeuArgGlyLeuPheLeuHisAspAsnGlyLeuValGlyIleGlnGln 428
Oy      13230 TTCTTG---GGCTTAGAACCACTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACA 13286
Db      429 SerLeuTyrGlyLeuAlaGlnLeuLeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
Oy      13287 ATGAGTAGTTTCAAGTATTTCTTACTCACTCAAAACCTCATTTACCTTGACATTTTCAT 13346
Db      446 ----- 446
Oy      13347 ACTCACACAGAGTGTGCTTCAATGGCATTTCAATGGCTTTGTCAGTCTGAAAGTCTG 13406
Db      447 ThrHisLeuPro-----HisArgLeuPheGlnGlyLeuGlyLysLeuGlnTyrLeu 463
Oy      13407 AAAATGCTGCGCAATTTCTTCCAGAAATACTTCTTCCA---GATATCTTCCAGAGCTG 13463
Db      464 LeuLeuSerArgAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeu 481
Oy      13464 AGAAACTTGACCTTCTCGACCTCTCTCAGTGTCACTGACGACGCTGTCTCCACACACA 13523
Db      482 GlnArgAlaPheThrPheLeuAspValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeu 501
Oy      13524 TTTAATCACTCTCAGTCTTCAATATGAGCCACACAACTTCTTTTCATTTG 13583
Db      502 LeuAlaProLeuGlyArgLeuArgTyrLeuSerLeuArgAsnAsn-----SerLeu 518
Oy      13584 GATACGTTTCTTAAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAACAGTCAATCAC 13643

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Db      519 ArgThrPheThrProGln----- 524
Oy      13644 ATATGACTTCCAAAAACAGAACTACAGACATTTTCCAGTACTGACTTCTTAAT 13703
Db      525 -----ProProGlyLeuGlnArgLeuTyr 532
Oy      13704 CTTACTCAGAAATGACTTTGCTTGTACTTGTGAACACAGAGTTTCTGCAATGATCAG 13763
Db      533 LeuGlnGlyLeuAsnProTyrPheAspCysGlyCysPro-----LeuLysAlaLeuArg 548
Oy      13764 GAC-----CAGAGCAGCTCTTGTGTGGAAGTTGAACGA 13796
Db      549 AspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCysGlnGly 568
Oy      13797 ATGGAATGTCAACCTTCAGATTAAGCAGGACATGCTGCTGAGTTGAATATCAC 13856
Db      569 AspAspCysGlnProProAlaTyrThrTyrAsn-----AsnIleThr 582
Oy      13857 TGTCAAGTAAATAGAACATCATTTGCTGTGTGCTC 13892
Db      583 CysAlaSerProProGlnValValGlyLeuAspLeu 594

RESULT 15
US-08-477-346-49
/ Sequence 49, Application US/08477346
/ Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theroef
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Alignment Scores:
Pred. No.: 1,2e-18 Length: 605

```

Score: 258.00 Matches: 139
 Percent Similarity: 39.16% Conservative: 85
 Best Local Similarity: 24.30% Mismatches: 220
 Query Match: 0.78% Indels: 128
 DB: 3 Gaps: 23

US-09-396-985b-47 (1-18989) x US-08-477-346-49 (1-605)

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QY 12237 AGGGTGAATTCAGATTAAGATGGGGCAATAGAGCCTTAGCCTTCTACC 12296
DB 131 ArgnglnleuargserleuAlaleuGlyThrPheAlahisthProAlaleuAlaser 150
QY 12297 TTAATATTGACAGAAACCCATCCAGATTAGCCCTGGAGCCTTTTCTGACATCA 12356
DB 151 LeuGlyleuSerleuAenAenArgleuSerArgleuGlnuArglyleuPheGlnuGlyleuGly 170
QY 12357 AGTTTACAGAACTGGTGGCTGTGGAGACAAATCTAGCATCTCTAGAAACCTTCCCAT 12416
DB 171 SerleuThrAspIeuAenLeuGlyTTrpAsnSerleuAlaValleuProAspAlaAlaPhe 190
QY 12417 GGAATCTCAAACTTTGAAAGAACTTAATGTGGCTGACAACTTATCCAACTTTTCAA 12476
DB 191 ArgGlyleuGlySerleuArgGlnleuValleuAlaGlyAsnArgleu--AlaTyrleu 209
QY 12477 TTAACCTGAGTATTTTCTTAATCTGACCAATCTAGAGACTTGGACCTTTCCAGCAACAG 12536
DB 210 GlnProAlaleuPheSerGlyleuAlaGlnleuArgGlyleuAspIeuSerArgAsnAla 229
QY 12537 ATTCAAAGTATTTATTGACACAGACTTGGGGTCTACATCAAAATGCCCTTACATCTC 12596
DB 230 LeuArgAlaIle-----LysAlaAsnValPheValGlnleuProArgleuGln--- 245
QY 12597 TCCTTAAAGCTGTCCTGAAACCCATAGACTTTATCCAAACGAGGTGATTAAGAAAT 12656
DB 246 LysleuTyrleuAspArgAsnleuIleAlaValAlaProGlyAlaPheleuGlyleu 265
QY 12657 AGG---CTTCATTAAGCTGACTTTAAGAAATTAATTTGATAGTTTAAATGTAATGAAACT 12713
DB 266 LysAlaIleuArgTrpIleAspIeuSerHisAsn---ArgValAlaGlyleuGlnAsp 284
QY 12714 TGATTCAGGCTGGCTGGCTGTTTGAAGATCCATGTTGGTCTGGAGAAATTTAGAAAT 12773
DB 285 ThrPheProGlyleuLeuGlyleuArgValleuArgleu----- 297
QY 12774 GAAAGAACTTGGAAAGTTTGACAAATCTGCTAGAGGGCTGTGCAATTGACCAT 12833
DB 298 -----SerHisAsnAlaIleAserleuArgProArgTrpPhe 310
QY 12834 GAAGAAATCCGATTAGCATTAAGTACTACTGATGATTAATTTGACTTTTAAT 12893
DB 311 LysAspIeu-----HisPheleuGlnuIleu----- 319
QY 12894 TGTTCGACAAATGTTTCTTCATTTTCCCTGGTGAAGTGACTATTTGAAAGGGTAAAGAC 12953
DB 320 -----GlnleuGlyHisAsnArgGlyleuArgGlnleuAlaGln 331
QY 12954 TTTTCTTATATTTCCGATGGCAACATTAGATTAGTTACTGTAATTTGACAGATT 13013
DB 332 ArgSerPheGln---GlyleuGlyGlnleuGlnuValleuThrLeuAspHisAsnGlnleu 350
QY 13014 CCCACATTGAAACTCAATCTCTCAAAAGCCTTACTTCACTTCC-----ACAAAGGT 13067
DB 351 GlnGlnuVallyLysAlaGlyAlaPheleuGlyleuThrAsnValAlaValMetAsnleuSer 370
QY 13068 GGGAACTGTTTTCAGAAATTGATTCACAAAGCCTTGAATTCTAGATCTCAGTAGA-- 13124
DB 371 GlyAsnCySerleuArg-----AsnleuProGlnuGlnuAlaPheArgGlyleuGlyLysleu 388
QY 13125 AATGCTTGAAGTTTCAAGTTGCTGT-----TCGCAAGTGATTTTGGG 13169
DB 389 HistserleuHisleuGlnuGlySerCySerleuGlyArgIleArgProHisThrPheThrCly 408
QY 13170 ACAACGAGCTAAAGTATTTAGATCTGAGTTCAATGGTGTATTATACCATGAGTTCAAC 13229

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DB 409 LeuSerGlyleuArgArgleuPheleuLysAspAsnGlyleuValGlyIleGlnuGln 428
QY 13230 TTCTTG---GGCTTAAACAACATCAGAAACATCGGATTTCCAGATTCGAATTTGAACAA 13286
DB 429 SerleuTrpGlyleuAlaGlnleuLeuGlyleuAspIeuThrSerAsnGlnleu----- 446
QY 13287 ATGATGATGATTTTCAGTATTTCTATCATCAGAAACCTGATTTTACCTTGACATTTCTCAT 13346
DB 446 ----- 446
QY 13347 ACTCAACACAGACTTCTTTCATATGCAATCTTCAATGCTTGTCCAGTCTCCAAAGCTTG 13406
DB 447 ThrHisleuPro-----HisArgleuPheGlnuGlyleuGlyLysleuGlnuTyrleu 463
QY 13407 AAAATGGCTGGCAATCTTTCCAGAAACCTTCCCA--GATATCTTCCAGAGGCTG 13463
DB 464 LeuLeuSerArgAsnArgleuAlaGln-----LeuProAlaAspAlaLeuGlyProleu 481
QY 13464 AGAACTTGACCTTCTCTGGACCTCTCTCAGTGTCACTGAGCAGAGTGTCTCCACAGCA 13523
DB 482 GlnArgAlaPheThrleuAspValSerHisAsnArgleuGlnuAlaleuProAsnSerleu 501
QY 13524 TTTAAGTCTCTCCAGTCTTTCAGGTACTTAATATGACCAACAACCTTTCTTTGATTG 13583
DB 502 LeuAlaProleuGlyArgleuArgTyrleuSerleuArgAsnAsn-----Serleu 518
QY 13584 GATACGTTTCTTATAGTGTCTGAATCCTCCCTCAGGTTCTTGATTAAGTCTCAATCAC 13643
DB 519 ArgThrPheThrProGln----- 524
QY 13644 ATATGACTTCCAAAAACAGAACTACAGACTTTTCCAGTAGTCTAGTCTTTTAAAT 13703
DB 525 -----ProProGlyleuGlnuArgleuTrp 532
QY 13704 CTTACTCAGAAATGACTTGTGCTTGTACTTGTGAACACACAGATTCTCGCAATGATCAG 13763
DB 533 LeuGlnuGlyAsnProTrpAspCyGlyCyPro-----LeuYsAlaleuArg 548
QY 13764 GAC-----CAGAGCAGCTCTTGGTGAAGTTGAACGA 13796
DB 549 AspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCySerGlnuGly 568
QY 13797 ATGAAATGTGCAACACCTTTCAGATTAAGCAGGGCATGCTGTGCTGAGTTGAATATCAC 13856
DB 569 AspAspCySerleuProProAlaTyrThrTyrAsn-----AsnIleThr 582
QY 13857 TGTCAATGAATAAGACATCATTTGGTGTGCGTC 13892
DB 583 CyAlaSerProProGlnuValAlaGlyleuAspIeu 594

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Search completed: March 29, 2005, 19:53:21
 Job time : 437 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:51:33 ; Search time 185 Seconds
(without alignments)
19752.001 Million cell updates/sec

Title: US-09-396-985B-47

Perfect score: 33065
Sequence: 1 tccaccattctctcacatt.....catgaabydcabydcabydc 18989

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Xgapop 6.0 , Ygapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame_n2p.model -DEV=x1h
-Q=/cg12_1/USPRO.spool/US09396985/runatc.28032005.155743.21159/app_query.fasta_1.85098
-DB=PIR 79 -QMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOPEX=0 -LIST=45
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09396985.0CCN_1.1364.0runatc.28032005.155743.21159 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563.5	1.7	661	2	RP105 - mouse
2	474	1.4	786	2	Toll protein-like
3	441	1.3	1097	2	Toll protein precu
4	389	1.2	1389	2	gene wheeler prote
5	377	1.1	1385	2	tlr protein - trui
6	360	1.1	1280	2	hypothetical prote
7	355	1.1	712	2	retrovirus-related
8	348	1.1	1066	2	hypothetical prote
9	347	1.0	1275	2	reverse transcript
10	346.5	1.0	275	2	probable pol polyp
11	345	1.0	1275	2	reverse transcript
12	344	1.0	1275	2	line-1 protein ORF
13	338	1.0	1259	4	retrovirus-related
14	333.5	1.0	1281	1	retrovirus-related

15	323.5	1.0	1260	4	GNMRL1	retrovirus-related
16	320.5	1.0	1134	1	A29944	chaoptin precursor
17	310	0.9	603	2	T24315	hypothetical prote
18	287.5	0.9	1112	2	T10504	disease resistance
19	286	0.9	853	2	T17461	disease resistance
20	285.5	0.9	994	2	H96510	probable disease r
21	284	0.9	622	2	JC7973	synleuxin - human
22	282	0.9	855	2	T07015	Cf-4a protein - to
23	278	0.8	855	2	T17460	disease resistance
24	278	0.8	1531	2	T42218	slit-1 protein hom
25	276.5	0.8	768	2	T17462	disease resistance
26	276	0.8	845	2	T07039	Hcr9-0 protein - t
27	272.5	0.8	143	2	E41925	hypothetical prote
28	271	0.8	1143	2	T10636	hypothetical prote
29	270.5	0.8	890	2	T00800	disease resistance
30	269	0.8	1027	2	B85089	receptor protein k
31	267.5	0.8	863	2	A55173	ci-9 protein precu
32	267	0.8	605	2	JC5239	insulin-like growt
33	266.5	0.8	1019	2	C96519	probable disease r
34	262.5	0.8	907	2	JE0176	orphan G protein-c
35	262.5	0.8	1051	2	T13174	gpl50 protein - fr
36	260	0.8	1134	2	T04587	hypothetical prote
37	259	0.8	907	2	JG0193	G protein-coupled
38	258	0.8	605	2	A41915	insulin-like growt
39	256.5	0.8	1784	2	C96615	hypothetical prote
40	256.5	0.8	1839	1	OYBYX	adenylate cyclase
41	254	0.8	771	2	T02565	disease resistance
42	254	0.8	910	2	G84648	probable disease r
43	253	0.8	890	2	C96654	hypothetical prote
44	253	0.8	983	2	G84524	probable disease r
45	251.5	0.8	603	2	JC1282	insulin-like growt

ALIGNMENTS

RESULT 1:
156258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revastion 26-Jul-1996 #ext_change 09-Jul-2004
R/Accession: 156258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: 156258; PMID:95204928; PMID:7897216
A/Accession: 156258
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BA07043.1; PID:g761711

Alignment Scores:

Pred. No.: 1.7e-38
Score: 563.50
Percent Similarity: 44.91%
Best local Similarity: 27.86%
Query Match: 1.70%
DB: 2
Gaps: 18

US-09-396-985B-47 (1-18989) x 156258 (1-661)
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DB 58 LeuGlubPheSerPheAsnValLeuProThr11eGlnAsnThrThrPheSerArgLeu11e 77
QY 12210 AGATAATCATGCTTTTATTTCC--TGTAGGTGTAATCCAGCAATTGAGATGGG 12266
DB 78 -----AsnLeuThrPheLeuAspLeuThrArgCysGln11eYrTrp11eHsGluAsp 95
QY 12267 GCATATCAGACCTTAAGCAACCTCTTACCTTAATTTGACAGGAACCCCATCCAGACT 12326
DB 96 ThrPheGlnSerGlnHsArgLeuAspThrLeuValThrAlaAsnProLeu11ePhe 115

QY	12327	TTAGCCCTGGGAGGCTTTTTCGACATTCAGATTTCACAAAGCTGGTGGTCGAGACA	12386
Db	116	MetIaGluThrIaLeuSerGlyProIySaIaLeuIyHrIeLeuPheIleGlnThr	135
QY	12387	AATCGACATCTCGAGAACTTCCCATTTGAGCATCTCAAAACTTTGAAAGACTTAT	12446
Db	136	GlyIleSerSerIleAerPheIleProIeHrIaSmGlnIyHrIeLeuIserLeuYr	155
QY	12447	GTGGCTCAACATCTTAATCCCATCTTTCAAATTACCTGAGATTTTCTAATCGACAA	12506
Db	156	LeuGlySerAsnHrIaIleSerSerIleIyLeuProIyGlyPheProThr---GluIyS	174
QY	12507	CTAAGACACTTGGACCTTTCACGACACAGATTCAAAAGTATTATTGACACACTTGGG	12566
Db	175	LeuIySaIaLeuAerPheGlnAaSmHrIaIleHrIeIyLeuSerIyGluIyAspIleSer	194
QY	12567	GTTCATCAACAAATGCCCTATCAATCTCTCTTTCAGCTGTCGCTGAAACCTTGAAC	12626
Db	195	SerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnIySaIyAsnSpIleAla	212
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Db	213	GlyIleGluProGlyIaIaPheAerSerAlaValaPheGlnSerLeu-----Asn	228
QY	12687	TTTGATAGTTTAAATGTATGAATAACTGTATTCAGAGCTGCTGCTGTTAAGATCCAT	12746
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QY	12807	CTAAGAGGCTCTGTCGAATTTGACCATTTGAAGAAATTCGATACATATCTAGACTATAC	12866
Db	268	PheGluGlyLeuCyGluMetSerValGluSerIleAsnLeu---GlnIyHrIyTrPhe	286
QY	12867	CTCGATGATATTATGACTTATTATTTATTTGTTTGAACAAGTGTCTTCATTTCCCTGGTG	12926
Db	287	PheAsnIleSerSerAsnThrPheHrIeCyPheSer-----	298
QY	12927	AGTGGACTATTGAAAGGTAAAGACTTTCTTATATTTGGATGGGACATTTAGAA	12986
Db	299	-----GlyLeuGlnGluLeuAsp	304
QY	12987	TTAGTTAATCTGAATTTTGGACAGTTTCCACAC-----TTGAATCTCAATCTGCTCAA	13040
Db	305	LeuThrIaIaThrIeLeuSerGlnLeuPheProSerGlyLeuValGlyLeuSerThrIeLeuS	324
QY	13041	AGGCTTACTTCACTTCCACAAAGGTGGAAAT---GCTTTTCAAGAGTTATCTTA	13094
Db	325	IyLeuValIaLeuSerIaAeIyIaPheGluAsnLeuCyGlnIleSerIaIaSerAsnPhe	344
QY	13095	CCAGCCTTGAAGTT-----	13109
Db	345	ProSerLeuThrIeLeuSerIleIyGlyIaAsnThrIyAerGluLeuGlnIyThrGly	364
QY	13110	-----CTAGATCTCAGTGAAGATGGCTTGAAGTTTC	13139
Db	365	CysLeuGluAaLeuLeuGluAaLeuAerGluLeuAspLeuSerIaIaSerPheIleGluThr	384
QY	13140	AAAGGTGCTGTCTTCAAAAGTATTTTGGACAAACAGCTTAAAGTATTATAGTGTGAC	13199
Db	385	SerAerCySvSaLeuLeuGlnLeuAerGlnLeuAerIeLeuGlnSerIeLeuGlnLeuSer	404
QY	13200	TTCAATGATGTATTATTCATAGACTTCAAC---TTCCTGGGCTTAAACAATAGAAACAT	13256
Db	405	TyAerGluProLeuSerLeuIyThrGluIaIaPheIyGlnCyAerProGlnIeLeuGluLeu	424
QY	13257	CTGATTTTCAGACATTCCAATTTTGAACAATAGAGTTCACAGATTTTCCATATCAC	13316
Db	425	LeuAspLeuAlaIaPheThrAerGluLeuValIyAerPheAlaGlnIaSerProPheGlnIaSmLeu	444
QY	13317	AGAAACCTCATTTACTTGAACATTTTCCATATCTCACACAGAGTGTCTTCAATGGCAC	13376

Dd		445	HleuleuuluyValleuabnuLeuserShisSerleuAberliserSergluInleu	464
Oy	13377	TTCAGTGGCTTTGTCACGCTTCGAAAGTCTGAATAATGGCTGGCAATCTTTCCAGAAAAAC	13436	
Dd	465	PheabrglyleueroAlaleuglnHsyleAbnleuglnglyAbnHiepherolygely	484	
Oy	13437	TTCCCTT-----CGAGATATTCTCACAGACTGCAGAAACTTGACCTTCTGTGACCTCTCT	13490	
Dd	485	AsnlleclnlyeThrAnserleuglnThrIuglyArgleugluileuValleuser	504	
Oy	13491	CAGGTCAATGGAGAGAGTTGTCCACAAGCATTTTAATCACTGCTCCAGTGTTCAGGTA	13550	
Dd	505	PheCyabrspeuseerSerillearglnHsyalapeThrSerleuysweckesbnHs	524	
Oy	13551	CTAAATATGACCACAACAACCTCTTTGATTCGATACCTTTCTTATTAAGTGTGAAC	13610	
Dd	525	ValaspleuserHsbshmg-----LeuthrSerSerlleglualaleuser	541	
Oy	13611	TTCCCTCAG-----GTTCTTGATTAACGTTCTTCATCATAATAAGACTTCCAAAAAACAG	13664	
Dd	542	HleuleuysglylerYreuleuendulaaserAnhsHlsleSerllele-----	558	
Oy	13665	GAACTNAGACTTTTCCAGTAGCTACGTTCTTA-----AATCTT	13706	
Dd	559	-----LeuproSerleuProIlleleuserGlnglnArgThrIleabneu	574	
Oy	13707	ACTCAGAATGACTTTGCTGTTGATCTTGATCTTGACAACACAGATTTCTCGCAATGATCAAGAC	13766	
Dd	575	ArgglmamproleuabryCythrTybserAbnlleryPhleuglnvtrpyrlrysglu	594	
Oy	13767	CAGAGCAGCTCTTGGTGAAAGTTGAACAAATGAATGTGCCAACCTTCAGATNAGCAG	13826	
Dd	595	AsmectlnlyeIleuglnAprThrgIdnapTrhleucyGluasnProbleuLeudarg	614	
Oy	13827	GGCATGCTTGCTGCTGAGTTGAATATCACCTGTGCAGATGAATNAAGCATCTTGGTGTG	13886	
Dd	615	GlyvalArgleuserAprValThrleuserCyssermetalalavalglyllephepe	634	
Oy	13887	TCGGTCTCTGAGCTCTTGATGATCTGTGTGAGCAGTTCTGCTGATNAGTTCTAT	13943	
Dd	635	LeullevalPheuleuValPhealalleuLeullePhealVallysyrrhe	653	
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CAccession: T08664				
R.Pousterka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.				
submitted to the Protein Sequence Database, May 1999				
A.Reference number: Z16466				
A.Accession: T08664				
A.Molecule type: mRNA				
A.Residues: 1-786 <POU>				
A.Cross-references: UNIPROT:Q15399; EMBL:AL050262				
A.Experimental source: fetal brain; clone DKFZps4710610				
C.Genetics:				
A.Note: DKFZps4710610.1				
Alignment Scores:				
Pred. No.: 6,02e-31 Length: 786				
Score: 474.00 Matches: 204				
Percent Similarity: 41.80% Conservative: 130				
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Query Match: 1.43% Indels: 162				
DB: 2 Gaps: 32				
US-09-396-985B-47 (1-18989) x T08664 (1-786)				
Oy	12345	TCGTGACTATCAAGTTTACGAAGCGTGCGCTGTGGAACAATCTAGCATCTTGAG	12404	
Dd	34	AsmllyleuileHsValProlybAprleuserGlnlyeThrThrIleuabnHieser	53	

QY 12405 AACTGCCCATGACATCTCAAACT-----TTGAAAGAA 12440
DB 54 GlnAsnTrpIleSerGluLeuTrpThrSerAspIleLeuSerLeuSerIleValArgIle 73
QY 12441 CTTAATGGCTCAACATCTTATGCAATCTTCAAAATTACCTGAGTATTTTCTAATCTG 12500
DB 74 LeuIleIleSerHisAsnArgIleGlnTrpLeuAspIleSerValPheIysPheAsn--- 92
QY 12501 ACCAATAGAGCACTTGACCTTTCAGAGCAAGAAATTAACATATTATTTATGACAGAC 12560
DB 93 GlnGluLeuGlnTrpLeuAspLeuSerHisAsnIleValIleValIleSerCys----- 110
QY 12561 TTGGGGTTTACATCAAAATGCCCTACTCATCTCTCT---TTAGACTGTCCCTGAAC 12617
DB 111 -----HisProThrValAsnLeuIleValAsnLeuAspLeuSerPheAsn 124
QY 12618 CCTATGAACTTTATC-----CAACCAAGTCGATTTAAAGAAATTAGGCTTCAT 12665
DB 125 AlaPheAspAlaLeuProIleCysIleGluPheGluIleAsnMetSerGlnLeuIleValPheLeu 144
QY 12666 AAGCTGCTTTAAGAAATTAATTTGATAGTTAATGAAATGAAACTGTGATTCAGAGT 12725
DB 145 GlyLeuSer-----ThrThrHisIleuGlnIlySerSerValLeuPro 158
QY 12726 CTGGCTGGTTTGAAGTCCATCGTTGGTTCTG-----GGAGAAATT 12767
DB 159 IleIleHisIleuAsnIleSerIleValIleuValIleuGlnIleTrpIleGlnIleValIle 178
QY 12768 AGAATGAGAGAACTTGAAGAAAGTTTGACAAATCTGCTGAGGCGCTGCGCAATTTG 12827
DB 179 GluAspProGluGlyLeuGlnIleAspPheAsnThrGluSerIleHisIleValPheProThr 198
QY 12828 ACCATGAAAGAAATTCGATTAGACACTACTACCTCGATGATATTATTGACTTA 12887
DB 199 AsnIleGln----- 201
QY 12888 TTTAATGTTTGAAGAAATGTTTCTTCAATTTCCCTGGTGAAGTGAATATGAAAGGTA 12947
DB 202 PheHisIleHisIleuAspValSerValIleThrValAlaAsnLeuGluLeuSerHisIle 221
QY 12948 AAAAGACTTTTCTAATAATTCGAGTGCACATTTAGAAATTAATTAATTAATTTGA 13007
DB 222 LysCysValIleuGlnIleAspSerIleCysSerTrpPheLeuSerIleLeuAlaIleValGln 241
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DB 242 ThrAsnProIleuLeuSerSerIleuThrLeuAsnAsnIleGluTrpThrTrpAsnSerPhe 261
QY 13065 -----GGTGGGAATGCTTTTTCAGAGTT 13088
DB 262 IleArgIleLeuGlnIleuValTrpHisIleThrValTrpTrpSerSerIleSerAsnVal 281
QY 13089 GATCTACAA---AGCCTTGAAGTTTAGATCTCAGTGAAGATGCGCTTGAAGTTCAAGGT 13145
DB 282 LysLeuGlnGlnIleuLeuAspPheArgAspPheAspTrpSerGluThrIleSerIleuIleVal 301
QY 13146 TGCCTTTCTCA-----AGTGAT----- 13163
DB 302 LeuSerIleHisGlnValIleSerAspValPheGluPheProGlnSerTrpIleTrpGln 321
QY 13164 -----TTTGGGACAAACCGCTTAAG----- 13184
DB 322 IlePheSerAsnMetAsnIleIleValAsnPheThrValSerGluThrArgMetValHisMet 341
QY 13185 -----TATTAGATCTGAGCTTCAATGCGTGTATT----- 13214
DB 342 LeuCysProSerLysIleSerProPheLeuHisIleuAspPheSerAsnAsnLeuLeuThr 361
QY 13215 ---ACCATGATTCAACTTTGGCTTGAAGAACTTAAGAACTGAGATTTCCAGCAT 13271
DB 362 AspTrpValPheGlnIleuSerCysGluHisIleuThrGluLeuGlnThrLeuIleLeuGlnMet 381

QY 13272 TCCAAATTGAACAATGAGTGAATTTCA---GTAATCTTATCATCAGAAACCTCAT 13328
DB 382 AsnGlnLeuIleuSerGluLeuSerIleValAlaGluMetThrGlnMetIleSerLeuGln 401
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DB 402 GlnLeuAspIleSer-----GlnAsnSerValSerTrpAspGluIleValIleAspCys 419
QY 13380 AATGGCTTTCGACGTCGAAAGCTTGAAGAAATGCGTGGCAATCTTTCAGGAAACCTTC 13439
DB 420 SerTrpThrIleSerIleuSerIleuSerIleuAsnMetSerAsnIleLeuThrAspThrIle 439
QY 13440 -----CTTCCAGATATCTTCAAGAGCTGAGAAACTTGAACCTTCTGAGCTCTCT 13490
DB 440 PheArgCysLeuProPro-----ArgIleIleValIleuAspLeuHis 453
QY 13491 CAGTGTCACTGACAGCAATTTGCTCCAAAGCAATTAATCACTTCCAGCTTTCAGAGTA 13550
DB 454 SerAsnIleIleuSerIle-----ProIleGlnValIleValIleuGlnIleValGlnIle 472
QY 13551 CTTAATATGACCAACAACAACTTTTCACTTGGATACCTTCT-----TAT 13598
DB 473 LeuAsnValAlaPheAsn-----SerLeuThrAspLeuProGluCysGlySerPhe 489
QY 13599 AAGTGTCAACTCCCTCCAGGTTCTTGATTAACAGTCTCATCATCAATAGACTTCCAA 13658
DB 490 SerSerLeuSerValIleuIleIleAspHisAsnSerValSerHisProSerAlaAspPhe 509
QY 13659 AAAAGAACTACAGCAATTTTCCAGTACTGTATTTCTTAATCTTACTCAGAAATGAC 13718
DB 510 PheGlnSerCysGlnIleuSerMetArgSer-----IleValAlaGluAspAsnPro 525
QY 13719 TTTGCTTGTATCTTGAACCAAGATTTCTTCCATGATCAAGACCAAGGCGCTC 13778
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QY 13779 TTGGTGAAGTT-----GAACGAATGAAATGTGCAACACCTTCAGATTAAG 13823
DB 543 SerSerGlnValIleuGlnIleuGlnTrpProAspSerTrpIleCysAspTrpProGluSerTrp 562
QY 13824 CAGGSC-----ATGCTGTGCTGAGTTTGAATATCATCCTTCAG 13862
DB 563 ArgGluThrLeuLeuIleuIleAspPheHisMetSerGlnLeuSerCysAsnIleThrLeuLeu 582
QY 13863 ATGAATTAAGACATCATGTGTGTGTGCTGCTTCAAGTGTGTTAGATGTGTTTGAAGA 13922
DB 583 IleValThrIleValAlaThrMetLeuValIleValThrValThrIleSerIleCysIle 602
QY 13923 GTTCTGTATTAAGTCTATATTTCACCTGATGCTTCTTCTGCTGCTGCATTAAGTATGT 13982
DB 603 TrpLeuAspLeuProTrpTrpIleuArg---MetValCysGlnTrpHisGlnThrArgArg 621
QY 13983 AGAGTGAAATCATC-----TATGATGCGCTTTTGT 14012
DB 622 ArgAlaArgAsnIleProLeuGlnIleuGlnIleuGlnArgAsnLeuGlnPheHisAlaPheIle 641
QY 14013 ATCTACTCAAGCAGATGAGACTGGTGAAGAAAGAGCTTAAGAAATTAAGAA--- 14069
DB 642 SerTrpSerGluHisAspSerPheTrpValIleValAsnGlnIleuLeuProAsnLeuGlnIle 661
QY 14070 GAAGGGGTGCTTCATTTCAAGCTGCTGCTTCACTAAGAGACTTTATCCCGGTGGGCC 14129
DB 662 GlnGluMet-----GlnIleCysLeuHisGlnIleuArgAsnIleValProGluIlySer 678
QY 14130 ATTGCTGCACAACTCATCATGATGAAGTTTCCATTAAGCGGAAAGTATGTTGTGTGGT 14189
DB 679 IleValGlnAsnIleIle---ThrCysIleGlnIleuSerTrpIleSerIlePheValLeu 697
QY 14190 TCCAGACATTCATCCAGAGCGCTGTATGTTTGAATATGAAATGCTCAGACACTGG 14249
DB 698 SerProAsnPheValGlnIleSerGlnTrpCysHisIleuIleuIleuTrpPheHisAsnIleAsn 717
QY 14250 CAGTTTCTGAGCAGTGTGCTGATCATCTTCAATGTCTGCGAAGGTC---GAGAG 14306


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QY 13389 -----TCCAGTCTGAGAGTCTTGAAGAAAGTGGCAATTC 13424
Db 636 AenCyshIsvAlaRgThrTyAspIlyeValleuValIleAenCyshIseRglYasnIle 655
QY 13425 TTCACGAGAAACCTTCCTCCGATATCTTCACAGAGCTGAGAACTTGACCTTCCTGAC 13484
Db 656 ThrHsValProArGleuProAsnIleHis-----LysAsnMetGlnLeuMetGln 672
QY 13485 CTC-----TTCAGTGTCACTGGAGAGCTGTTGCTCCACAGACATTAAC 13529
Db 673 LeuHsIleuGluAenAenThrLeuLeuArGleuProSerAlaAenThrProGlyTyGlu 692
QY 13530 TCACTCCGACTTCCTGAGTACTAATATGAGCAACAATCTTTTCAATGATAGC 13589
Db 693 SerValThrSer-----LeuHsIleuAglYasnAenLeuThrSerIleAspVal 709
QY 13590 -----TTCTCTTAAGTGTCTGAACCTCCCTCCAGGTTTGTATATACAGTCAATCAC 13643
Db 710 AspGlnLeuPro-----ThrAsnLeuThrHsIleuAspIleSerTrpAsnHs 725
QY 13644 ATAAAGACTCCCAAAAAACAGAACTACAGCATTTCCAGTACTGTTCTTAAT 13703
Db 726 Leu-----GlnMetLeuAsn-----AlaThrValLeuGlyPheLeuAsn 738
QY 13704 -----CTTACTGAGATGACTTGTGCTGTGACTTGTGAA 13736
Db 739 ArgThrMetLysTrpArgSerValIlyeLeuSerGlyAsnProTrpMetCysAspCysThr 758
QY 13737 CACCAAGGTTTCTCGCATGATCAAGACAGGAGGAGCTTTGGTGGAACTTGAACGA 13796
Db 759 AlaLysPheLeuLeuPheThrGlnAspAsnPheGlnArgIleGlyAspArgAsnGlu 778
QY 13797 ATGGAATGTGCAACACCTTCAGATAGAGGAGGAGCTGCTGAGTGTGAATATACAC 13856
Db 779 MetMetCysValAsnAlaGluMetProThrArgMetValGluLeuSerThrAsnAspIle 798
QY 13857 TGTCAATGATAGAACCATC--ATTGCTGTGTGGTC-----CTCAGTGTGCTT 13904
Db 799 CysProAglGluYasnGlyValPheIleAlaLeuAlaValIleAlaLeuThrGlyLeu 818
QY 13905 GTAGTATCTGTGAGAGTCTGTGCTATTAAGTTC----- 13940
Db 819 LeuAglPheThrAlaAlaLeuTyTrpLysPheGlnThrGlnIleLysIleTrpLeu 838
QY 13941 TATTTACCTGAGTCTTCTGCTGGCTGATAAAGATGAGGATGAAATC-- 13997
Db 839 TyrAlaHsIleAsnLeuLeu-----TrpPheValThrGluGluAspLeuAsp 854
QY 13998 -----TATGATGCTTGTATATCTACTCAAGCAAGATGAGATGAG 14045
Db 855 LysAspLysLysPheAspAlaPheIleSerTySerHsIlyAspGlnSerPheIleGlu 874
QY 14046 AATGAGCTAGTAAAGATTTGAAGAAAGGGAGGCTCCATTTACGCTGTGCTCACTAC 14105
Db 875 AspTyLeuValProGlnLeuGlnHsIleGlyProGlnLysPheGlnLeuCysValHsIleGlu 894
QY 14106 AGAGACTTATCCCGGTGGTGGCCATGCTGSCCAACATCATGAAAGTTTCCATAAA 14165
Db 895 ArgAspTrpLeuValGlyGlyHsIleProGlnAsnIleMet--ArgSerValAlaAsp 913
QY 14166 AGCGGAAGGTGATTTGTGTGTGTCTCCACAGACTTCACAGACCGCTGTGATCTTT 14225
Db 914 SerArgArgThrIleIleValleuSerGlnAsnPheIleLysSerGluTrpAlaAspLeu 933
QY 14226 GAATATGATTTGCTCAGACCTGGCACTTTCTGACAGCTGTGCTGTATCATTTCAAT 14285
Db 934 GluPheArgAlaAlaHsIArgSerAlaLeuAsnGlnLysArgSerArgIleIleValIle 953
QY 14286 GTC-----CTGCAAGAAAGTGGAGAGACCTGCTGAGCAAGGAGGTGAGAGCTAC 14336
Db 954 IleTySerAspIleGlyAspValGlnLys-----LeuAspGlnGluLeuValAlaTy 971
QY 14337 CGCCTTCTCAGCAAGAACCTTAACCTGAGTGGAGAGACAGTCTCTGGGGCGGACATC 14396

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Db 972 -----LeuLysMetAenThrTyLeuTyLeuTrpGlyAspPro-----Trp 984
QY 14397 TTCCTGAGAGACTCCGAAAAAGCCCTGCTGATGCTTAATCATCGAATCCAGAGAGACA 14456
Db 985 PheTrpAspLysLeuAglPheAlaLeuProHsIArgArg-----ProValGlyAsn 1001
QY 14457 GTGGGTACAGCA 14468
Db 1002 IleGlyAsnGly 1005

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Elton, E.; Kooyer, S.; D'aveylyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Beilen, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking siml.
A:Reference number: 217796; MUID:95324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <ELD>
A:Cross-references: UNIPROT:Q24591; EMBL:L21171; NID:g415682; PID:g1019104; PIDN:AAA792;
C:Genetics:
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Alignment Scores:
Pred. No.: 9,85e-24 Length: 1389
Score: 389.00 Matches: 222
Percent Similarity: 38.28% Conservative: 139
Best Local Similarity: 23.54% Mismatches: 363
Query Match: 1.18% Indels: 219
DB: Gaps: 38

US-09-396-985b-47 (1-18989) x T13852 (1-1389)
QY 12065 GGGCTTCTTATTTGCTTATTTCCATCATCATCTGTCTCTTGAATGCTTTCCTATGAC 12124
Db 301 GlyLeuLeu-----HsIArgLeuGlnGlnLeuLeuValleuAspLeuSer 315
QY 12125 ---AATCATATGACCCATCATCATCTGTATGAAAGCTGATGACTAGATTAATA----- 12176
Db 316 GlyAsnGlnLeuThrSerHsIleValAspAsnSerThrPheAla-GlyLeuIleArgLe 335
QY 12176 ----- 12176
Db 335 uIleValleuAsnLeuSerHsAsnAlaLeuThrArgIleGlySerLysThrPheLysGlu 355
QY 12177 ---TCTATTTAGGTTCTTATTCAGCAGAAATATTAGATTAATCAATGCTTTTATTC 12232
Db 355 uLeuTyPheLeuGlnIleLeuAspMetArgAsn----- 366
QY 12233 CTGTAGTGTGAATTCACAGACATTTGAAGATGGGGCATATCAGAGCTTAAGCCACTTC 12292
Db 367 -----AsnSerIleGlyHsIleIleGlnGlnGlyAlaPheLeuProLeuTyTrpAsnLeuHsI 384
QY 12293 TACCTTAATATTGACAGAAACCCATCCAGATTTAGCCCTGAGAGCTTTTCTGACT 12352
Db 384 eThrLeuAsnLeuAlaGluAsnArgLeuHsIThrLeuAspAsnArgIlePheAsnGlyLe 404
QY 12353 ATCAAGTTTACAGAGCTGTGCTGTGAGACAAATTTAGCATCTTA---GAGAACTT 12409
Db 404 uTyValleuThrLysLeu---ThrLeuAsnAenLeuValSerIleValGlnSerGlu 423
QY 12410 CCCCATGAGCATCTCAAAAACCTTGAAGAAGACTTAATGTGGCTCACAATCTTATCCAATC 12469
Db 423 nAlaPheArgAsnCysSerAspLysGlnLeuAspLeuSerSerAsn---GlnIle 441
QY 12470 TTTCAATTATTCAGTATATTTTCTAATCTGACCAATCTAGACACTTGACCTTCCAG 12529

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[illegible][illegible]

QY 14315 CAGGACAGGTGAGCTGTACCGCTTTCAGCAGAACTTACCTGAGTGGAGGA 14374
 Db 1143 lserAlaGluAlaGluAspValAlaGluLeuSer-----ProTyrLeuS----- 1158
 QY 14375 CAGTGTCTGGGGCGGCAGATC-----TTTGGAGACGACTCGAAGA 14416
 Db 1159 -SerValProSerAsnArgLeuThrCysAspArgTyrPheTrpGluTyrSLeuArgTyr 1178
 QY 14417 AGCCCTG 14423
 Db 1178 rAlaIle 1180
 RESULT 5
 T13887
 Clr protein - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T13887
 R/Chiang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A/Title: Expression of a novel Toll-like gene spans the parasegment boundary and controls
 A/Reference number: Z17805; MUID:95151581; PMID:7848870
 A/Accession: T13887
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1385 <CHI>
 A/Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AA83383
 C/GeneticB:
 A/Cross-references: FlyBase:FBgn0004364
 A/Note: Clr
 Alignment Scores:
 Pred. No.: 1 01e-22 Length: 1385
 Score: 377.00 Matches: 218
 Percent Similarity: 37.96% Conservative: 140
 Best Local Similarity: 23.12% Mismatches: 366
 Query Match: 1.14% Indels: 219
 DB: 2 Gaps: 37
 US-09-396-985b-47 (1-18989) x T13887 (1-1385)
 QY 12065 GGGCTTCTTATTTGCTTATTCATCATCTGTCTGCTGATGCTTTGCCATAC 12124
 Db 301 GlyLeuLeu-----HisArgLeuGluGluLeuLeuValLeuAspLeuSer 315
 QY 12125 ---ATCATATGACCCATCATCATCTGTATGAGAGCTGAGTACTAGATTAATA----- 12176
 Db 316 GlyAsnGluLeuThrAspHisValAspAsnSerThrPheAla-GlyLeuIleArgLe 335
 QY 12176 ----- 12176
 Db 335 uIlleValLeuAsnLeuSerAsnAsnAlaLeuThrArgIleGlySerIleThrPheArgI 355
 QY 12177 ---TTCTATTTTATGCTTCTTATTCAGAGAAATATAGATTAATCAATGCTTTTATTC 12232
 Db 355 uLeuTyrPheLeuGlnIleLeuAspMetArgAsn----- 366
 QY 12233 CTGTAGGTGTAATTCAGACATTTGAAGATGGGGCATATCAGAGCTTAAGCCACTTC 12292
 Db 367 -----AsnSerIleGlyHisIleGluGluGlyAlaPheLeuProLeuTyrAsnLeuH 384
 QY 12293 TACCTTAATTTGACAGGAACCCCATCCAGAGTTTACCTGGAGACCTTTCTGACT 12352
 Db 384 strIleuAsnLeuAlaGluAsnArgLeuHisThrLeuAspAsnArgIlePheAsnArgLe 404
 QY 12353 ATCAAGTTTACAGAGCTGGGTGCTGTGAGACAAATCTAGACTCTA---GAGAATT 12409
 Db 404 uTyrValLeuThrIleValLeu---ThrLeuAsnAsnLeuValSerIleValGluSerG 423
 QY 12410 CCCCATTTGACATCTCAAACTTTGAAGAACTTAATGTGGCTCACAATCTTATTCATC 12469
 Db 423 nAlaPheArgAsnCysSerAspLeuTyrSLeuAspLeuSerSerAsn-----GlnLe 441

QY 12470 TTTCAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTGGACCTTCCAG 12529
 Db 441 uThrGluValProGluAlaIleAlaGluAspLeuSerMetLeuLeuThrIleuAspLeuGlyG 461
 QY 12530 CAACAGATTCAAGATTTATTTATTCACAGACTTGGGGTTCTACATCAATGCCCTACT 12589
 Db 461 uAsnGlnIleSerGluPheLeuAsnAsnThrPheArgAsnLeuAsnGlnIleuThrGlyLe 481
 QY 12590 CAATCTC----- 12596
 Db 481 uArgLeuIleAspAsnArgIleGlyAsnIleThrValGlyMetPheGlnAspLeuProAr 501
 QY 12597 -----TCTTACCTGCTGCTGACAGCCCTGACACTTATTCACAGCTGACTT-- 12647
 Db 501 gLeuSerValLeuAsnLeuAlaGluAsnArgIleGlnSerIleGluArgIleAlaPheAs 521
 QY 12648 -AAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATTAATTGATGATTAATGTAAT 12706
 Db 521 pLysAsnThrGluIleGluAlaIleArgLeuAspLysLeuPhe----- 535
 QY 12707 GAAACCTGTATTCAGAGCTGCTGCTGTTTGAAGTCCATCGTTGGTTCGGAGAAAT 12766
 Db 536 -LeuThrAspIleAsnGlyIlePheAlaThrLeuAlaSerLeuLeuThrLeuAsnLeuSe 555
 QY 12767 TAGAAATGAA-----GAAACTTGGAAAGTTTGA 12796
 Db 555 rGluAsnHisLeuValThrPheAspTyrAlaPheIleProSerAsnLeuTyrTrpLeuAs 575
 QY 12797 C-----AAATCTGCTGTAGAGGCTGTGCAATTGG-----ACCATTAAGAAATTCG 12844
 Db 575 pIleHisGlyAsnTyrIleGluAlaLeuGluAsnTyrTyrLeuLeuGlnGluIleAr 595
 QY 12845 ATTAGCATCTTATGACTACTACCTCCATGATATTTATGACTTATTTAATGTTTGACAAA 12904
 Db 595 gValIThrThrLeuAspAlaSerHisAsnArgIleIleGluIle---GlyAlaMetSerVa 614
 QY 12905 TGTTTCTCATTTTCCCTGGAGTGGAGTACTATGAAAGGTAAGAACTTCTTTCTTAA 12964
 Db 614 lProAsnSerIleGluLeuLeuPheIleAsnAsnAsnIleIleGlyGlnIleGlnAlaAs 634
 QY 12965 T-----TTGAGATGGCAACTTGAATTAAGTAACTGTAATTTGAGACATTTCCAC 13018
 Db 634 lThrThrPheValAspLysThrArgLeuAlaArgValAspLeuTyrAlaAsnValLeuSerLy 654
 QY 13019 ATTGAAATCAAAATCTCTCAAAAGGCTTACTTTCATCCAAACA----- 13064
 Db 654 sIleSerLeuAsnAlaLeuArgValAlaProValIleValGluIleProValProGluPh 674
 QY 13065 -----GGTGGAAATGCTTTTCA----- 13082
 Db 674 eTyrLeuGlyGlyAsnProPheGluCysAspCysSerMetGluTrpLeuGlnArgIleAs 694
 QY 13083 -----GAAGTTGATCTCAAGCCCTGAGTTTCTA-- 13112
 Db 694 nAsnLeuThrThrArgGlnHisProHisValValAspLeuGlyAsnIleGluCysLeuMe 714
 QY 13113 -----GATCTCAAGAAATGCGCTTGAG 13135
 Db 714 cProHisSerArgSerAlaProLeuArgProLeuAlaSerLeuSerAlaSerAspPheVa 734
 QY 13136 TTTCAAA-----GGTGGTGTCTCAAGATGATTTTGG 13168
 Db 734 lCysLysTyrGluSerHisCysAspProThrCysHisCysGluTyrGluGlnCysG 754
 QY 13169 GACAAACAGCCTTAAGATTTAGATCTGAGCTTCAATGGGTGTTATTCACATGAGTTCAAA 13228
 Db 754 uCysGluValIleCysValroGlyAsnCysSerCysPheHisAspAlaThrTrpAlaPheAs 774
 QY 13229 CTTCCTG-----GCTTGAACAATGAAATCTGGAATTTCCAGCATTCGAATTTGAA 13282
 Db 774 nIleValAspCysGlyArgGlnAspLeuAlaIleu-----ProAsnArgIle 790

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QY 13283 ACAATGAGTAGTTTTCAGTATTCCTATCATCAGAAACCTCATTTACCTTGACATTC 13342
      |||:|||||
      790 eProglInAspValSerAspLeuYrLeuAspRglValAsnAsnMetProgluLeuGluValG1 810
QY 13343 TCATPACTACACAGAGAGTTCTTCAATGGCATCTTCAATGGCTTGCTCCAGTCTCGAAGT 13402
      |||:|||||
      810 yH1LeuThrGlyArgAsnLeuValG1ValLeuYrLeuAsnAlaSerAsnLeuMetL1 830
QY 13403 CTGGAAAATGGCTGGCAATCTTCCAGAAAACCTTCCTCCAGATCTTCCACAGAGCT 13462
      |||:|||||
      830 rLeuGlnAsnGlySer-----LeuAlaGlnLe 839
QY 13463 GAGAACTTGACCTTCCCTGAGACCTTCTCAGTGTCAATGACAGAGAGTTGTCTCCAAAGC 13522
      |||:|||||
      839 uValAsnLeuArgValLeuHisLeuGluuAsnLeuValLeuThrAlaLeuGluGluYrH1G1 859
QY 13523 ATTTAACTCACTCCAGTCTTCAAGGTATTAATATGACGCAACAATCTTTTCATT 13582
      |||:|||||
      859 uPheArgSerLeuGlyLeuLeuArgGluLeuYrLeuHisAsnAsnMetLeuThrHis11 879
QY 13583 GGATACGTTCTTATAGTGTGAGTCCCTCCAGAGTTCTGATACAGTCCATCA 13642
      |||:|||||
      879 eSerAsnAlaThrPheGluProLeuValSerLeuGluValLeuArgLeuAspAsnAr 899
QY 13643 CATATGACTTCCAAAAACAGAACTACATATTTCCAAAGTACTGACTTCTTCAAA 13702
      |||:|||||
      899 gLeuSerSerLeuProHisLeuGluYrArgHis-----SerLeuGlnGlyLeuTh 916
QY 13703 TCTTACTCAGATGACTTTGCTGTTACTTGTGAACAC--CAGAGTTTCTCGACATGAT 13759
      |||:|||||
      916 rLeuGlyArgAsnAlaThrSerCysArgCysGlnGluLeuArgGluLeuAlaGlnPheVa 936
QY 13760 CAAAGACCAAGGAGAGCTTTGTGGAAGTTGAACGAAGGAAGTGCACACCTTCAGA 13819
      |||:|||||
      936 lSerAspAsnAlaMetValValArgAspAlaHisAspIleYrCysLeuAspAlaGly11 956
QY 13820 TAAGCAGGAGCATGCTGTGCTG----- 13841
      |||:|||||
      956 eLyAspArgGluLeuGluLeuLeuGlyLeuAsnLeuAlaAsnGlyProAspCysSerAspLeuLe 976
QY 13842 -----AGTTGAATATCACCTGTGCAGATGAAT-----AA 13870
      |||:|||||
      976 uAspAlaSerAlaSerAsnIleSerSerSerGlnAspLeuAlaGlyGlyYrArgLeuPr 996
QY 13871 GACCATCATGTCGTGTCGCTGCGCTCAGTGTCTTGTAATCTGTAGACAGTTCGTG 13930
      |||:|||||
      996 oLeuLeuAlaAlaValLeuValLeuIlePheLeuAspValValLeuIleIleValPheVa 1016
QY 13931 CTATTAAGTTCTATTTTCACTGATGTTCTTGTGCTGTCGTCATTAAGTATGCT 13982
      |||:|||||
      1016 lPheArgGlnSerValArgMetTrpLeuPheAla-----HisYrGlyValArgVa 1033
QY 13983 -----AGAGGTGAAAAC-----ATCTATGATGCCCTTTGATCTACAG 14023
      |||:|||||
      1033 lCysGluProArgPheGluAspAlaGlyLyLeuYrAspAlaIleIleLeuHisSerG1 1053
QY 14024 CCGAGTAGAGAGACGTGGTAAGGATGAGCTTGAAGATTTAGAAGAGGGGCTCC 14083
      |||:|||||
      1053 uLyAspYrGluuPheValCysArgAsnIleAlaGluLeuGluHisGlyArgPropR 1073
QY 14084 ATTTACACTCTGCTTCACTACATCAGAGACTTTATTCGCGTGTGSCCATTTGCTGCAACAT 14143
      |||:|||||
      1073 oPheArgLeuCysIleGlnGlnArgArp---LeuProProGlnAlaSerHisLeuGlnLe 1092
QY 14144 CATCCATGAAGGTTTCCATTAAGCCGAAGAGTATGTTGTGTCGCCAGCATTTCAT 14203
      |||:|||||
      1092 uVal---GluGlyAlaArgAlaSerArgLyIleIleLeuValLeuThrArgAsnLeuLe 1111
QY 14204 CCAAGACCGCTGTGTATCTTTGAATATGAGATTTGCTCAGACCTGGCAGTTTCGAGAG 14263
      |||:|||||
      1111 uAlaThrGluThrAspAsnArgIleGluPheArgAsnAla-----PheHisGluSe 1127
QY 14264 TCGTGTGTGATCATCTTCATTTGCTGTCGACAGAG-----GTGAGAAAGACCTGTCT 14314
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Db 1127 rLeuArgGlyLeu-----AlaGlnLyLeuValIleIleGluGluThrSerVa 1143
QY 14315 CAGGACGAGAGGTGGAGCTGTACCGCTTCTCAGACGAGAACTATTCGAGTGGAGGA 14374
      |||:|||||
      1143 lSerAlaGluAlaGluAspValAlaGluLeuSer-----ProYrLeuLyS----- 1158
QY 14375 CAGTGTCTGTGGGCGGCAGCATC-----TTCTGAGACGACTCAGAAA 14416
      |||:|||||
      1159 -SerValProSerAsnArgLeuLeuThrCysAspArgYrPheTrpGluLyLeuArgYr 1178
QY 14417 AGCCTTG 14423
      |||:|||||
      Db 1178 rAlaIle 1180

RESULT 6
B34087
hypothetical protein (L1H 3' region) - human
C/Species: Homo sapiens (man)
C/Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C/Accession: B34087
R/Scott, A.F.; Schmeckeeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rosolter, J
Genomics 1, 113-125, 1987
A/Title: Origin of the human L1 elements: proposed progenitor genes deduced from a cons
A/Reference number: A34087; PMID:88085185; PMID:3692483
A/Accession: B34087
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-1280 <SCD>
A/Cross-references: UNIPROT:Q9Y5K0
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 2 66e-21 Length: 1280
Score: 360.00 Matches: 70
Percent Similarity: 64.67% Conservative: 27
Best Local Similarity: 46.67% Mismatches: 53
Query Match: 1.09% Indels: 1
DB: 2 Gaps: 0

US-09-396-985b-47 (1-18989) x B34087 (1-1280)
QY 2697 AGACGAAAGATATATATAGTGTGTAAGTGAAGTGAAGAACTCCTGATCAC 2756
      |||:|||||
      1128 LyLySerSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1147
QY 2757 CATTGTGGAAATGTAATATGTATACAGATCTGTGGAAATCTATATGCTGGCTCAAA 2816
      |||:|||||
      1148 CysTrpTrpAspCysLySLeuValGlnProLeuTrpLyThrValTrpArgPheLeuLyS 1167
QY 2817 AAATTAATAATATGATTTTACACATGATCCAGAACTCACTTCTGAGTACGATCCAAA 2876
      |||:|||||
      1168 AspLeuGluLeuGluIleProPheAspProAlaIleProLeuLeuGlyIleYrProLyS 1187
QY 2877 GAATTAAGAAACAGAGACTTTAAGATATTTGTACAAACATGTTTATGGCAGATTAATC 2936
      |||:|||||
      1188 AspYrLySerCysCysYrLyAspTrpCysThrArgMetPheIleAlaLeuPhe 1207
QY 2937 ACAATAGCTTACGCTGTGGCAACAATGCAAGTGTCCATGAACAGACAAATGATTAAGCAA 2996
      |||:|||||
      1208 ThrIleAlaYsThrTrpAsnGlnProLyCysProSerMetIleAspTrpIleLyLyS 1227
QY 2997 ATGTGCTATACATCAATGAATATTTGTCAGCTTTAAAGAAAGAGGCTTGATC 3056
      |||:|||||
      1228 MetTrpHisIleYrThrMetGluYrYrAlaAlaIleLyAsnAspGluPheMetSer 1247
QY 3057 TATATACACACAGAAAGAACTTGAAGACATTATGAAATTAATAGCCAGTGAACA 3115
      |||:|||||
      1248 PheValGlyThrTrpMetCysLeuGluThrIleIleLeuSerLySLeuSerGlnGlyGln 1267
QY 3116 AAAGATACATACGTATGATTCACATTCTA 3145
      |||:|||||
      Db 1268 LyThrLyHisIleArgMetPheSerLeuIle 1277
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RESULT 7

US-09-396-985B-47 (1-18989) x S23650 (1-712)

Cited as: retrovirus-related hypothetical protein II - human retrotransposon LINE-1
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
A:Accession: M23650
R:Hohjoh, H.; Minakami, R.; Sakaki, Y.
Nucleic Acids Res. 18, 4099-4104, 1990
A>Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences which
A:Reference number: S23649; MUID:90332398; PMID:2165587
A:Accession: S23650
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-712 <HOh>

A:Cross-references: UNIPROT:Q15604, UNIPROT:O9UN80, UNIPROT:Q12881, UNIPROT:O00363, UNIPROT:Q14754, UNIPROT:O9Y5K0, UNIPROT:O00366, UNIPROT:Q8TE30, UNIPROT:O00375, EMBL:X52235
P:Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1990
C:Genetics:
A:Mobile element: LINE-1
A:start codon: GTG
C:Superfamily: pol polyprotein

Alignment Scores:

Pred. No.:	6.07e-21	Length:	712
Percent Similarity:	35.00	Matches:	69
Best Local Similarity:	46.00%	Conservative:	28
Diversity Match:	1.07%	Mismatches:	53
	2	Indels:	1
	Gaps:		0

Db

Oy 2697 AGACCGAAATAATTAAGTGTGGGAAGATGTGAAAAATAGAAAATTCTTGTCATAC 2756
::: ||||| :::: |::| :||| :||| :||
560 lylsysserglyaaenlaerxgcystrparqglycsglygiullleglythrleulehdls 579
2757 CATTGTGGGAATGTAAATAGTACAGATGCTGTGAGAATCATATGATGGTGGTCTCAA 2816
||||| :::::: ::::| ::::| ::::| ::::|
580 cystriprrparpcyblyvalaulvalglrproleutrlpybservaltlrpargphleuarlg 599
Dl 2817 AAATTTAAATAGATTATTCACATGATCCAGCAATCTTCACCTTGACTAGATCCAAA 2876
::: ::::| ::::| ::::| ::::| ::::|
600 Aspleugluiprogguilleprropheaspprolalleprroleuulgilyletyprrplys 619
Oy 2877 GAATTGAAAAAGAGACTTTAAGAGATATTGTACAACAGTTTATGGAGCATTTATTC 2936
::: ||||| ::::| ::::| ::::| ::::| ::::|
620 Asperlysrseryscysetyrllysaprhrctyethrmgtmetpheilealaaleuphe 639
Db 2937 ACATTAGCTACGTCGTGCACACATGCAAGTGTCCATGAACAGACAATGGATPAAGCAA 2996
||||| ||| ||| ||||| ||| ||||| |||
640 ThrlleaialaystnrtpasnglnProlyesyrrohmrtlleaprtlllelyls 659
Oy 2997 ATGTGCTGTATACATACATGSAATVATTGTTCAGCTTTAAAAAGAAAGAGCGTTGATC 3056
||||| :::::: ::::| ::::| ::::| ::::|
660 MettrphisilietythrmerglutytyzmlaalielelysaanaerpGlupheValser 679
Oy 3057 TATATCAC-AAGAGAAAAGAACCTTGAGAGCACTTATGCAATGMAATGAATAGCCATGACAA 3115
::: ||||| ||||| ||||| ::::| ::::| ::::| ::::|
680 Phevalgluytrrmpetmelyslengullellelleuleuserylseuserginglughn 699
Db 3116 AAGATACATACCTGATGATTCACCTTCTA 3145
||| ::::| ::::| |||||
700 Lythrlyshisicysliepherterleuille 709

RESULT 8

T13864
hypothetical protein C56B6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13864
R:Pultom, L.

Submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C56B6.
A:Reference number: S69019
A:Accession: T15864
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1066 <FRL>
A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA81
C:Genetics:
A:Gene: CESP:C56B6.6
A:Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3;

Alignment Scores:

Pred. NO.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.6e-20	348.00	43.64%	26.57%	1.05%	1066	140	90	205	92	22

US-09-396-985B-47 (1-18989) x T15864 (1-1066)

OY 12243 GAATTCAGACAAATTGGAAGATGGGCGCATATCAGAGCCCTTACGCCACTCTTACCTTAATA 12302
:::|||||:::|||||:::|||||:::|||||
Db 179 Glnlleglnlrvalgluaspserspheglnlrhvalglghlsmeeglnserleuasp 198
OY 12303 TTGCAGGAACCCCACATCAGAGTTTAGCCCTGGGAGGCTTTTGACGTATCAAGTTTA 12362
|||:::|||||:::|||||
Db 199 Leusertyrhnaaglllealrtytleuproargly----- 210
OY 12363 CAGAAGCTGTGGCTGTGGAGACAATCTTACATCTCTAGAGAACTTCCCATTTGGACAT 12422
|||:::|||||
Db 211 -----Metleuylsrnph----- 215
OY 12423 CTCAAAATTGGAAGAATTAAATGTGGCTCACATCTTATCCATCTTTCAAATTACT 12482
|||||:::|||||:::|||||:::|||||
Db 216 Alalystrleuylstrhleuylaelgluasnetllehsala----ThirPro 233
OY 12483 GAGTATTTTTCTATATGACCACATCTAGACACTTGACACTTTCACAGAACAAAGTTGAA 12542
|||||:::|||||:::|||||:::|||||
Db 234 Glualaleuarglauleuarxasnhleuthrlshleuanleuanlglyashnyleuan 253
OY 12543 AGTATT-----TATTGCACAGACTTGGCGTTCTACATCAAAATGCC 12584
|||:::|||||
Db 254 Argllleaprglyaservalleunlyegllycysrhrrspthrleuval----- 268
OY 12585 CTACTCATCTCTCTTAAAGACTGTCCCTGAACCTTAAGAACTTATCCACACAGTGA 12644
|||:::|||||:::|||||
Db 269 -----Gluleupheillealasnbnayrleugluhnsilerprohisglyal 284
OY 12645 TTTAAGAAATTTAGGCTTCATPACGTGACTTAAAGAAATTAATTTGATGAGTTTAATGTA 12704
|||:::|||||
Db 285 leusertglymetlys-----Glnleugluhnieuanprlle 296
OY 12705 ATGAAAATTGATATCAAGGTCTGGCTGTTTGAAGTCCATCGTTGGTCTGGAGAA 12764
|||:::|||||
Db 297 Serlyrsenlyslilemetsereu----- 304
OY 12765 TTTGAAATGGAAGAACTTGGAAAAAGTTTGACAAATCTGCTAGAGAGGCTGTGCAT 12824
|||:::|||||
Db 305 ---lysyprorhrrserleuenseerlleThrlysglugluhrserThrValarArg 323
OY 12825 TTGCACATTTGAAGATTTCCGATAGCATACTTAACTACTACCTCGATGATATTTATGAC 12884
|||:::|||||:::|||||
Db 324 leuansneulanlaglyasnargllleasnbnsetserhapryga-----Ilephedgu 341
OY 12885 TTATTTAATTGTTGACAAATGTTTCT---TCATTTTCCCTGGAGGTGACTATTTGAA 12941
|||:::|||||
Db 342 HiswetrProleueneutrhyrvalaspyalserspheasnargllleargpheilleserPro 361
OY 12942 AGGTTAAAGACTTTTCTTATTTTTCGAGATGGCAATTTAGAAATTTGTTAACTGTAA 13001
|||||:::|||||:::|||||
Db 362 ArgylaRhegulyrseulyrsenleu-----Gluaserleupheleughnasbnancln 379


```
QY 13002 TTGGACAGTTTCCCATGTTG---AAATCAAAATCTCTCAAAAGGCTTACTTTCACCTTCC 13058
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 380 LeuAlaHisPheProSerLeuPheArgLeuArgHisLeuArgHisLeuMetLeuAspAsn 399
QY 13059 AAC-----AAAGTGGGAATGCTTTTTCAGAACTGATATACCAAGCTTGAAGTTT 13109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 400 AsnGlnIleGlnHisLeuAspAsn---PheSerLeuAlaAspLeuProLysLeuGlnHis 418
QY 13110 CTGATCTGCAATGAATGCTTGAAGTTCAGTTGCTGCTTCTCAAAAGTATTTGGG 13169
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 419 LeuSerLeuAlaGlnAsnGlnLeuAspIle-----IleThrGlnAsnMetPheGly 435
QY 13170 ACAACACGAC-----CTAAAGTATTAGATCTGACGTTCAATGCTGTATTAATACATG 13220
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 436 SerSerSerSerSerGlnLeuLysSerLeuAsnLeuAlaHisAsnLysIleHisSerIle 455
QY 13221 AGTTCA--AACTTCTTGCGGCTTAGAACAATAGACATCTGATTTCCAGCATTTCAAT 13277
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 456 SerSerArgSerPheSerAspLeuAspAsnLeuGlnGlnLeuArgLeuSerHisAsnAsn 475
QY 13278 TTGAAACAAATGAGTGAAGTTTTCAGTATCTCTATCATCTCAGAAACCTTACCTTAC 13337
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 476 IleArgThrIleThrSerMetThr---PheSerAsnLeuArgAsnLeuArgLysLeuAsp 494
QY 13338 ATTTCTCATCTACACACAGAGTTGCTTTCATGAGCATCTTCAATGCGCTTGTCCAGTCTC 13397
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 495 LeuSerHisAsnArgIleIleLysIleLeuProSerAlaLeuArgLysLeuProAlaLeu 514
QY 13398 GAACTCTTGAATAATGCGCTGCAATCTTTCCAGAAATCTCTTCCAGATATCTTACA 13457
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 515 AspValIleuHisIleLeuAspHisAsnAsnLeuAsnGlu---IleAspArgAspAlaPheArg 533
QY 13458 GAGCTGAGAAACTTGACCTTCTCGACCTCTCTGACGTGCAAGTGCAGACGAGCTGTCCCA 13517
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 534 SerPheSerAspLeuGlnSerLeuLysLeuSerHisAsnAlaPheArgArgPheSerCys 553
QY 13518 ACAAGCATTTAACTCATCTCTCCAGTCTTCAGGTAATAATAGACCAACAATCTTCTTT 13577
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 554 GluPheLeuGlnSerIleSerGlnValHisGlnLeuAspLeuSerSerAsnGlnIleAsn 573
QY 13578 TCATGGATACGTTTCTTATAGTGTCTG---AACTCCCTCCAGGTTCTTGATTAACAGT 13634
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 574 GluIleAspIlePhe-----CysIleAlaArgGlyIleArgLysLeuSerLeuAla 590
QY 13635 CTCATGACATATGATCTCCAAAAACAGAACTATACAGCTTTTCCAGTATAGTCTAGCT 13694
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 591 SerAsnSerValGlnLysIleAsnArgLysLeuLeuGlnAsp---AlaThrGlnLeuThr 609
QY 13695 TTCTTAATCTTACTCAGAAAT-----GACTTGTGCTTGTACTTGT 13733
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 610 SerIleAspIleSerHisAsnGlyIleIleAspValaAspSerAspAlaPheCysGlnCys 629
QY 13734 GAACACCAAGGTTTCTTGCAA 13754
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 630 ArgLysLeuSerHisIleLys 636
RESULT 9
S65824
reverse transcriptase homolog - human transposon L1.1
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65824
R:Domroski, B.A.
submitted to the EMBL Data Library, January 1992
A:Description: Isolation of an active human transposable element.
A:Reference number: S65823
A:Accession: S65824
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1275 <DOM>
A:Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AAA51622.1; PID:g3397
C:Superfamily: pol polyprotein
```

```
Alignment Scores:
Pred. No.: 3,3e-20 Length: 1275
Score: 347.00 Matches: 68
Percent Similarity: 64.00% Conservative: 28
Best Local Similarity: 45.33% Mismatches: 54
Query Match: 1.05% Indels: 1
DB: 2 Gaps: 0
US-09-396-985b-47 (1-18989) x S65824 (1-1275)
QY 2697 AGACCAAGAAAGTATATATAGTCTTGTAAGATGTGAAAAATGCAACTCTGTACAC 2756
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGlnIleGlyThrLeuLeuHis 1142
QY 2757 CATTTGGGAAGTAAATGAGTACGATGCTGAGATGATCATATAGTGGGTGCTCAAA 2816
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1143 CysTrpTrpAspCysLysLeuValGlnProLeuThrLysSerValThrArgPheLeuArg 1162
QY 2817 AAATTAATAATAGATTATACCATGATCCAGCAATCTCACTTGTGAGTACGATCCAAA 2876
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1163 AspLeuGlnLeuGlnIleProPheAspProAlaIleProLeuLeuGlyIleTyProAsn 1182
QY 2877 GAAATGAACAAGACATTTAGAGATATTGTTCACACCATGTTTATGCGACATTTATTC 2936
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1183 GluTyLysSerCysCysTyLysAspTrpCysThrArgMetPheIleAlaLeuPhe 1202
QY 2937 ACAATGCTTAACGTGTGGCAACAATGCAAGTGTCCATGAAACAGACAAATGATATAGCAA 2996
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1203 ThrIleAlaLysThrTrpAsnGlnProLysCysProThrMetIleAspTrpIleLysLys 1222
QY 2997 ATGTGCTTATATACATCAATGAAATATGTTCTTCACTTTAAAAAGAAAGAGCTTGATC 3056
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1223 MetTrpHisIleTyThrMetGlnTyTyAlaAlaIleLysAsnAspGlnPheIleSer 1242
QY 3057 TATACTAC-ACAGAAAAAACCCTTGAGACATTTATGCAAAAGTAAATAGCCGCTGACAA 3115
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1243 PheValGlyThrTrpMetLysLeuGlnThrIleIleLeuSerLysSerGlnGlnGln 1262
QY 3116 AAAGATACATACGTATGATTCACCTTCA 3145
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1263 LysThrLysHisArgIlePheSerLeuIle 1272
RESULT 10
S21348
probable pol polyprotein-related protein 4 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21348
R:Schmitz, E.; Mohr, E.
submitted to the EMBL Data Library, June 1990
A:Reference number: S21345
A:Accession: S21348
A:Molecule type: DNA
A:Residues: 1-275 <SCH>
A:Cross-references: UNIPROT:Q63306; EMBL:X53581; NID:g56586; PIDN:CAA37647.1; PID:g5659
C:Superfamily: pol polyprotein
C:Keywords: polyprotein
Alignment Scores:
Pred. No.: 2,49e-20 Length: 275
Score: 346.50 Matches: 68
Percent Similarity: 67.81% Conservative: 31
Best Local Similarity: 46.58% Mismatches: 46
Query Match: 1.05% Indels: 2
DB: 2 Gaps: 1
US-09-396-985b-47 (1-18989) x S21348 (1-275)
QY 2709 AATTAATAGTGTGTGTAAGATGTGAAAAATGAGAATCTCTGTACCAATTTGTGGAA 2768
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 AspAsnArgCysTrpArgGlyCysGlyGlnArgGlyThrLeuLeuHisCysTrpTrpAsp 147
QY 2769 TGTAATATGTACAGATGTGTGAGAAATCATATGTGTGGTGTCAAAAATTAATAATA 2828
```

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Db      148 CysylsleuValIglProPheTrpLysSerValITrpArgPheLeuArgLysleuAspIle 167
Qy      2829 GATTACACATGATGCAGCATATCCTCATCTGAGTACGTATCCAAAAGATTGAAAACA 2888
Db      168 GluIleuProGluAspProIalIleProIeuIeuGlyIleTyProIleAspAlaProThr 187
Qy      2889 GAGACTTAAAGATATTGTACCAACCATGTTTATGAGCATTTATTCACATAGCTAAC 2948
Db      188 TyrLys--LysAspThrCysSerThrMetPheIleAlaIleuPheIleIleAlaArg 206
Qy      2949 GTGGGCAACAATGACATGTCATGAAACAGACAAATGATPAGCAAAATGTGCTTATA 3008
Db      207 SerTrpLysGluProArgCysAspSerThrGluGluTrpIleGlnLysMetTrpTyrIle 226
Qy      3009 CATACAAATGAATATTGTTCAGCTTTAAAAAGAAAGAGGCTTGATCTATACACACAG 3068
Db      227 TyrThrMetGluTrpTyrSerAlaIleLysAsnAsnGluPheMetLysPheValGlyLys 246
Qy      3069 AA-AAGAACCTTGAAGACATTTATGCAAAAGTAAATPACCCAGTACAAAAGATTACATAC 3127
Db      247 TrpIeuGluIeuGluAsnIleIleIeuSerLysIeuThrGlnSerGlnLysAspIleHis 266
Qy      3128 TGTAATGATTCACCTTCTA 3145
Db      267 GlyMetHisSerLeuIle 272

```

RESULT 11

```

138588 reverse transcriptase homolog - human retrotransposon L1
N/Alternate names: ORF2 protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I38588
R/Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
A/Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q
A/Reference number: I38587; MUID:95004577; PMID:7920631
A/Accession: I38588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:9483914; PIDN:AAB60345.1; PID:94839
C/Superfamily: pol polypeptide

```

Alignment Scores:

```

Pred. NO.: 4.87e-20 Length: 1275
Score: 345.00 Matches: 67
Percent Similarity: 64.67% Conservative: 30
Best Local Similarity: 44.67% Mismatches: 53
Query Match: 1.04% Indels: 1
DB: 2 Gaps: 0

```

US-09-396-985B-47 (1-18989) x I38588 (1-1275)

```

Qy      2697 AGACCAGAAAGTAAATTAAGTGTGGAAGATGTGAAAAATGAGAACTCTGTACAC 2756
Db      1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1142
Qy      2757 CATTGTGGGAATGTAATAGTACAGATGCTGTGAGAAATCATATGGTGGTCTCAAA 2816
Db      1143 CysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSerValITrpArgPheLeuArg 1162
Qy      2817 AAATTAATAATAGATTATTCACATGATCCAGCATCTTCATCTTGAGAGTACATCCAAA 2876
Db      1163 AspIeuGluIeuGluIleProPheAspProIalIleProIeuIeuGlyIleTyProGln 1182
Qy      2877 GAATTGAAAACAGAGACTTTAAGAGATTTGTACAAACATGTTATGAGAGATTATTC 2936
Db      1183 AspTrpLysSerCysCysTrpLysAspThrCysThrArgMetPheIleAlaIleuPhe 1202
Qy      2937 ACAATAGCTAAAGTGTGCAACATGCAAGTGTCCATGAAACAGAAATGATPAGCAAA 2996

```

```

Db      1203 ThrIleAlaLysThrTrpAsnGlnProLysCysProThrMetIleAspTrpIleLysLys 1222
Qy      2997 ATGTGCTATATACATACAAATGAAATATTGTTACGCTTTAAAAAGAAAGAGCTTTGATC 3056
Db      1223 MetTrpHisIleTyThrMetGluTrpTyrAlaIleLysAsnAspGluPheIleSer 1242
Qy      3057 TATATCTAC-ACAGAAAAGAACTTGAGACATTTATGCAAAATGAAATPAGCCAGTACAA 3115
Db      1243 PheValGlyThrTrpMetLysLeuGluThrIleIleIeuSerLysLeuSerGlnGluGln 1262
Qy      3116 AAAGATACATACCTGTATGATTCACCTTCTA 3145
Db      1263 LysThrLysHisArgIlePheSerLeuIle 1272

```

RESULT 12

```

B28096 line-1 protein ORF2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Accession: B28096
R/Skowronski, J.; Panning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A/Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A/Reference number: A28096; MUID:88246405; PMID:2454389
A/Accession: B28096
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1275 <SKO>
A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:Q00363; UNIPROT:Q9Y5K0; UNIPROT:Q00366; UNIPROT:Q8TB30; UNIPROT:Q00375
C/Superfamily: pol polypeptide

```

Alignment Scores:

```

Pred. NO.: 5.91e-20 Length: 1275
Score: 344.00 Matches: 67
Percent Similarity: 64.00% Conservative: 29
Best Local Similarity: 44.67% Mismatches: 54
Query Match: 1.04% Indels: 1
DB: 2 Gaps: 0

```

US-09-396-985B-47 (1-18989) x B28096 (1-1275)

```

Qy      2697 AGACCAGAAAGTAAATTAAGTGTGGAAGATGTGAAAAATGAGAACTCTGTACAC 2756
Db      1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1142
Qy      2757 CATTGTGGGAATGTAATAGTACAGATGCTGTGAGAAATCATATGGTGGTCTCAAA 2816
Db      1143 CysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSerValITrpArgPheLeuArg 1162
Qy      2817 AAATTAATAATAGATTATTCACATGATCCAGCATCTTCATCTTGAGTACATCCAAA 2876
Db      1163 AspIeuGluIeuGluIleProPheAspProIalIleProIeuIeuGlyIleTyProAsn 1182
Qy      2877 GAATTGAAAACAGAGACTTTAAGAGATTTGTACAAACATGTTATGAGAGATTATTC 2936
Db      1183 AspTrpLysSerCysCysTrpLysAspThrCysThrArgMetPheIleAlaIleuPhe 1202
Qy      2937 ACAATAGCTAAAGTGTGCAACATGCAAGTGTCCATGAAACAGAAATGATPAGCAAA 2996
Db      1203 ThrIleAlaLysThrTrpAsnGlnProLysCysProThrMetIleAspTrpIleLysLys 1222
Qy      2997 ATGTGCTATATACATACAAATGAAATATTGTTACGCTTTAAAAAGAAAGAGCTTTGATC 3056
Db      1223 MetTrpHisIleTyThrMetGluTrpTyrAlaIleLysAsnAspGluPheIleSer 1242
Qy      3057 TATATCTAC-ACAGAAAAGAACTTGAGACATTTATGCAAAATGAAATPAGCCAGTACAA 3115
Db      1243 PheValGlyThrTrpMetLysLeuGluThrIleIleIeuSerLysLeuSerGlnGluGln 1262
Qy      3116 AAAGATACATACCTGTATGATTCACCTTCTA 3145
Db      1263 LysThrLysHisArgIlePheSerLeuIle 1272

```


A:Reference number: A93381; PMID:86230917; PMID:2423883

A:Accession: B25313

A:Status: conceptual translation of pseudogene

A:Molecule type: DNA

A:Residues: 1-1260 <HAT>

A:Cross-references: UNIPROT:P08548

A>Note: This sequence was constructed from an alignment of six sequences, determined by

C:Keywords: reverse transcriptase; pseudogene

Alignment Scores:

Pred. No.:	3,13e-18	Length:	1260
Score:	323.50	Matches:	62
Percent Similarity:	66.67%	Conservative:	28
Best Local Similarity:	45.93%	Mismatches:	44
Query Match:	0.98%	Indels:	2
DB:	4	Gaps:	1

US-09-396-985b-47 (1-18989) x GNLRL1 (1-1260)

```

QY 2709 AATATAAGTGTGTGTAAGATGTGAAAAAATGAGAACTCTGTACACCATTTGTGGGA 2768
    ||| :||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1126 AsnGlnArgCysTrpArgGlyCysGlyGlyLysGlyThrLeuLeuHisCysTrpTrpGln 1145
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2769 TGTAAATGTGACAGAGCTGTGAGAAATCATATGTGGTGTCAAAAAATTAAATA 2828
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1146 CysProLeuIleArgSerPheTrpLysAspValTrpArgIleLeuArgAspLeuIle 1165
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2829 GATTACACATGATCCGACATCTCATCTTGTGAGTACGTATCCAAAAAATGAAACA 2888
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1166 AspLeuProPheAspProIleIleProLeuLeuGlyLeuTyProGluAspGlnLysSer 1185
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    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 2949 GTGTGGCAACATGCAAGTGTCCATGAAACAGACAATGATAGCAAAATGTGCTATA 3008
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1206 SerTrpLysLysProLysCysProSerThrIleGluTrpThrSerLysLeuTrpTyrMet 1225
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QY 3009 CATACATGGAATTTGTTGACGCTTT-AAAAGAAGAGAGGCTTTGATCTATAC--TAC 3064
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1226 TyrThrMetGluTyTyAlaAlaLeuLysLysAspGlyAspPheThrSerPheMetCphe 1245
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3065 ACAGAAAAAGAACTTGAGAGACATTATGCAAGTGAATTAAGCCAG 3109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1246 ThrTrpMetGluLeuGluHisIleLeuLeuSerLysValSerGln 1260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: March 29, 2005, 19:47:42
Job time : 445 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 964.5 Seconds

(without alignments)
20163.549 Million cell updates/sec

Title: US-09-396-985B-47

Perfect score: 33065

Sequence: 1 tccctactcttcacatc.....catgaabdcabdcabdc 18989

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=UniProt_03 -QFMT=fastaan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03: *
1: uniProt_sprot: *
2: uniProt_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3905.5	11.8	839	1	TLR4_HUMAN
2	3891.5	11.8	839	1	TLR4_HUMAN
3	3878.5	11.7	837	2	Q8P5E8
4	3750.5	11.3	828	1	TLR4_PONPY
5	3621.5	11.0	826	1	TLR4_PAPAN
6	2977.5	9.0	843	1	TLR4_HORSE
7	2971.5	9.0	841	1	TLR4_BOVIN
8	2968.5	9.0	841	2	Q8S0S5
9	2966.5	9.0	841	2	Q8WCD5
10	2957.5	8.9	841	2	Q8WCD4
11	2937	8.3	833	1	TLR4_FELICA
12	2867	8.7	841	1	TLR4_PIG
13	2753.5	8.3	839	2	Q8M1Q2
14	2738	8.3	838	1	TLR4_CRIGR
15	2599	7.9	835	2	Q8K2T5
16	2594	7.8	835	1	TLR4_MOUSE

17	2579.5	7.8	835	1	TLR4_RAT
18	2206	6.7	836	2	Q8SOH3
19	1696.5	5.1	843	2	Q7ZTG5
20	1173.5	3.5	819	2	Q6TS41
21	1162.5	3.5	817	2	Q6NV08
22	834.5	2.5	258	2	Q70EK4
23	637.5	1.9	991	2	Q6RSN8
24	626.5	1.9	961	2	Q76CT9
25	620.5	1.9	945	2	Q8T753
26	618.5	1.9	940	2	Q8O1F9
27	618.5	1.9	961	2	Q76CT7
28	595.5	1.8	973	2	Q6KCC7
29	575.5	1.7	785	2	Q76L24
30	571.5	1.7	784	2	Q6YGM2
31	570.5	1.7	784	2	TLR2_MOUSE
32	569.5	1.7	784	2	Q8K3D9
33	566.5	1.7	784	2	Q8L1T5
34	564.5	1.7	785	2	Q6TN21
35	563.5	1.7	781	1	CI80_MOUSE
36	562	1.7	781	1	TL22_CHICK
37	560.5	1.7	784	1	TLR2_HUMAN
38	560.5	1.7	793	1	TL21_CHICK
39	553.5	1.7	784	1	TLR2_CRIGR
40	549	1.7	784	2	Q6T752
41	548.5	1.7	784	1	TLR2_MACFA
42	545.5	1.6	661	2	Q8C251
43	543.5	1.6	785	2	Q889D1
44	543.5	1.6	1032	1	TLR8_MOUSE
45	536	1.6	1050	1	TLR7_MOUSE

ALIGNMENTS

RESULT 1
ID TLR4_HUMAN STANDARD; PRT; 839 AA.
AC 000206; Q9UK78; Q9UW57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll1-like receptor 4 precursor (Toll1).
GN Name=TLR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlbut P., Janeway C.A. Jr.;
RT "A human homologue of the Drosophila Toll protein signals activation
RT of adaptive immunity.";
RL Nature 388:394-397(1997).
RN [2]
RP SEQUENCE OF 41-839 FROM N.A.
RC TISSUE=Fetal liver, Lung, and Placenta;
RA MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RC MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan R.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RC MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;
RA Abour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,

RA Freese K, Mart J.L., Schwartz D.A.;
RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in humans.";
RL Nat. Genet. 25:187-191(2000).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP MUTAGENESIS OF GLU-697; ARG-710; ASP-711 AND PRO-714.
RX MEDLINE=20531768; PubMed=11081516; DOI=10.1038/35040600;
RA Xu Y., Tao X., Shen B., Horig T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domains";
RL Nature 408:111-115(2000).
RN [7]
RP CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
RX MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
RA da Silva Correia J., Ulevitch R.J.;
RT "MD-2 and TLR4 N-linked glycosylations are important for a functional 11polysaccharide receptor.";
RL J. Biol. Chem. 277:1845-1854(2002).
RN [8]
RP VARIANTS ARG-188; SER-246; GLY-299; SER-329; ILE-399; LEU-443;
RX LYS-474; HIS-510; ARG-694; HIS-763 AND HIS-834.
RL MEDLINE=21405531; PubMed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4 in humans.";
RL Genetics 158:1657-1664(2001).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response.
CC -1- SUBUNIT: Belongs to the 11polysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen and peripheral blood leukocytes. Detected in monocytes, macrophages, dendritic cells and several types of T-cells.
CC -1- PPM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to be necessary for the expression of TLR4 on the cell surface and the LPS-response. Likewise, mutants lacking two or more of the other N-glycosylation sites were deficient in interaction with LPS.
CC -1- POLYMORPHISM: Allele TLR4B (Gly-299, Ile-399) is associated with a blunted response to inhaled LPS.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copy-right. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U93091; AAC80327.1; -;
DR EMBL: U88880; AAC34135.1; -;
DR EMBL: AF177765; AAF05316.1; -;
DR EMBL: AF177786; AAF07823.1; -;
DR EMBL: AF172171; AAF89753.1; -;
DR EMBL: AF172169; AAF89753.1; JOINED.
DR EMBL: AF172170; AAF89753.1; JOINED.
DR HSSP: O60603; 1FTW.
DR Genew: HGNC:11850; TLR4.

DR	MIM; 603030; -;	C:integral to plasma membrane; TAs.
DR	GO: 00005687;	C:integral to plasma membrane; TAs.
DR	GO: 0046696;	C:lipopolysaccharide receptor complex; NAS.
DR	GO: 00001530;	F:lipopolysaccharide binding; NAS.
DR	GO: 0004888;	F:transmembrane receptor activity; NAS.
DR	GO: 00007250;	P:activation of NF-kappaB-inducing kinase; ISS.
DR	GO: 00016046;	P:detection of fungi; NAS.
DR	GO: 00009598;	P:detection of pathogenic bacteria; NAS.
DR	GO: 0006955;	P:immune response; TAs.
DR	GO: 00042116;	P:macrophage activation; IMP.
DR	GO: 00045571;	P:negative regulation of osteoclast different. . ; NAS.
DR	GO: 00045671;	P:negative regulation of interleukin-1 biosyn. . ; ISS.
DR	GO: 00045084;	P:positive regulation of interleukin-12 biosyn. . ; NAS.
DR	GO: 00045368;	P:positive regulation of interleukin-13 biosyn. . ; ISS.
DR	GO: 00045410;	P:positive regulation of interleukin-6 biosyn. . ; ISS.
DR	GO: 00007165;	P:signal transduction; TAs.
DR	GO: 00042088;	P:T-helper 1 type immune response; NAS.
DR	InterPro; IPR001611;	LRR.
DR	InterPro; IPR000483;	LRR_Cterm.
DR	InterPro; IPR003591;	LRR_Typ.
DR	InterPro; IPR001571;	TIR.
DR	Pfam; PF00560;	LRR; 12.
DR	Pfam; PF01463;	LRRCT; 1.
DR	Pfam; PFO1582;	TIR; 1.
DR	PRINTS; PR00019;	LEURICHRPT.
DR	SMART; SMO0369;	LRR_Typ; 2.
DR	SMART; SMO0082;	LRRCT; 1.
DR	SMART; SMO0255;	TIR; 1.
DR	PROSITE; PS50104;	TIR; 1.
KM	Direct protein sequencing; Glycoprotein; Immune response; Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;	
KW	Inflammasome response; Leucine-rich repeat; Polymorphism; Receptor;	
KW	Repeat; Signal; Transmembrane.	
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FT	CHAIN	24 839
FT	DOMAIN	24 631
FT	TRANSMEM	632 652
FT	DOMAIN	653 839
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 /FTID=VAR_018733.
 Q -> H.
 /FTID=VAR_018734.
 K -> R.
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 FT VARIANT 474 474
 FT VARIANT 510 510
 FT VARIANT 694 694

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 Score: 3905.50 Matches: 773
 Percent Similarity: 93.46% Conservative: 13
 Best Local Similarity: 91.91% Mismatches: 20
 Query Match: 11.81% Indels: 35
 Gaps: 6

US-09-396-985B-47 (1-18989) x TLR4_HUMAN (1-839)
 QY 11992 TGCTTATCATATGATGCGCTTAACATGACAAAGAGCCATTCATTCATTCGACCCAGTATGATTA 12051
 D 29 CysValGluValValProAsnIleThrTyrGlnCysMetGluLeuAsn----- 44
 QY 12052 TACTCAGCTGTGGGGCTTCTTATTTGGCT-----ATTTCATCATCATCTGTCTGTG 12102
 D 45 -----PheTyrLysIleProAspAsnLeuProPheSerThrLysAsn 58
 QY 12103 CTGATGCTTTGGCTTATGACCAATCATATGACCA---TCACATCTGTATGAAAGAGCTG 12159
 D 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
 QY 12160 GATACATGAGTATATATTCATTTTATTTAGGTTCTTATTC---GCAGAAATTTAGATTAAT 12216
 D 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 12217 CAATGCTTTTATTCCTGTAGTGTGAATCCAGACAAATGAGATGGGCGATATGACA 12276
 D 81 GlnValLeuAspLeu---SerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlns 100
 QY 12277 GCCTTAAGCACTTCTTACCTTAATATTGACAGAAACCCCATCCAGAGTTTACCCCTGG 12336
 D 100 erLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuG 120
 QY 12337 GAGCTTTTTCGACACTATCAAGATTACAGAAAGCTGTGGCTGTGGAGACAAATTCAGAT 12396
 D 120 LysAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThrAsnLeuAlaS 140
 QY 12397 CTCTAGAGAACTTCCCATTTGAGATCTCAAACTTTGAAGAACTTAATGTGGCTACA 12456
 D 140 erLeuGluAsnPheProIleGlyAlaSerLeuThrLeuLysGlnLeuAsnAlaAlaHisA 160
 QY 12457 ATCTTATCCATCTTTCAATTAACCTGATTTTCTTCAATCTGACCAATTCAGACAT 12516
 D 160 snLeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisL 180
 QY 12517 TGGACCTTTCCAGACAAAGATTTATTTGACAGACATTCGGGGCTTTTACATC 12576
 D 180 euAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisG 200
 QY 12577 AAATGCCCTACTCAATCTCTTTAGACCTGTCCCTGGAACCTTATGAACTTTATTCGAAC 12636
 D 200 InMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnP 220
 QY 12637 CAGGTGCAATTTAAAGAAATTTAGGCTTCATAGCTGACTTTTAAAGAAATTTTGTATGTT 12696
 D 12637 CAGGTGCAATTTAAAGAAATTTAGGCTTCATAGCTGACTTTTAAAGAAATTTTGTATGTT 12696

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 D 240 euAsnValMetLysThrCysIleGlnIleLeuAlaGlyLeuGluValHisArgLeuValL 260
 QY 12757 TGGGAGAAATTTAGAAATGAAGAAACTTGAAGAAAGTTTGAACAAATCTGCTTGAAGGCC 12816
 D 260 euGlyGluPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyL 280
 QY 12817 TGTCAATTTGACCATTTGAAGAAATTCGATTTAGCATCTTGACTTACTTCCATGATA 12876
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 D 420 LysLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluP 440
 QY 13297 TTTTCAGATTTCTATCACTCAGAAACCTCAATTAACCTTGAACATTTCCATCTCAGACCA 13356
 D 440 heSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrA 460
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 D 460 rGlyAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
 QY 13417 GCATTTCTTTCAGAAAACTTCTCTTCAGATATCTTCAACAGAGCTGAGAAACTTGAACCT 13476
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 D 500 heLeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuS 520
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 D 540 YrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerL 560
 QY 13657 AAAACAGAACTACAGCAATTTTCAAGATGTCTAGCTTTCTTAAATCTTACAGATG 13716
 D 560 YsLysGlnGlnLysGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnA 580
 QY 13717 ACTTTGCTGTACTTGTGAACACCAAGATTTCTGTCAATGATCAAGAGACCAAGGAGGC 13776
 D 580 spPheAlaCysThrCysGlnIleGlnSerPheLeuGlnIleTyrIleLysArgGlnArgGlnL 600

QY	13177	TCCTGGTGAAGTTGAACGAATGGAAATGTGCAACACCTTCACATTAAGCAGGGACCTG	13836
Db	600	euleuValGIuValGIuArgMetGIuCySAIaThrProSerAspLyGIuGlyMetProV	620
QY	13837	TGCGAGATTGGAAATATCACCTGTGCAGATGAATGAAGCAATCATTTGGTGTGTGGCTCTCA	138966
Db	620	alleuSerLeuAenIIeThrCyGIuMechAsnLySthrIIeIIeGlyValSerValIeUS	640
QY	13897	GTGTGCTTGTAGTATCTGTGTGAGAGTTCTGGCTATTAAGTTCTAATTTTCACTGTATGC	139566
Db	640	erValIeValIaSerValIaIaValIeValIaLyTrLySPhenLyPhenIIeMetI	660
QY	13957	TTCTTGTGGCTGCAATAAAGTATGATGAGGTGAAAAACATCTATGATGCTTTGTATATCT	140166
Db	660	euleuValGIuCyValIeLyStryGIuArgGIuGlyuAsnIIeLyTrAspAlaIphenValIeT	680
QY	14017	ACTCAACGCCAGATGAGAGCATGGGTATGAAGAAATAGCATGATTAAGATTATTAAGAAAGGGG	140766
Db	680	yrSerSerGIuAspGIuAspTrIprValAArgAsnGIuIeValIaLySAsnIIeGIuGlyIy	700
QY	14077	TGCCTCCATTTACAGCTGTGCCTTCACATACAGAGACTTATTTCCGGGTGTGCCATTTCTG	141366
Db	700	alPProPhoNegIIeUcyLeuHIIeLyTrArgSerPhelIeProGIuValaIIeAlaI	720
QY	14137	CCAAATCATTCATGAAGAGTTTCCATTAAGACCCGAAAGGTGATGTTGTGGTGTGCCAC	141866
Db	720	IaenIIeIIeHArgIIuGIuLyphenIIeLySerAspLySValIeValIaValIaSerGIuH	740
QY	14197	ACCTCATCCAGAGCGCGGTGGTGTATCTTTGAATATGATGATGTGTGCAGACCTGGCAGTTTC	142566
Db	740	IsPhelIeIIeGInSerAspLyTrProCyAlIePhelIuTrGIuIIeAlaGInThrIprGIuPhel	760
QY	14257	TGAGCAGTCTGTCTGTATATCTTCAATTTGTCTCTGCAGAAAGGTGAGAAAGACCTGTCTCA	143166
Db	760	eusSerAspArgAlaGIuIIeIIePhelIeValIeGIuIuSValIeGIuLySthrLeuIeUdA	780
QY	14317	GGCAGCAGGTGGAGCTGTACCGGCTTTCAGACGGAAACAATTACCTGGAGTGGAGAGACA	143766
Db	780	rGIuGIuIuValGIuIeUTrLyArgIeUeUeSerAspLySthnTrLyLeuGIuIuTrGIuIuAsS	800
QY	14377	GTGTCTGTGGCGGACATCTTCTGTGAGAGCACTCAAGAAAGCCCTGTGATGTATTAAT	144386
Db	800	erValIeUeGIuLyArgHIIeIIePhelIeTrArgIeUdArgLySAlaIeUeAspGIuLyS	820
QY	14437	CATGGAAATCCAGAAAGAAACAGTGGTTCAGAGATGCAATTTGGCAGAAAGCAACATCTATC	14495
Db	820	erTrpAsnProGIuGIuThrValGIuIuHrGIuCySAsnTrGIuGIuIuAlaThrSerIle	839
RESULT 2			
TLR4_PANPA	STANDARD;	PRT;	839 AA.
AC	Q9T7NO;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Toll-like receptor 4 precursor.		
GN	Name=TLR4;		
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.		
OX	NCBI_TaxId=9597;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEUJINE=20558910; PubMed=11104518;		
RA	Smirnova I., Poltorak A., Chan E.K.D., McBride C., Beutler B.;		
RT	"Phylogenetic variation and polymorphism at the Toll-like receptor 4		
RT	locus (TLR4).";		
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).		
CC	-I- FUNCTION: Cooperates with MyD and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	My88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (by similarity).		

CC	-1	SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via their respective TIR domains (By similarity).	
CC	-1	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).	
CC	-1	SIMILARITY: Belongs to the Toll-like receptor family.	
CC	-1	SIMILARITY: Contains 21 leucine-rich (LRR) repeats.	
CC	-1	SIMILARITY: Contains 1 TIR domain.	
CC		-----	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).	
CC		-----	
DR	EMBL	AF179220; AAF05320.1; -	
DR	EMBL	AF179218; AAF05320.1; JOINED.	
DR	EMBL	AF179219; AAF05320.1; JOINED.	
DR	HSSP	Q15399; 1PXY.	
DR	GO	GO:0046656; C:lipopolysaccharide receptor complex; ISS.	
DR	GO	GO:0001530; F:lipopolysaccharide binding; ISS.	
DR	GO	GO:0004888; P:transmembrane receptor activity; ISS.	
DR	GO	GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.	
DR	GO	GO:0009598; P:detection of fungi; ISS.	
DR	GO	GO:0009598; P:detection of pathogenic bacteria; ISS.	
DR	GO	GO:0045216; P:macrophage activation; ISS.	
DR	GO	GO:0045576; P:mast cell activation; ISS.	
DR	GO	GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.	
DR	GO	GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO	GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.	
DR	GO	GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO	GO:0042088; P:T-helper 1 type immune response; ISS.	
DR	InterPro	IPR001611; LRR	
DR	InterPro	IPR000483; LRR_Cterm	
DR	InterPro	IPR003591; LRR_Typ.	
DR	InterPro	IPR001571; TIR.	
DR	Pfam	PF00560; LRR; 12.	
DR	Pfam	PF01463; LRRCT; 1.	
DR	Pfam	PF01582; TIR; 1.	
DR	PRINTS	PR00019; LEURICRPT.	
DR	SMART	SM00369; LRR_Typ; 2.	
DR	SMART	SM00082; LRRCT; 1.	
DR	SMART	SM00255; TIR; 1.	
DR	PROSITE	PS0104; TIR; 1.	
KW	Glycoprotein; Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Signal; Transmembrane.		
FT	SIGNAL	1 23	Potential.
FT	CHAIN	24 839	Toll-like receptor 4.
FT	DOMAIN	24 631	Extracellular (Potential).
FT	TRANSMEM	632 652	Potential.
FT	DOMAIN	633 839	Cytoplasmic (Potential).
FT	REPEAT	52 76	LRR 1.
FT	REPEAT	77 100	LRR 2.
FT	REPEAT	101 124	LRR 3.
FT	REPEAT	128 149	LRR 4.
FT	REPEAT	150 173	LRR 5.
FT	REPEAT	174 197	LRR 6.
FT	REPEAT	203 225	LRR 7.
FT	REPEAT	228 252	LRR 8.
FT	REPEAT	277 303	LRR 9.
FT	REPEAT	307 330	LRR 10.
FT	REPEAT	332 350	LRR 11.
FT	REPEAT	351 372	LRR 12.
FT	REPEAT	373 398	LRR 13.
FT	REPEAT	400 421	LRR 14.
FT	REPEAT	422 445	LRR 15.
FT	REPEAT	447 469	LRR 16.
FT	REPEAT	470 494	LRR 17.
FT	REPEAT	495 518	LRR 18.
FT	REPEAT	520 541	LRR 19.

FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 205 205 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 282 282 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 309 309 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 497 497 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 526 526 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 624 624 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 630 630 N-linked (GlcNAc...) (potential)
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 5,38e-305 Length: 839
 Score: 3891.50 Matches: 770
 Percent Similarity: 93.34% Conservative: 15
 Best Local Similarity: 91.56% Mismatches: 21
 Query Match: 11.77% Indels: 35
 DB: 1 Gaps: 6

US-09-396-985B-47 (1-18989) x TLR4_PANPA (1-839)

QY 11992 TGCTTATCATGATGCTTAAACGCAAAAGAGCTATCATTCAGCCAGTATGATTA 12051
 DB 29 CysValaIGluValaProAsnIleThrIleGlyCysMetGluLeuAsn----- 44
 QY 12052 TACTCATGCTGTGGGCTTCTTATTTGCTT-----ATTCATCATCATCTGCTCG 12102
 DB 45 -----PheTyrIlePheProAsnLeuProPheSerThrIleAsn 58
 QY 12103 CTTCATGCTTTCCTTATGACATCATATGACCA---TCATCTGTATGAAAGAGCTG 12159
 DB 59 LeuAsnLeu-----SerPheAsnProLeuArgHis----- 68
 QY 12160 GATGACATGATTAATTTCTATTTAGTCTTATTTCA--GCAGAAATATTAGATAT 12216
 DB 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 12217 CAATGCTTTTATTCCTGTAGTGTGAATTCAGACATTTAGAGTGGGCTATTCAGA 12276
 DB 81 GluValaLeuAsnLeu--SerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlns 100
 QY 12277 GCCTAAGCACCTCTCTTACCTTAATATTGACAGGAAACCCATCCAGAGTTTACCCCTCG 12336
 DB 100 erLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuG 120
 QY 12337 GAGCCTTTTCTGACATATCAAGTTTACAGAGCTGTGGCTGTGAGCAAAATCTAGCAT 12396
 DB 120 LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValaAlaValaIleuThrAsnLeuAlaS 140
 QY 12397 CTTCAGACACTTCCCATTTGACATCTCAAAACTTTGAAAGACTTATATGTGCTCACA 12456
 DB 140 erLeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValaAlaHisSA 160
 QY 12457 ATCTTATCAATCTTTCAATTAAGTATTTTCTAATCTGACCAATCTAGAGCACT 12516
 DB 160 snLeuIleGlnSerHisLeuSerProGluLysPheSerAsnLeuThrAsnLeuGlnHisSL 180
 QY 12517 TGACCTTTTCTGACAGCAAGATTCAAGATTTATTCAGACAGACTTGGGGGTTCTACATC 12576
 DB 180 euAsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAsnLeuArgValaLeuHisSG 200
 QY 12577 AAATGCCCTTACTCATCTCTTTTGAACCTGTCCCTGAACCCCTATGAACCTTATCCAAC 12636
 DB 200 LmetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsnPheIleGlnP 220
 QY 12637 CAGGTGCAATTTAAAGAAATTTAGGCTTCAATGACTTAAAGAAATATTTGATAGTT 12696
 DB 220 roGlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerL 240

QY 12697 TAAATGATGAAAACTTGATTCAGAGCTGTGGTGGTTTGAAGACTCGTTGGTTC 12756
 DB 240 euAsnValMetLysThrCysIleGlnGluLeuAlaGlyLeuGluValaHisSerGluValL 260
 QY 12757 TGGAGAAATTTGAAGATGAGAAACCTTGAAAACTTTGACAAATCTGCTTACAGGGCC 12816
 DB 260 euGlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyL 280
 QY 12817 TGTGCAATTTGACATTTGAAGAAATTCGATAGCAATCTTACAGTACCTGATGATA 12876
 DB 280 euCysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspI 300
 QY 12877 TTAATGACTTAAATGTTTGAACAATGTTTCTTCAATTTCCCTGTGATGATGACTA 12936
 DB 300 LeuLeuAsnLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrI 320
 QY 12937 TTGAAGGGTAAAGACTTTTCTTATTAATTTGGATGGCAACATTTAGATTAAGTAACT 12996
 DB 320 LelysSerValLysAspPheSerTyrAsnPheGlyTyrGlnHisIleuGluLeuValaGnc 340
 QY 12997 GTAAATTTGACAGTTTCCCATTTGAAACCTGAAATCTCAAAAGCTTACTTTCACTT 13056
 DB 340 LysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrS 360
 QY 13057 CCAACAAAGTGGGAATGCTTTTTCAGAACTTGATCTTACCAAGCTTGAGTTTCTAGATC 13116
 DB 360 erAsnLysGlyGlyAsnAlaPheSerGluValaLeuPheProSerLeuGluIleuLeuAspL 380
 QY 13117 TCAGTGAATATGCTTGAGTTTCAAGGTTGCTGTCTCAAAAGTATTTGGACACCA 13176
 DB 380 euSerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrS 400
 QY 13177 GCCTAAGTATTTAGATCTGAGCTTCAATGGTGTATTAACATGATTTCAAACTTCTTG 13236
 DB 400 erLeuLysTyrLeuAsnLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420
 QY 13237 GCTTAGAACATCTGAACATCTGATTTCCAGATTTCCAAATTTGAAACAAATGAGTAGT 13296
 DB 420 LysLeuGluGlnLeuGlnHisIleuAspPheGlnHisSerAsnLeuLysGlnMetSerGluP 440
 QY 13297 TTTCAATTTCTTATCACTCAAGAAACCTCATTTAATCTTGAATTTCTCAATCAACCA 13356
 DB 440 heserValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrA 460
 QY 13357 GAGTTGCTTGAAGGCACTTCAATGCTTGTCCAGTCTGGAAGTCTTGAAGTGGCTG 13416
 DB 460 rGlyAlaAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValaLeuLysMetAlaG 480
 QY 13417 GCAATTTCTTTCAGAAAACTTCTCCAGATATCTTCAAGAGCTGAGAACTTGAACCT 13476
 DB 480 LysAsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrP 500
 QY 13477 TCGTGACCTTCTCACTGTCAACTGAGACAGTTGTCTCAACAGACTTAACTACTCT 13536
 DB 500 heLeuAspLeuSerGlnCysGlnLeuGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuS 520
 QY 13537 CCAATCTTCAAGTCTTAATTAAGCCACCAACACTTCTTTCATGGAATCGTTCTCTT 13596
 DB 520 erSerLeuGlnValaLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProT 540
 QY 13597 ATAAGTGTGGAATCTCCCTCAGAGTTCTTGATTAACAGTCAATCAACATTAATGACTTCA 13656
 DB 540 YLysCysLeuAsnSerLeuGlnValaLeuAspTyrSerLeuAsnHisIleMetThrSerL 560
 QY 13657 AAAAAGAGAACTACAGCAATTTTCAAGTATGACTTTTCTTAATCTTACAGAAATG 13716
 DB 560 YLysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnA 580
 QY 13717 ACTTGCTGTACTTGTGGAACACCAAGATTTCCTGCAATGGAATTAAGAACCAAGAGCAGC 13776
 DB 580 sPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleTyrIleLysAspIleArgGlnL 600
 QY 13777 TCTTGATGAAGTGAACGAATGGAATGTGCAACACTTTCAGATTAAGAGGAGCATGCTG 13836

Db	600	euleuValIGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProV	620
Qy	13837	TGCTGAAGTTTGAATATACACCTGTCCAGATGAAATAGAACCATCATTTGGTGTGGCTCTCA	13896
Db	620	allEuSerLeuAsnIleThrCysGlnMetCAsenLysThrIleIleGlyValSerValLeuS	640
Qy	13897	GTCGTCTTGATNGATTCCTGTTGTAGACAGTTCTTGGCTCTATAAGTTCTATTTTCCACTGATG	13955
Db	640	eValIleuValValSerValValAlaValIleuValLysLysPheThrPheHisLeuMetC	660
Qy	13957	TTCTTGTGCTGGCTGATTAAGATGATGATGAGTGAGTGAAACATCTATAGATGCTTGTATATCT	14016
Db	660	euleuValAGlyCysIleLeuThrCylArgGlyGluAsnIleThrAspAlaPheValIleT	680
Qy	14017	ACTCAAGCCAGATAGAGAGACTGGGTAAAGATGACATGACTAGTAAAGAAATTTAGAAGAGGG	14076
Db	680	yrSerSerGlnAspGlnAspArgPyrAlaArgAsnGluIleuValLysAsnLeuGluGly	700
Qy	14077	TGCTCTCCATTTACAGCTCTGCTCTTACATACAGAGACTTATATCCGGTGTGGCATTTGCTG	14133
Db	700	alProProPheGlnLeuCysLeuHisThrArgAspPheIleProGlyValAlaIleAla	720
Qy	14137	CCAACATCATCATGAAAGGTTTCCATTAAGCCGAAGAGATGATGTTGGTGTGCCAG	14196
Db	720	laasnIleIleHisGlnGlyPheHisLysSerSerGlyValIleValValValSerGlnH	740
Qy	14197	ACTTCATCCAGAGCCGCTGGTGTATCTTTGAAATATGAGATTGGTCAGACCTGGACATTC	14255
Db	740	IsPheIleGlnSerArgTrpCysIlePheGlnLysTrpGluIleAlaGlnThrTrpGlnPhe	760
Qy	14257	TGACGAGTCGTGCTGTGATCATCTTCAATTTGCTGTCCGAAGAGGTGGAGAGACCTGTCTCA	14311
Db	760	eusSerSerArgAlaGlyIleIlePheIleValIleuGlnLysValGlnLysThrLeuLeuA	780
Qy	14317	GGCAGCAGGTGGAGCTGATCCGCTTCCAGCAGGAGACACTTTCCTGGAGTGGAGGAGCA	14376
Db	780	rGArgGlnValGlnLeuLysTrpGluLeuSerSerArgAsnThrTrpLeuGlnTrpGlnAspS	800
Qy	14377	GTCGTCCTGGGCGGCGACATCTTCTGAGAGACGACTCAGAAAAGCCCTGCTGATGTGTAAT	14433
Db	800	eValIleuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysS	820
Qy	14437	CATGGAATCCAGAAAGAACTGGGTCTACAGATGCAATTGGCAGGAAGCAACATCTATC	14495
Db	820	eTrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle	839
RESULT 3			
QSPSP8	PRELIMINARY;	PRT;	837 AA.
AC	QSPSP8;		
DT	01-JUN-2002 (TREMBlrel. 21, Created)		
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)		
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	Toll-like receptor 4.		
GN	Name=TLR4;		
OS	Gorilla gorilla (gorilla).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.		
OX	NCBI_TaxID=9593;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21405531; PubMed=11514453;		
RA	Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;		
RT	"Excess of rare amino acid polymorphisms in the toll-like receptor 4		
RT	in humans";		
RL	Genetics 158:1657-1664(2001).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;		
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF497565; AAA18617.1; -		
DR	EMBL; AF497563; AAA18617.1; JOINED		

DR	HSPB1; AFA97564; AAM18617.1; JOINED.
DR	HSPG; O60603; I077.
DR	GQ; GQ:0046596; C:lipopolysaccharide receptor complex; ISS.
DR	GQ; GQ:0001530; F:lipo-polysaccharide binding; ISS.
DR	GQ; GQ:0000488; F:transmembrane receptor activity; ISS.
DR	GQ; GQ:00007250; P:activation of NF-kappa-B-inducing kinase; ISS.
DR	GQ; GQ:0016046; P:detection of fungi; ISS.
DR	GQ; GQ:0009598; P:detection of pathogenic bacteria; ISS.
DR	GQ; GQ:0044216; P:mactrophage activation; ISS.
DR	GQ; GQ:0045576; P:mast cell activation; ISS.
DR	GQ; GQ:0045671; P:negative regulation of osteoclast different. . ; ISS.
DR	GQ; GQ:0045567; P:positive regulation of interleukin-1 biosyn. . ; ISS.
DR	GQ; GQ:0045584; P:positive regulation of interleukin-12 biosy. . ; ISS.
DR	GQ; GQ:0045568; P:positive regulation of interleukin-13 biosy. . ; ISS.
DR	GQ; GQ:0045410; P:positive regulation of interleukin-6 biosym. . ; ISS.
DR	GQ; GQ:0042088; P:T-helper 1 type immune response; ISS.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR003591; LRR_cyp.
DR	InterPro; IPR00157; TIR.
DR	Pfam; PF01463; LRCT; 1.
DR	Pfam; PF00560; LRR_1; 10.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SMO0082; LRCT; 1.
DR	SMART; SMO0369; LRR_TYF; 2.
DR	SMART; SMO0255; TIR; 1.
DR	PROSITE; PSS0104; TIR; 1.
RW	Receptor.
QO	SEQUENCE 837 AA; 95497 MW; 5A117BAB34136DD CRC64;

Alignment Scores:	
Pred. No.:	6 04e-304
Score:	3878.50
Percent Similarity:	98.31%
Best Local Similarity:	97.79%
Query Match:	11.73%
DB:	2
US-09-396-985B-47 (1-18989) x Q8SPD8 (1-837)	
Length:	837
Matches:	752
Conservative:	4
Mismatches:	4
Indels:	9
Gaps:	1

QY	12216	TCAAATGCTTTTATATCC-----TGATGGCTGAATAC	12247
		:::	
Db	69	SerTyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle	88
QY	12249	CAGACAAATTGAAGATGGGCATATCAAGCCCTTACCTTCAATAATTGACA	12308
Db	89	GlnThrIleGluMetGlyAlaTyrArgIleSerLeuSerHisLeuSerThrIleLeuThr	108
QY	12309	GGAAACCCCATCCAGAGATTAGCCCTGGAGCCTTTTCTGGACTATCAAGTTACGAG	12366
Db	109	GlyAsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys	128
QY	12369	CTGGTGGCTGGGAGACAATATTCAGATCTCTGAGAGAACTTCCCAATTGGACATCTCAAA	12428
Db	129	LeuValAlaValGluThrAsnMetLeuAlaSerLeuGluAsnPheProIleGlyHisLeuLys	148
QY	12429	ACTTTGAAGAATCTTAATGTGGCTCACATCTTATTCCAATCTTTCAAAATTACTCGAGTAT	12488
Db	149	ThrIleuysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyr	168
QY	12489	TTTTTCTAATCTGACCAATCTTAGAGCACTTGGACTTTCACGGACAAGAATTCAAGATT	12546
Db	169	PheSerAsnLeuThrAsnLeuGluTyrLeuAspLeuSerSerAsnLysIleGlnSerIle	188
QY	12549	TATTGACACAGACTTGGCGGTTCTACATCAAAATGCCCTACTCATCTCTTTAGACCTG	12606
Db	189	TyrCysThrAspLeuArgValIleuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu	208
QY	12609	TCCTGTAAACCCCTATGAACCTTATCCAAACGAGTGACATTTAAGAAATTAGGCTTCATAG	12666
Db	209	SerLeuAsnProMetThrPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys	228

QY 12669 CTGACTTAAAGAAATATTTGATGATTTAAATGTAAGAACTTGATTTCAAGGCTG 12728
 Db LeuThrLeuAArgAsnPhaSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
 QY 12729 GCTGGTTTGAAGATCCATCGTTTGGTTCTGGGAGAAATTTAGAAATGAAGAACTTGGA 12788
 Db AlaGlyLeuGluValArgArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGlu 268
 QY 12789 AAGTTTGAACAATCGCTCTGAGAGGGCTGCAATTTGACATTTGAAGAAATTCGATTA 12848
 Db LysPheAspLysSerAlaLeuGluCysAsnLeuThrIleGluGluPheArgLeu 288
 QY 12849 GCATATTTAGACTACTGATCGATGATATTAATGACTTATTTAAATGTTTGAACAATGTT 12908
 Db AlaTyrLeuAspTyrTyrLeuAspAspIleIleLeuAspPheAsnCysLeuThrAsnVal 308
 QY 12909 TCTTCATTTTCCCTGGTGAAGTGTGACTTGTAAAGGGTAAAGACTTTCTTATTAATTC 12968
 Db SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 328
 QY 12969 GGATGGCAACATTTAGAAATTTGTAACGTAAATTTGACAGTTTCCACATTTGAACCTC 13028
 Db GlyTyrGlnHisLeuGluLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 348
 QY 13029 AATATCTCAAAAGGCTTACTTCTTCACTTCCAAACAAGGTGGAAATGCTTTTTCAGAAAT 13088
 Db LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluVal 368
 QY 13089 GATCTACCAAGCTTGAAGTTCTTGAATCTGATGAAATGGCTTGAAGTTCAAGTTTC 13148
 Db AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 388
 QY 13149 TGTCTCAAAAGTATTTGGGACAACAGCTTAAAGTATTTAGATTCGAGCTTCAAGT 13208
 Db CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 408
 QY 13209 GTTATTAACATGAGTTCAAACTTCTTGGCTTAGAACAACATGAACTTGAATTCAG 13268
 Db ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHisLeuAspPheGln 428
 QY 13269 CATTCAATTTGAAACAATGAGTGAAGTTTTCAGTATTCCTATGACTCAGAACTTCAT 13328
 Db HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIle 448
 QY 13329 TACCTTGAACATTTCTCACTACACACAGAGTTCCTTCAATGAGCTTCAAGGCTTG 13388
 Db TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
 QY 13389 TCCAGTCTCGAAGCTTGAATAATGGCTGCAATCTTCCAGAAACTTCTCCAGAT 13448
 Db SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 488
 QY 13449 ATCTTCACAGAGCTGAGAACTTGAACCTTCTGAGACCTCTCTCAGTGTCAACTGAGACG 13508
 Db IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 508
 QY 13509 TTGCTCCACACAGATTTAATCACTCTCCAGCTTTCAGGTAATTAATTAAGCCACAC 13568
 Db LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
 QY 13569 AACTCTTTTTCATTTGATGATGCTTCTTAATAGTGTGAACTCCCTCCAGAGTCTTGAT 13628
 Db AsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuArgValLeuAsp 548
 QY 13629 TACAGTCTCAATCAATATGACTTCCAAAAACAGAACTTACAGACTTTTCCAGTAGT 13688
 Db TyrSerLeuAsnHisIleMetThrSerLysGlnGluLeuGlnHisPheProSerSer 568
 QY 13689 CTACCTTTTCTTAATCTTACTCAGAAATGACTTGTGTAATTTGTGAACACCAAGTTTC 13748
 Db LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 588
 QY 13749 CTGCAATGATCAAGACCAAGACGAGCTTGTGTGAAGTTGAACGAATGAGATGTGCA 13808

Db 589 LeuGlnThrPheLysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 608
 QY 13809 AACCTTCAGATTAAGCAAGGGCAGACCTGCTGAGTTTGAATATCACCTGTCAGATGAAT 13868
 Db ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
 QY 13869 AAGACATCAATGGTGTGTCGCTCCAGTGTGCTTGAATATCTGTTAGACAGTTCTG 13928
 Db LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 648
 QY 13929 GCTTAATGTTCTTATTTTCACTGATGCTTCTTGTCTGCTGCTGATTAAGTATGAGGT 13988
 Db ValTyrLysPheTyrPheHisLeuMetLeuValAlaGlyCysIleLysTyrGlyArgGly 668
 QY 13989 GAACAACATCATGATGCTTGTGTTATCTCAAGCCAGATGAGCACTGGGTAAAGAAAT 14048
 Db GluAsnValTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAsn 688
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 Db GluLeuValLysAsnLeuGluGluGlyValProProPheGlnLeuCysLeuHisTyrArg 708
 QY 14109 GACTTATTCCTCGGTGTGGCATTGCTGCCAACAATCATGAGAGGTTTTCATTAAGC 14168
 Db AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGluGlyPheHisLysSer 728
 QY 14169 CGAAGGTGATTTGTGTGTGTGTCCAGACTTCAATCCAGAGCCGTGTATTTTGA 14228
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 QY 14229 TATGAGATTCCTGAGACTGAGCTTCTGAGAGTGTGCTGATCATCTTCAATGTC 14288
 Db TyrGluIleAlaGlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
 QY 14289 CTGCAAGGTGAGAAAGACCTGCTCAGCAGCAGGTGAGCTGTACCGCTTCTGACG 14348
 Db LeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 788
 QY 14349 AGGAACCTTACTGAGGTGAGAGACAGTGTCTGTGGGGCGGCACATCTTCTGAGACGA 14408
 Db ArgAsnThrTyrLeuGluTyrGluAspSerValLeuGlyArgHisIlePheThrArg 808
 QY 14409 CTCGAAAGACCTGCTGATGTGAATCATGGAATCCAGAGGAACAGTGGGACAGGA 14468
 Db LeuArgLysAlaLeuLeuAspGlyLysSerTyrAsnProGluGlyThrValGlyThrGly 828
 QY 14469 TGCATTTGGCAGAGCAACATCTATC 14495
 Db 829 CysAsnThrPheGlnGluAlaThrSerIle 837
 Db 829 CysAsnThrPheGlnGluAlaThrSerIle 837
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 TLR4_PONPY ID TLR4_PONPY STANDARD; PRT; 828 AA.
 AC OSSEP9;
 DT 05-JUN-2004 (Rel. 44, Created)
 DT 05-JUN-2004 (Rel. 44, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OK NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21405531; Pubmed=11514453;
 RA Smirnova I., Hamblin M.T., McBrier C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 RL in humans."
 CC Genetics 158:1657-1664(2001).
 CC -I- FUNCTION: Cooperates with LY6 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via

CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TLR4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 DR EMBL: AF497562; AAM18616.1; -
 DR EMBL: AF497560; AAM18616.1; JOINED.
 DR EMBL: AF497561; AAM18616.1; JOINED.
 DR HSPB: O60603; IFLW.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007280; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:mast cell activation; ISS.
 DR GO: GO:0045571; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF00560; LRR_12.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR00619; LEURICHRP.
 DR SMART: SMO0369; LRR_Typ; 1.
 DR SMART: SMO0082; LRRCT; 1.
 DR SMART: SMO0255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR GlycoProtein: Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 828 Toll-like receptor 4.
 FT DOMAIN 24 629 Extracellular (Potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 651 828 Cytoplasmic (Potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.
 FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.

FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DF CRC64;
 Alignment Scores:
 Pred. No.: 1,33e-293 Length: 828
 Score: 3750.50 Matches: 728
 Percent Similarity: 96.97% Conservative: 9
 Best Local Similarity: 95.79% Mismatches: 14
 Query Match: 11.34% Indels: 9
 DB: 1 Gaps: 1
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 QY 12216 TCAGTGGTGTATATCC-----TGATGGTGTGAATC 12248
 Db 69 SerTyrSerPheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 88
 QY 12249 CAGACATTTGAAGATGGGCGATATCAGAGCTTAAGCCATCTTCAATTTATTTGACA 12308
 Db 89 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleThr 108
 QY 12309 GGAACCCCATCCAGAGTTTATGCCCTTGGAGCCTTTTCTTGACTATCAATTTACAGAAG 12368
 Db 109 GlyAsnProIleGlnIleAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
 QY 12369 CTGGTGGCTGTGAGACCAATCTAGCATCTCTAGAGACTTCCCATTTGACATCTGAAA 12428
 Db 129 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuLys 148
 QY 12429 ACTTTGAAAGACTTATATGTGGCTCACAATCTTATCCATCTTCAATTTACCTGATAT 12488
 Db 149 ThrLeuLysIleLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyr 168
 QY 12489 TTTTCTAATCTGACCAATCTTAGAGCACTTGACCTTTCCAGACAAGATTCAAGATT 12548
 Db 169 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 188
 QY 12549 TATTTGCACACATTTGGGGGTTCTTCAATCAATGCCCTTACTCAATCTCTTTAGACCTG 12608
 Db 189 TyrCysLysAspLeuGlnValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
 QY 12609 TCCCTGAACCTTATGAACTTTATCCAAACAGGTGATTTAAAGAAATTAGCTTCATTAAG 12668
 Db 209 SerLeuAsnAlaMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
 QY 12669 CTGACTTAAAGAAATAATTTGATGATTTAAATGTAATGAAAATTGTATTTCAAGCTCTG 12728
 Db 229 LeuThrLeuArgAsnSerPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
 QY 12729 GCTGGTTTAAAGTCCATCTTTGGTTCGGGAAATTTGAATGAAGAAATTCGGA 12788
 Db 249 AlaGlyLeuGlnValHisHisLeuValLeuGlyGlnPheArgAsnGlnLysAsnLeuGln 268
 QY 12789 AAGTTTGACAAATCTGCTTAGAGGGCTTGCAATTTGACCAATTGAAGAAATTCGGA 12848
 Db 269 LysPheAspThrSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeu 288
 QY 12849 GCATTTAGACTTACTACTGATGATATTTAGCTTATTTAATTTGTTGACAAATGTT 12908
 Db 289 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnLysLeuAlaAsnVal 308

QY 12909 TCTTCATTTCCCTGGAGTGTGACTATTGAAAAGGTAAGAACTTTTCTTAATATTC 12968
 DB 309 SerSerPheSerLeuValSerValThrIleYSerSerValIysAspPheSerIleAsnHe 328
 QY 12969 GGAATGCAACATTGAAATTAGTTAACTGTAAATTGACAGTTTCCACATTTGAAATC 13028
 DB 329 G1YTPG1nH1sLeuG1nLeuValAsnCyS1yPheG1nLeuPheProTh1LeuG1nLeu 348
 QY 13029 AAATCTCCAAAAGGCTTACTTCACTTCCAAAAGGTTGGAATGCTTTTTCAGAAAT 13088
 DB 349 LysSerLeuLysAlaG1nLeuThrPheThrAlaAsnYsG1yG1yAsnAlaPheSerG1yVal 368
 QY 13089 GATCTACCAAGCCTTGAGTTTCTAGATCTCAGTAGAAATGCTGAGTTTCAAGGTTC 13148
 DB 369 AspLeuProSerLeuG1nLeuPheLysPheSerIleAsnG1yLeuSerPheLysG1yCyS 388
 QY 13149 TGTTCCTCAAGTATTTGGGACAAACAGCCTAAAGTATTAGATCTGAGCTTCAGTGT 13208
 DB 389 CysSerG1nSerAspPheG1yThrThrSerLeuYsTy1LeuAspLeuSerPheAsnAsp 408
 QY 13209 GTTATTACAGAGTTCAAACTCTTGGGCTTAAAGCACTTGAACATCTGATTTCCAG 13268
 DB 409 ValIleThrMetG1ySerAsnPheLeuG1yLeuG1nLeuG1nLeuH1sLeuAspPheG1n 428
 QY 13269 CATTCCTCAATTTGAAACAAATGAGTGTTCAGATTCTATCACTCAGAAACCTCAT 13328
 DB 429 HisSerAsnLeuLysG1nLeuSerG1nLeuSerValPheLeuSerLeuAspAsnLeuIle 448
 QY 13329 TACCTTGACATTTCTCATACTCACAACAGAGTGTTCATGAGCATCTTCAGTGT 13388
 DB 449 Ty1LeuAspI1eSerH1sThrH1sThrArgValAlaPheAsnG1yI1ePheAsnG1yLeu 468
 QY 13389 TCCAGTCTCGAAGCTTGAATAATGCTGGCAATTTTTCACAGAAACTTCTTCAGAT 13448
 DB 469 SerSerLeuLysValLeuLysMetAlaG1yAsnSerPheG1nLeuAspPheLeuProAsp 488
 QY 13449 ATCTTCACAGAGCTGAGAAACTTGACCTTCTGAGCCTCTGAGTGTCAACCTGAGAG 13508
 DB 489 I1ePheThrG1nLeuArgAsnLeuThrPheLeuAspLeuSerG1nCyS1nLeuG1nLeu 508
 QY 13509 TTGCTCCACAGCAATTAACTCACTCTCAGTCTTCAGTACTTAATATGAGCCACAAC 13568
 DB 509 LeuSerProThrAlaPheAsnSerLeuSerLeuG1nValLeuAsnMetSerH1sAsn 528
 QY 13569 AACTTTCTTTTATTGATGATGTTCTTAAAGTGTCTGAACCTCCCTCAGGTTCTTGAT 13628
 DB 529 AsnPhePheSerLeuAspThrPheProTy1LysCyS1eAsnAsnSerLeuG1nValLeuAsp 548
 QY 13629 TACAGTCTCATCATATATGACTTCCAAAACAGCAACTACAGCAATTTCCAAAGTGT 13688
 DB 549 Ty1SerLeuAsnH1sI1eMetThrSerIysYsG1nLeuG1nH1sPheProSerSer 568
 QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTCTGTACTTGTGAACACAGAGTTTC 13748
 DB 569 LeuAlaPheLeuAsnLeuThrG1nAsnAspPheAlaCyThrCyS1nH1sG1nSerPhe 588
 QY 13749 CTGCAATGATCAAGGACCAAGGAGCTTGTGGAAGTTGAACGAATGGAATGTGCA 13808
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 QY 13809 ACACCTTACAGTAAGGAGGAGGATGCTGTGAGTTGATATTCACCTGTCAATGAT 13868
 DB 609 ThrProSerAspLysG1nG1yMetProValLeuSerLeuAsnI1eThrCyS1nMetAsn 628
 QY 13869 AAGACCATCATTTGTGTGCTCCTCAGTGTGCTTGTAGTATCTGTGTGAGAGTTCTG 13928
 DB 629 LysThrValI1eG1yValSerValPheSerValLeuValSerValAlaValLeu 648
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 DB 649 ValTy1LysPheTy1PheH1sLeuMetLeuLeuAlaG1yCyS1yLeTy1G1yArgG1y 668

QY 13989 GAAACATCTATGATGCTTTGTATTATCTCAAGCAGATGAGACTGGGTAGAGAT 14048
 DB 669 GluAsnThrTy1AspAlaPheValI1eTy1SerSerG1nAspG1uAspTrpValArgAsn 688
 QY 14049 GAGCTAGTAAAGATTTGAAGAAAGGGTGCCTTCATTTCACTCTGCTTCACTACAGA 14108
 DB 689 GluLeuValLysAsnLeuG1nG1yValProThrPheG1nLeuCyS1eH1sTy1Arg 708
 QY 14109 GACTTTATCCCGGTGGCCATGTGCTGCCAAACTCATTCATGAAGTTTCCATTAAGC 14168
 DB 709 AspPheI1eProG1yValAlaI1eAlaAlaAsnI1eH1sG1nG1yPheH1sLysSer 728
 QY 14169 CGAAGGTGATTTGTGTGTGCTCCACAGACTTCATCCAGAGCCCTGATATCTTGA 14228
 DB 729 ArgLysValI1eValValSerG1nH1ePheI1eG1nSerArgTrpCyS1ePheI1u 748
 QY 14229 TATGAGATGCTCAGACCTGGCAGCTTCTGAGCAGTGTGTGATTCATTTCAATGTC 14288
 DB 749 Ty1G1nLeuAlaG1nTrpG1nPheLeuSerSerArgAlaG1yI1eI1ePheI1eVal 768
 QY 14289 CTGCAAGAGTGGAGAGACCTGCTCAGCAGCAGGAGTGAAGCTTACCGCTTCAGC 14348
 DB 769 LeuG1nLysValG1uLysThrLeuLeuArgG1nValG1uLeuTy1ArgLeuLeuSer 788
 QY 14349 AGAACACTTACCTGAGTGGAGAGACAGTGTCTCGGCGCGCACATCTTCTGAGACA 14408
 DB 789 ArgAsnThrTy1LeuG1nTrpG1uAspSerValLeuG1nArgH1sI1ePheTrpArgArg 808
 QY 14409 CTCGAAAAGCCTGCTGATGTGTAATCATGAATCCAGAAAGAGAGTGGTACAGA 14468
 DB 809 LeuArgLysAlaLeuLeuAspG1yLysSerTrpAsnProG1nG1yThrValG1yThrG1y 828

RESULT 5

TR4_PAPAN STANDARD; PRT; 826 AA.
 AC Q9TSP2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Papio.
 NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20558910; PubMed=11104518;
 RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 RT locus (TLR4).";
 RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TR4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
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Accession	Protein	Length	Score	Alignment	Score	Alignment
DR EMBL AF180964	AA07059.1	283	826	3.56e-283	826	3.56e-283
DR EMBL AF180962	AA07059.1	283	826	3.56e-283	826	3.56e-283
DR EMBL AF180963	AA07059.1	283	826	3.56e-283	826	3.56e-283
DR HSSP Q15399	1FVY	283	826	3.56e-283	826	3.56e-283
DR GO GO:0046696	C:lipopolysaccharide binding	283	826	3.56e-283	826	3.56e-283
DR GO GO:0001530	F:lipopolysaccharide receptor activity	283	826	3.56e-283	826	3.56e-283
DR GO GO:0004888	F:transmembrane receptor activity	283	826	3.56e-283	826	3.56e-283
DR GO GO:0007250	P:activation of NF-kappa-inducing kinase	283	826	3.56e-283	826	3.56e-283
DR GO GO:0016046	P:detection of fungi	283	826	3.56e-283	826	3.56e-283
DR GO GO:0009598	P:detection of pathogenic bacteria	283	826	3.56e-283	826	3.56e-283
DR GO GO:0042116	P:macrophage activation	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045576	P:mast cell activation	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045671	P:negative regulation of osteoclast different	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045362	P:positive regulation of interleukin-1 biosyn	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045084	P:positive regulation of interleukin-12 biosyn	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045368	P:positive regulation of interleukin-13 biosyn	283	826	3.56e-283	826	3.56e-283
DR GO GO:0045410	P:positive regulation of interleukin-6 biosyn	283	826	3.56e-283	826	3.56e-283
DR GO GO:0042088	P:T-helper 1 type immune response	283	826	3.56e-283	826	3.56e-283
DR InterPro IPR001611	LRR	283	826	3.56e-283	826	3.56e-283
DR InterPro IPR000483	LRR Cterm	283	826	3.56e-283	826	3.56e-283
DR InterPro IPR003591	LRR typ	283	826	3.56e-283	826	3.56e-283
DR InterPro IPR000157	TIR	283	826	3.56e-283	826	3.56e-283
DR Pfam PF04463	LRR 13	283	826	3.56e-283	826	3.56e-283
DR Pfam PF01463	LRRCT 1	283	826	3.56e-283	826	3.56e-283
DR Pfam PF01582	TIR 1	283	826	3.56e-283	826	3.56e-283
DR PRINTS PRO0019	LEURICRPT	283	826	3.56e-283	826	3.56e-283
DR SMART SM00369	LRR typ 2	283	826	3.56e-283	826	3.56e-283
DR SMART SM00082	LRRCT 1	283	826	3.56e-283	826	3.56e-283
DR SMART SM00255	TIR 1	283	826	3.56e-283	826	3.56e-283
DR PROSITE PS50104	TIR 1	283	826	3.56e-283	826	3.56e-283
KW Glycoprotein	Immune response; Inflammatory response	283	826	3.56e-283	826	3.56e-283
KW Lactinase-rich repeat	Receptor; Repeat; Signal; Transmembrane	283	826	3.56e-283	826	3.56e-283
FT SIGNAL	1	283	826	3.56e-283	826	3.56e-283
FT CHAIN	24	826	631	3.56e-283	826	631
FT DOMAIN	24	631	652	3.56e-283	631	652
FT TRANSMEM	632	652	652	3.56e-283	632	652
FT DOMAIN	653	826	76	3.56e-283	653	826
FT REPEAT	53	76	100	3.56e-283	53	76
FT REPEAT	77	100	124	3.56e-283	77	100
FT REPEAT	101	124	149	3.56e-283	101	124
FT REPEAT	128	149	173	3.56e-283	128	149
FT REPEAT	150	173	197	3.56e-283	150	173
FT REPEAT	174	197	225	3.56e-283	174	197
FT REPEAT	203	225	252	3.56e-283	203	225
FT REPEAT	228	252	303	3.56e-283	228	252
FT REPEAT	277	303	350	3.56e-283	277	303
FT REPEAT	327					

Score:	3621.50	Matches:	716
Percent Similarity:	90.80%	Conservative:	34
Best Local Similarity:	86.68%	Mismatches:	41
Query Match:	10.95%	Indels:	35
DB:	1	Gaps:	6
US-09-396-985B-47 (1-18989) * TLR4_PAPAN (1-826)			
QY 11992	TGCTTATCATGTATGCTCTTAATCATGACAAAAAGCCATATCTTATGACGCCAGTATGATTA	12051	
DB 29	CysValGluValValProLeuIleThrTyrGlnCysMetGluLeuAsn-----	44	
QY 12052	TACTACGTCTGTGGGGCTTTATTTGGCT-----ATTCCATCATCATCTGTCCG	12102	
DB 45	-----PheTyrLysIleProAspAsnIleProPheSerThrLysAsn 58		
QY 12103	CTTGATGCTTTGGCCTATGACACATATATGACCCA---TCACATCTGTATGAAGCTG	12159	
DB 59	LeuAspLeu-----SerPheAsnProLeuArgHis-----68		
QY 12160	GATGACTAGGATTAATATCTTATTTAGGTTCTTATTC--GCAGAAATATAGATAT	12216	
DB 69	-----LeuGlySerTyrSerPheLeuArgPheProGluLeu 80		
QY 12217	CAATGCTCTTTTATCTCTGATGGTGCGAATCCAGACATTTGAAGATGGGGCATATCAG	12276	
DB 81	GluValLeuAspLeu--SerArgCysGluIleGlnIleThrIleGlnuSpGlyAlaTyrGlns 100		
QY 12277	GCCTAAGCAACCTCTACCTTAATTTTGAACAGAAACCCCATCCAGATTAGCCCTGG	12336	
DB 100	erLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuG 120		
QY 12337	GAGCCTTTTGTGACTATCAAGTTTACAGAACTGGGTGGCTGTGAGACAAATCTAGCAT	12396	
DB 120	LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlas 140		
QY 12397	CTCTAAGAACTTCCCATTTGGACATCTCAAACTTTGAAGAATTATATGGGCTCACA	12456	
DB 140	erLeuGluAsnPheProIleGlnIleLeuIleThrLeuLysGluLeuAsnValAlaHisAs 160		
QY 12457	ATCTTATCCAAATCTTCAAAATTAACCGAGATTTTCTATGCTGACCAATCTTAGAGCACT	12516	
DB 160	snLeuIleGlnSerPheLysLeuProGluTyrPheSerHisLeuThrAsnLeuGluHisL 180		
QY 12517	TGCACTTTCCAGACACAGATTCAAAGTATTTATGACACAGACTTCCGGGTTCTACATC	12576	
DB 180	euaBrLeuSerSerAsnLysIleGlnAsnIleTyrCysLysAspLeuGlnValLeuHisG 200		
QY 12577	AAATGCCCTTACTCAATCTCTTTTGAACCTGTGCCCTGAACCTTATGAACCTTATGCAAC	12636	
DB 200	ImetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnPheIleGlnP 220		
QY 12637	CAGGTGCAATTTAAAGAAATTAAGGCTTCATAGGCTGACTTTAAGAAATATTTTGGATAGTT	12696	
DB 220	roGlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuAspGSerAsnPheAspAspL 240		
QY 12697	TAAATGTATGAAGAAACTTGTATTCAAAGTCTGGCTGGTTTATGAGATGCCATCGTTGGTTC	12756	
DB 240	euaAsnValMetLysThrCysIleGlnIleLysLeuAlaGlyLeuGlnValHisArgLeuValL 260		
QY 12757	TGGAGAAATTTAGAAATGAGAGAACTTGGAAAAATTGAACAAATCTGCTCTAGAGGGCC	12816	
DB 260	eugIyGluPheArgAsnGluArgAsnLeuGlnIlePheAspLysSerAlaLeuGlnGlyL 280		
QY 12817	TGTGCAATTTGACCATTTGAGAAATTCGGATTTACACATTTAGACTTACCTCGATGARGA	12876	
DB 280	eucYasnLeuThrIleGlnIlePheArgLeuThrTyrLeuAspLysTyrTyrLeuAspAsnI 300		
QY 12877	TTATTTGACTTATTTATTTGTTTGAACAAATGTTTCTTCATTTTCCCGTGAAGTGACATA	12936	
DB 300	IeIleAspLeuPheAsnCysLeuAlaAsnAlaSerSerPheSerIleValIleSerValAsnI 320		
QY 12937	TTGAAGGGTAAAAAGCTTTTCTTATTAATTTGGATGGACAACTTTAGATTAGTTAACT	12996	

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Db      320  l e y s a r v a l g l u a s p h e s e r t y r a s n p h e a r g t r p g l n h i s e u g l u e u v a l a a n c 340
Qy      12997  G T A A T T T G G A C A G T T T C C A C A T T G A A A C T C A A A G G C T T A C T T C A C T T 13056
Db      340  y l y s p h e g l u g l i n h e p r o h n r l e u g l u e g l u s e r l e u y a r g l u e u t h r p h e i n r a 360
Qy      13057  C C A A C A A G G T G G A A T C T T T T C A G A G T T G A T C T C A A G C C T T G A G T T C T A G A T C 13116
Db      360  l a a n l y g l y g l y a s n l a p h e s e r g l u v a l a s p l e u p r o s e r l e u d l u h e l e u a p l 380
Qy      13117  T C A G T A G A A A T G G C T T G A G T T C A A A G G T G C T T C C A A A G T A T T T T G G A C A C C A 13176
Db      380  e u s e r a r g a n g l y l e u s e r p h e u y s g l y c y s e r g l n s e r a p h e g l y t h r t h s 400
Qy      13177  G C C T A A A G T A T T T G A T C T G A G C T T C A A T G G T A T T A C C A T G A G T T C A A A C T T C T T G 13236
Db      400  e r l e u y s t r l e u a s p l e u s e r p h e a s n a p v a l l e t h r m e c l y s e r a s n p h e l e u g 420
Qy      13237  G C T T A G A C A C T A G A C A T C T G A T T T C C A G A T T C C A A T T T G A A C A A T G A T G A G T 13296
Db      420  l y l e u g l u g l i n h e u g l u h i s t e u a s p h e g l n h i s e r a s n l e u y s e g l n h e t s e r g l n p 440
Qy      13297  T T T G A T T C C T C A C T C A G A A C C T C A T T A C T T G A C A T T T C A T A C T C A C A C C A 13356
Db      440  h e s e r v a l p h e l e u s e r l e u a r g a n l e u i l e t y r l e u a s p l e s e r h i s t h r h s t h r t 460
Qy      13357  G A G T T G C T T C A A T G G C A C T T C A A T G G C T T G C C A G C T C G A A G C T T G A A A T G G C T G 13416
Db      460  h r v a l a l a p h a s n g l y l e p h e a s p g l y l e u l e u s e r l e u y a l l e u l y s m e t a l a g 480
Qy      13417  G C A A T T C T T T C C A G A A A A C T T C C T C C A G A T A T C T T C A C A G A G C T G A A A C T T G A C C T 13476
Db      480  l y a s e n s e r p h e g l n g l u a s n p h e l e u p r o a p l l e p h e t h r a s p l e u l y a s n l e u t h r p 500
Qy      13477  T C T G G A C C T C T C A G T G T C A C T G A G C A G T T G T C C A A C A G A C A T T T A C T C A C T T 13536
Db      500  h e l e u a s p l e u s e r g l n c y s g l n e u g l u g l i n l e u s e r p r o t h r a l a p h a s p h r l e u a 520
Qy      13537  C C A G T T T C A G G T A T A A T A T G A G C C A C A C A C T T T T C A T T G A T C A C T T G C T T 13596
Db      520  s n l y s l e u g l n v a l l e u a s m e t s e r h i s a a n a n p h e p h e s e r l e u a s p a l a p h e p r o t 540
Qy      13597  A T A A G T G T C G A C T C C C T C C A G A T T C T T G A T T A C A G T C A T C A T C A T A T G A C T T C C A 13656
Db      540  y t l y s c y s l e u p r o s e r l e u c l n v a l l e u a s p t y r s e l e u a s h i s l l e t h i s e r l 560
Qy      13657  A A A A A C A G A A C T A C A G A T T T C C A A G T A G T T A G C T T T T T A A T C T T A C T C A G A T G 13716
Db      560  y s a n g l n g l u p r o g l n h i s p h e p r o s e r l e u a l a p h e l e u a s n l e u t h r g l n a s n a 580
Qy      13717  A C T T G C T T G A C T T G A A C C A G A G T T T C C G C A A T G A T C A A G A C C A G A G C A C 13776
Db      580  s p r h e a l a c y s t h c y s g l n h i s g l n s e r p h e l e u g l n t r p l l y l s p s g l n a r g l n l 600
Qy      13777  T C T T G T G A A G T T G A A C G A A T G A T G C A C A C C T T C A G A T A G A G G C G A T G C T G 13836
Db      600  e u l e u v a l g l u a l g l u h g m e c l u c y a l a t n r p r o s e r a s p l y s e g l n c l y e t p r o v 620
Qy      13837  T G C T G A T T T G A A T A T C A C C T G T C A G A T A A G A C C A T T G T G T G C G T C T C A 13896
Db      620  a l l e u s e r v a l a s n l e t h r c y s g l n m e c a e n l y s t h r l l e g l y a l s e r v a l p h e s 640
Qy      13897  G T G G C T T T G A T A T C T G T T G A C A G T T C G T G C T A T A A G T T T A T T T C A C C T G A T G C 13956
Db      640  e r v a l l e u v a l s e r v a l a l a v a l l e u v a l t y r l y s p h e t y r p h e h i s l e u n e t l 660
Qy      13957  T T C T T G C T G C T G A T A A G A T G T G A G G T G A A A C A T C A T A T G A G C C T T G T A T C T 14016
Db      660  e u l e u a l a g l y c y l l e y s t r l y a r g l y l u a n l l e t y r a s p l a p h e v a l l e t 680
Qy      14017  A C T C A G C C A G A T A G A C T G G G T A A G A A T G A T A A G A A T T T A A G A A G A G G G 14076

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Db      680  y r s e r g l n a s p l u a s p t r y v a l a r g a n g l u e u v a l l y a s n l e u g l u g l y v 700
Qy      14077  T G C C T C A T T T C A C T C G C C T T C A C T A C A G A C T T A T T C C G G T G G C A T T G C T G 14136
Db      700  a l p r o p r o p h e g l n e u c y s l e u h i s t y r a r g a s p h e i l e p r o g l y a l a l e a l a a 720
Qy      14137  C C A A C A T C A T C A T A G A G T T T C C A T A A A G C C A A A G C G A T T G T G T G T C C A G C 14196
Db      720  l a a n l l e l l e h i s g l u g l y p h e i s l y s e r a r g l y s v a l l e v a l a l a s e r g l n h 740
Qy      14197  A C T T C A T C C A G A C C C G T G T G T A T T C T T G A A T A T G A T T G C T C A G C C T G C A C T T T C 14256
Db      740  l s p h e i l e g l n s e r a r g t r p c y s i l l e p h e g l u r y g l u l e a l g l n t h r t r p g l n p h e l 760
Qy      14257  T G A C A G C G C G T G A T A C T T C A T T G C C G A G A G G T G A A G A C C C T G C T C A 14316
Db      760  e u s e r s e r a r g a l a g l y l e l l e p h e l l e v a l l e u g l n l y s v a l g l u y s t h r l e u e u a 780
Qy      14317  G G C A G A G T G A C C T T A C C G C C T T C A G A G A A C A C T T A C T G A T G G A G A C A 14376
Db      780  r g l n g l n v a l g l u e u t y r a r g l e u s e r a r g a n t h r t y r l e u g l u t r p g l n a s p s 800
Qy      14377  G T G T C T G G G C G C A C A C T T T C T G A G A C A C T C A G A A A C C C T G A T G A T A A T 14436
Db      800  e r v a l l e u g l y g l n h i s l l e p h e t r p a r g a r g l e u a r g l y s a l a l e u a s p l y a r g s 820
Qy      14437  C A T G A A T C C A G A A 14450
Db      820  e r t r a p a n p r o g l u 824

RESULT 6
TLR4_HORSE
ID_TLR4_HORSE STANDARD; PRT: 843 AA.
AC OSMYR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandeplass M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity). (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AY005808; MAF91076.1; -.
CC HSP: Q15399; LFYV.
CC GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
CC GO: GO:0001530; F:lipopolysaccharide binding; ISS.

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QY 13117 TCAGAGAAATGGCTGAGTTTCAAGGCTGCTTCAAGGATTTGGACAAACA 13176
 DB 381 euserArgAsnArgLeuSerPheIysSerCysGysSerGlnAlaAspLeuSerThrThra 401
 QY 13177 GCTTAAGATTTATTAATGATGAGCTTCAATGGTGTATTATTAACATGAGTTCAACTTTGG 13236
 DB 401 rGLeuYHnIleuAspLeuSerPheAsnArgValIleSerMetSerSerAsnPheMetG 421
 QY 13237 GCTTAAGACATTAATGATGAGTTTCCAGCATTTCCAAATTTGAAACAAATGAGTGTAGT 13296
 DB 421 lYLeuGlnGlnLeuGlnIleuAspPheGlnIleSerThrLeuYsglnIleSerAsp 441
 QY 13297 TTTCAAGTATCTTCACTGACCAAACTCATTTAGCTTGAATTTTCACTGACCA 13356
 DB 441 heProValPheLeuSerLeuYsAsnLeuArgIYLeuAspIleSerYThrAsnThra 461
 QY 13357 GAGTTGCTTCAATGAGCATTTCAATGGCTTTCAGTCTGCAAGTCTTGAAGAGGCTG 13416
 DB 461 rGValIValPheHnIsgIYIlePheAspGlyLeuValIleSerLeuGlnValIleuYsMetAlaG 481
 QY 13417 GCATTTCTTTCAGAGAAACTTCCCTGAGATTTTTCAGAGAGCTGAGAACTTGAAGCT 13476
 DB 481 lYAsnSerPheIysAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThrT 501
 QY 13477 TCCTGAGACCTCTCTCAGTGTCATCGAGAGTTGTCTCCAAAGCATTTAAGCTCACTCT 13536
 DB 501 hYLeuAspLeuSerIYsCysAsnLeuGlnValIleSerGlnGlnIleAspCysLeuLeuP 521
 QY 13537 CCAAGTCTTCAAGTATTAATTAATGAGCCAAACAATTTCTTTCATGAGTACGTTTCTCT 13596
 DB 521 rGValGlnArgValIleuAsnMetSerHISAsnAsnLeuLeuPheLeuAspMetLeuP 541
 QY 13597 ATAAGTGTCTGAACCTCCCTCCAGGTTCTTGATTTACAGTCTCAATGACATTAAGCTTCA 13656
 DB 541 YrLYsPProLeuHnIleSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPheL 561
 QY 13657 AAAAAGAGAGCTCAGCATTTTCCAGTATGAGCTTCTTAAATTTTCTAGAGATG 13716
 DB 561 YsTrpGlnGlnLeuGlnIlePheProSerSerLeuAlaSerLeuAsnMetThrGlnAsnA 581
 QY 13717 ACTTGTCTTGTACTTGTGAACACAGAGTCTCTGCAATGAGTCAAGGACGAGGCGAGC 13776
 DB 581 sPheAlaCysValCysGlnIYrGlnSerPheLeuGlnIYrValIYsAspGlnArgGlnL 601
 QY 13777 TCTTGTGGAAGTTGAAGATGGAATGGAATGCAACCTTCCAGATGAGACGAGGCTGCTG 13836
 DB 601 euleuValGlnValGlnIleuValCysAlaAlaIleProLeuGlnMetArgIYMetProV 621
 QY 13837 TGCTGAGTTTG---AATATGACCTGTGAGATTAAGCATGATGGTGTGCGGTC 13893
 DB 621 alIleuGlnPheAsnAsnAlaThrCysGlnIleSerYsThrIleValIleYIleYsValP 641
 QY 13894 TCAGTGTCTGTATGATCTGTGTAGAGAGTGTGTATTAAGTTCTATTTCACTGA 13953
 DB 641 heSerIleLeuMetValSerValIleAlaValIleuValIYIYsPheYrPheHnIleuM 661
 QY 13954 TGCTTTCTTGTGCTGCTCAATAAGTGTAGAGGTAAGGTAACATCTATGATGCTTTGTTA 14013
 DB 661 etIleuLeuAlaGlyCysIYsIYsIYrGlyArgGlyGlnSerIleYrAspAlaPheValI 681
 QY 14014 TCTATCAAGCAGAGGAGAGCTGGGTAAGATGAGCTGTAAAGATTAAAGAG 14073
 DB 681 lYrYsSerSerGlnAspIleuAspTrpValArgAsnGlnLeuValIYsAsnLeuGlnG 701
 QY 14074 GGGTGCCTTCATTTCACTGCTTCACTCACTCAAGAGCTTATTTCCCGGTGTGSCCATYTG 14133
 DB 701 lYValPProPheGlnLeuYsCysLeuHnIYrArgAspPheIleProGlyValAlaIleA 721
 QY 14134 CTGCCAATCATTCATTAAGTTTCCATTAAGCCGAAAGGTGATTTGTGTGTCCTC 14193
 DB 721 lAaIleAsnIleIleGlnGlnGlyPheHnIYsSerArgIYValIleValIValIleSerG 741

QY 14194 AGCACTTCATTCAGAGCCGCTGTGTATCTTGAATATGAGATTTGCTCAGACTGGCAGT 14253
 DB 741 lHnIspheIleGlnSerArgTrpCysIlePheGlnIYrGlnIleAlaGlnThrTrpGlnP 761
 QY 14254 TTTGAGACAGTCTGCTGCTGATTCATTTCACTTGTCTTGCAGAGAGTGAAGACCTGTC 14313
 DB 761 heLeuSerSerArgAlaGlyIleIlePheIleValIleuHnIYsYLeuGlnIYsSerLeuL 781
 QY 14314 TCAGAGCAGAGGTGAGCTGATCCGCTTTCAGCAGAGAACACTTACTGGAGTGGAGG 14373
 DB 781 euaYrGlnGlnValGlnLeuYrArgLeuLeuAsnArgAsnThrIYrLeuGlnIYrGlnI 801
 QY 14374 ACAGTCTCTGGGGCGGACATCTTCTGAGACGACTCAGAAAACCCCTGCTGAGTGA 14433
 DB 801 sPseValIleuGlyArgHISleIlePheTrpArgLeuAlaGlyValIleuLeuAspGlyL 821
 QY 14434 AATCATGAATCCAGAAAGAAACA 14456
 DB 821 YsProTrpSerProAlaGlyThr 828
 RESULT 7
 TR4 BOVIN STANDARD; PRT; 841 AA.
 ID TR4 BOVIN Q9GL65;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovine; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. Dubey C.T., Jungl T.W.;
 RA Guionaud C.T., Dubey C.T., Jungl T.W.;
 RT "Bovine Toll-like receptor 4 (TLR4).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MYD88, IRAK and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TR4.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and IRAK via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF310952; AAC32061.2; -.
 DR HSSP; 060603; LFYX.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macrophage activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biogen. . . ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biogen. . . ISS.

DR	GO:	GO:0045368;	P:Positive regulation of interleukin-13 biosyn. . . ; ISS.
DR	GO:	GO:0045410;	P:Positive regulation of interleukin-6 biosyn. . . ; ISS.
DR	GO:	GO:0042088;	P:T-helper 1 type immune response; ISS.
DR	InterPro:	IPR001611;	LRR.
DR	InterPro:	IPR000483;	LRR_Cterm.
DR	InterPro:	IPR003591;	LRR_typ.
DR	InterPro:	IPR001571;	LRR.
DR	Pfam:	PF00560;	LRR; 13.
DR	Pfam:	PF01463;	LRRCT; 1.
DR	Pfam:	PF01582;	TIR; 1.
DR	PRINTS:	PR00019;	LEUICHRPT.
DR	SMART:	SM00369;	LRR_Typ; 1.
DR	SMART:	SM00082;	LRRCT; 1.
DR	SMART:	SM00255;	TIR; 1.
DR	PROSITE:	PS50104;	TIR; 1.
KW	Glycoprotein:		Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT	SIGNAL:	1	23
FT	CHAIN:	24	841
FT	DOMAIN:	24	632
FT	TRANSMEM:	633	653
FT	DOMAIN:	654	841
FT	REPEAT:	53	76
FT	REPEAT:	77	100
FT	REPEAT:	102	124
FT	REPEAT:	149	173
FT	REPEAT:	174	197
FT	REPEAT:	203	225
FT	REPEAT:	277	300
FT	REPEAT:	310	334
FT	REPEAT:	350	372
FT	REPEAT:	373	398
FT	REPEAT:	400	421
FT	REPEAT:	422	445
FT	REPEAT:	446	469
FT	REPEAT:	471	494
FT	REPEAT:	495	518
FT	REPEAT:	520	542
FT	REPEAT:	544	566
FT	REPEAT:	568	592
FT	DOMAIN:	673	819
FT	CARBOHYD:	35	35
FT	CARBOHYD:	73	73
FT	CARBOHYD:	205	205
FT	CARBOHYD:	238	238
FT	CARBOHYD:	282	282
FT	CARBOHYD:	309	309
FT	CARBOHYD:	497	497
FT	CARBOHYD:	526	526
FT	CARBOHYD:	575	575
FT	CARBOHYD:	625	625
FO	SEQUENCE:	841 AA;	96026 MW; C5E1YCB9C798CD16 CRC64;

Predicted Score:	1.24e-230	length:	841
Pred. NO.:		Matches:	583
Score:	2971.50	Conservative:	77
Percent Similarity:	84.18%	Mismatches:	113
Best Local Similarity:	74.36%	Indels:	11
Query Match:	8.99%	Gaps:	4
DB:	1		
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Oy	12165 CTGAGATTAAATATTC--TATTTTAGGTCTTAATTCAGCAGAATAATTGATTAATCAATG	12221	
Dd	59 LeuapSerPheanTyLeudargHISleuGIYSerHisbnPhe-----Ser	75	
Oy	12222 TCCTTTTATTC-----TGAGGTGAATTCAGACAAATTGAAGAT	12263	
Dd	76 SerPheProGluLeuGINValLeuapSerPheSerGysGinUleuSIIellegIuaP	95	
Oy	12264 GGGGCATATACGAGCCCTTAAGCACCTTCTAACCCTTAATATTGACAGAAAACCCCATCGAG	12323	

Dd	96	AspThrPheGlnIleuYleuAsnH1sLeuSerThrLeuH1leuThrC1yLysnProH1leGln	115
Qy	12324	AGTTTACCCCTGGAGACCTTTTGTGACATATCAAGTTTACAGAACTGGTGGCTGGAG	12383
Dd	116	SeuLeuL1atPrG1yL1aPheSerG1yLeuSerSerLeuGlnYleuValAlaValGln	135
Qy	12384	ACAAATTCACATCTCTAGAGAACTTCCCATGGACATCTGAAACTTGGAAAGAACTT	12443
Dd	136	ThrAsnLeuVal1SerLeuAsnAapPheProH1leGlnH1sLeuYAsnLeuYsGlnLeu	155
Qy	12444	AATGGCTGACAAATCTTATTCCAATCTTTCAATTTGCTGAGATTTTCTAATCTGACC	12503
Dd	156	AsnValAlaH1sAsnPheH1leH1sSerPheYleuLeuProGlnYrPheSerAsnLeuPro	175
Qy	12504	AATCTAGAGCACTTGACCTTTTCCAGCAACAAGATTCAAGATTTATTTAGCACAGACTTG	12563
Dd	176	AsnLeuGlnH1sLeuAapPheLeuSerAAsnAAsnYH1leGlnAsnH1leYrYrGlnAapVal	195
Qy	12564	CGGGTTTCAATCAAAATGCCCTTACTCAATCTCTTTAGACCTGGCCCTGAACTCTAG	12622
Dd	196	LYsValLeuH1sGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu	215
Qy	12624	AACCTTATCCAAACAGGTGACATTTTAAAGAAATTAGAGCTTCAATGACTTTTAAAGAAAT	12683
Dd	216	AspPheH1leGlnProGlnYrPheYsGlnH1leYleuLeuAsnG1yLeuH1rLeuH1sSer	235
Qy	12684	AATTTTATAGTTTAAATGTATGAAAACTTGATTCAGAGTCTGGCTGGTTTAGAGTCT	12743
Dd	236	AsnPheAsnSerSerH1sValMetClyYrThrCyH1leGlnGlyLeuH1agYleuYsThr	255
Qy	12744	CATGCTTTGGTCTGGGAGAAATTTAGAAATGAAGAACTTGGAAAAATTGCAAAATCT	12803
Dd	256	AsnArgLeuValH1leuGlnYrPheYsAsnGlnArgYleuGlnArgPheAspArgSer	275
Qy	12804	GCTCTAGAGGCGCTGGTSCAATTTTGACATGGAAGATTCGATTAACATCTAGACTAG	12863
Dd	276	PheLeuGlnGlyLeuCyAsnLeuThrH1leGlnGlnPheArgH1leAtYrLeuAapYs	295
Qy	12864	TACCTCCATGATATTTATGTGACTTATTTAATTTGTTTGAACAATGTTTCTCATTTTCCCG	12922
Dd	296	PheSerGlnYAspArgThrAapPheLeuPheAsnCyLeuH1AsnValSerAlH1sSerLeu	315
Qy	12924	GTCAGTGTACATATGAAAAGGGTAAAAGACTTTTCTTATATTTGCGATGGCAACTTAA	12983
Dd	316	LeuSerH1leSerLeuGlnYSerLeuGlnAlaLeuLeuYsAspPheArgTrGlnH1sLeu	335
Qy	12984	GAATTAATTAACGTGAATTTTGACAGCTTTCCCAATTTGAACATCAAACTCTCAAAAGG	13043
Dd	336	GlnH1leAsnCyAspPheAapPheYrPheProAlaLeuYsLeuSerSerLeuYsYs	355
Qy	13044	CTTACTTTTCACTTSCAAACAAGGTGGGAATGCTTTTTCAGAAATTTGATCTACCAACCTT	13103
Dd	356	PheValH1rPheThrAapH1yAspH1leSerThrPheThrGlnH1eGlnLeuProSerLeu	375
Qy	13104	GAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAAAGTTGCTGTTCTCAAGTAT	13163
Dd	376	GlnYrPheAapPheLeuYsArgAsnH1sLeuSerPheYsG1yYsCySerH1sThrAap	395
Qy	13164	TTTGGGACAACAGCTTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTAACCAAGAGT	13222
Dd	396	PheGlnYrThrH1rAsnLeuYsH1sLeuAapPheLeuSerPheAsnAapValH1leThrLeuGly	415
Qy	13224	TCAAACTTCTGGGCTTAGAACAACATCTGAAATCTGGATTTTCCAGACTTSCAATTTGAAA	13283
Dd	416	SerAsnPheMetG1yLeuGlnGlnLeuGlnH1sLeuAapPheGlnH1sSerThrLeuYs	435
Qy	13284	CAAAATGTAGATTTTCAAGTATTTCTATCACTCAGAAACCTCATTTTACCTGCAATTTCT	13343
Dd	436	GlnH1eAsnH1aPheSerH1aPheLeuSerLeuArgAsnLeuArgYrLeuAapH1leSer	455
Qy	13344	CATATCTACACACAGAGTCTTTCATATGAGATCTTCAATGGCTTTCACAGTCTCGAAAGTCT	13403
Dd	456	YrThrH1rAsnH1eArgH1leValH1rAsnH1sG1yH1rPheThrG1yLeuValSerLeuGlnThr	475

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QY 13404 TTGAATGCTGGCAATTCCTTCAGAGAAAATTCTTCAGATATCTTCAGAGCTG 13463
DB 476 LeuysmetAlaGlyAsnSerPheGlnAsnLeuLeuProAspIlePheThrIleu 495
QY 13464 AGAACTTGACCTTCTGAGACTCTCTGAGTGTCACTGAGACACTTGTCTTCAACACA 13523
DB 496 ThrAsnLeuThrValLeuAspLeuSerIysCysGlnLeuGlnValAlaGlnThrAla 515
QY 13524 TTTAACTGACTCCAGCTTCAGTACTTAATAGACCCCAACACTTCTTTCATG 13563
DB 516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeu 535
QY 13584 GATAGCTTCCCTTAAGTGTGTCGAACTCCCTCCAGTTCCTTGAATGATCAAC 13643
DB 536 AspThrPheLeuTyrgluProLeuHisSerLeuAspGlyLeuAspCysSerPheAsnArg 555
QY 13644 ATTAATGACTCCAAAAAGAGAACTACAGCACTTTCCAGTAGTCTTAAAT 13703
DB 556 IleMetAlaSerLysGlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrThrLeuAsn 575
QY 13704 CTTACTGAGATGACTTGTGTTACTGTAACCAAGAGCTTCCTGATGATCAAG 13763
DB 576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLys 595
QY 13764 GACCAAGGAGAGCTCTTGTGGAAGTTGAACAAATGATGCAACACTTCAGATAG 13823
DB 596 AspGlnArgGlnLeuLeuValGlyAlaGlnGlnMetCysAlaGlnProLeuAspMet 615
QY 13824 CAGGCAATGCTGTGCTGAGTTTG--AATATCACTGTCAAGATGATGACATCAT 13880
DB 616 GluAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIle 635
QY 13881 GGTGTGCGTCCAGTGTCTGTAGTATCTGTGAGACAGTTCGTCTATTAAGTTC 13940
DB 636 SerValSerValValThrValLeuValSerValValGlyValLeuValTyrLysPhe 655
QY 13941 TATTTTCACTGAGCTTCTGTGCTGCTGCAATAAGTGTGAGAGGTAAGCACTCAT 14000
DB 656 TyrPheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyLysSerIleTyr 675
QY 14001 GATGCTTTGTTATCTACTCAAGCCAGATGAGCACTGGTGAAGATGACTGAATAG 14060
DB 676 AspAlaPheValIleTyrSerSerGlnAspGlnAspThrValArgAsnGlnLeuValLys 695
QY 14061 AATTGAAGAAGAGGGTCCCTCCATTCAGCTTCGCTTCACTACAGAGATTTATCCC 14120
DB 696 AsnLeuGlnGlnValProProPheGlnLeuCysLeuHisTyrArgAspPheIlePro 715
QY 14121 GGTGTGCTGCTGCTGCAATCATCATGATGAGTTTCCATTAAGCCGAAGAGTATT 14180
DB 716 GlyValAlaIleAlaIleAsnIleIleGlnGlnGlnPheHisLysSerAspGlyValIle 735
QY 14181 GTTGTGTGTCCAGCACTTCATCAGAGCCGCTGTGTATCTTGAATATGAGATTGCT 14240
DB 736 ValValValSerGlnHisPheIleGlnSerArgTyrPyrIlePheGlnTyrGlnIleAla 755
QY 14241 CAGACCTTGAGCTTTCGAGAGTGTGTGTATCATCTTCATTTGCTTCAGAGAGGTG 14300
DB 756 GlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeu 775
QY 14301 GAGAAGACCTGCTCAGAGCAGAGTGTGAGTGTACCGCTTCAGAGAGGACACTTAC 14360
DB 776 GluLysSerLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerAspAsnThrTyr 795
QY 14361 CTGAGTGGAGAGACAGTGTCTGTGGGCGGACACTTTCGAGAGCACTCAGAAAAGCC 14420
DB 796 LeuGlnTyrPgluAspSerValLeuGlyArgHisValPheTyrPargArgLeuArgValAla 815
QY 14421 CTGCTGATGCTAATATGTAATCCAGAGAGACAGTGGGTACAGATGCAATTTGGCAG 14480
DB 816 LeuLeuAlaGlyLysProGlnSerProGlnIleThrAlaAspAlaGlnThrAsnProGln 835

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QY 14481 GAGCAATCATCT 14492
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AC 08S055;
DT 01-JUN-2002 (TREMBLERel. 21, Created)
DT 01-JUN-2002 (TREMBLERel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLERel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RL Ito T., Morimatsu M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056444; BAB86840.1; -.
DR HSSP; 060603; 1077.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:Grammembrane receptor activity; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:mast cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF00560; LRR_1; 11.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Receptor.
SQ SEQUENCE 841 AA; 96054 MW; E08DCA840EA12D6F CRC64;
Alignment Scores:
Pred. No.: 2,16e-230 Length: 841
Score: 2968.50 Matches: 582
Percent Similarity: 84.18% Conservative: 78
Best Local Similarity: 74.23% Mismatches: 113
Query Match: 8.98% Indels: 11
DB: Gaps: 4
US-09-396-985b-47 (1-18989) x 08S055 (1-841)
QY 12165 CTAGATTAATATTC--TATTTAGGTTCTTATTCAGCAGAAATATGATATCAATG 12221
DB 59 LeuAspLeuSerPheAsnTyrLeuAlaGlnHisLeuGlySerHisAsnPhe-----Ser 75
QY 12222 TCTTTTATTC-----TTAGGTGTAATCCAGACAAATTTGAAGAT 12263
DB 76 SerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIleLysIleIleGlnAsp 95
QY 12264 GGGGCATATCAGAGCCTAAGCCACCTCTTACTTATATTTGACAGAAACCCCATCCAG 12323

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Db	96	AspThrheGlnGlyLeuAsnHisLeuSerThrLeuIleLeuThrCylAsnProIleGln	115
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Db	116	SeuLeuIaIatProGlyAlaPheSerGlyLeuSerSerLeuGlnHisLeuValAlaValGlu	135
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Db	136	ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuHisAsnLeuArgGlyLeu	155
Oy	12444	AATGTGGCTACAACTCTTAATCCAACTTTCAAAATTTGACGAAATTTTCTTAATCTGACC	12503
Db	156	AsnValAlaHisAsnPheIleHisSerPheLeuLeuProGlyIlePheSerAsnLeuPro	175
Oy	12504	AATCTAAGACACTTTGACCTTTTCCAGACAAATTCAAAGATTTATTTGACAGACACTTTG	12563
Db	176	AsnLeuGlnHisLeuAspLeuSerAsnAsnHisLeuIleGlnAsnIleTyrGlyAlaVal	195
Oy	12564	CGGGTTCTACATCAAAATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAACCTTAG	12623
Db	196	LeuValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspSerLeuAsnProIleu	215
Oy	12624	AACCTTTACCAACGAGGTGCATTTTAAAGAAATTAAGCTTCATTAAGCTCACTTAAGAAT	12683
Db	216	AspPheIleGlnProGlyIlePheLeuGlnIleLeuAsnAsnIleLeuThrLeuArgSer	235
Oy	12684	AATTTTATAGATTAAATGTAAAGAAACTTTGATTCAGAGTCTGGCTGGTTTAAAGATC	12743
Db	236	AsnPheAsnSerSerHisIleValMetLeuThrCysIleGlnGlyLeuAsnIleLeuLeuThr	255
Oy	12744	CATCGTTTGGTCTCGGAGAAATTTGAAATGAAGAAACTTGAGAAAAGTTTGACAAATCT	12803
Db	256	AsnArgLeuValIleGlnGlyIlePheLeuAsnGluArgIleLeuGlnArgPheAspArgSer	275
Oy	12804	GCTCTAAGAGGCGCTGTGCATTTTGAACATTTGAAGAAATTCGGATGACATCTTAAGATAC	12863
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Oy	12864	TACCTCGATGATATTTATGACTTATTTTAAATTTGTTTGAACAAATGTCTTCATTTTCCCG	12923
Db	296	PheSerGlyAspAspThrPhePheAsnHisCysLeuAlaAsnValSerValIleSerLeu	315
Oy	12924	GTGAGTGATATATTGAAGAGGTAAAGAACTTTTCTTATATTTTCCGATGGGACAACTTA	12983
Db	316	LeuSerIleSerLeuGlnGlySerLeuGlnAlaLeuLeuHisLeuAspPheArgIleGlnHisLeu	335
Oy	12984	GAATTAAGTTAACTGTAATTTTGGACAGTTTCCACATTTGAATCTCAAAATCTCAAAAG	13043
Db	336	GluIleIleAsnCysAspPheAspLeuPheProAlaLeuLeuLeuSerSerLeuLeuHis	355
Oy	13044	CTTACTTTCACTTCCAAAGAGGGGAAAGCTTTTTCGAAAGATGATCTACCAAGCCCTT	13103
Db	356	PheValPheThrAspAsnHisLeuAspIleSerThrPheThrCylPheGlnLeuProSerLeu	375
Oy	13104	GAGTTTCTAGATCTCAGTAGAAATAGGCTTGAAGTTTCAAAAGTTGCTGTCTCAAAAGTAT	13163
Db	376	GlnTyrLeuAspLeuLeuValArgAsnHisLeuSerPheLeuSerIleLeuCysSerHisThrAsp	395
Oy	13164	TTTGGGACACACGACCTTAAAGATATTAGATCTGAGCTTCATGSGTGTATTATACAGTACT	13223
Db	396	PheGlyThrThrAsnLeuLeuHisLeuAspLeuSerPheAsnAspValIleThrLeuGly	415
Oy	13224	TCAAACTCTTGGGCTTAAAGAACTGAATCATCTGGAATTTCCAGAGATTCGAAATTTGAA	13283
Db	416	SerAsnPheMetCylLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLeu	435
Oy	13284	CAAAATGAGTGAAGTTTCAAGTATCTTATCTACATGAAACCTCAATTATACCTTGACATTTT	13343
Db	436	GlnIleAsnAlaPheSerAlaPheLeuSerLeuAspArgAsnLeuArgTyrLeuAspIleSer	455
Oy	13344	CATATCTACACAGAGTTGCTTTCAATGAGCATTTCAATGGCTTTGTCCAGTCTCGAAGTC	13403

Db	456	lyThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr	475
QY	13404	TTGAAATAGGTGGCAATCTTTCCAGGAAAATTCTTCAGATATCTTCACAGAGCTG	13463
Db	476	LeuIysMetAlaGlyAsnSerPheGlnAsnIleLeuLeuProArgIlePheThrGlyLeu	495
QY	13464	AGAAACTGACCTTCTTGACCTCTCTCAGTGTCAACTGGAGCACTTGCTCCAAACGA	13523
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QY	13524	TTTAACTACACTCCAGCTTCAGGTACAAATATAGACCAACAACATCTTTCATTTG	13583
Db	516	PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnIlyLeuLeuSerLeu	535
QY	13584	GATACGTTCTTTAAAGTGTGTGAACCTCCCTCAGAGTTCTTGATTACAGTCCATCAC	13643
Db	536	AspThrPheLeuIyGlnProLeuHisSerLeuAspArgIleLeuAspCysSerPheAsnArg	555
QY	13644	ATAATGACTTCCAAAAACAGAACTACAGCAATTTCCAGTAGTGTACGTTCTTTAAAT	13703
Db	556	IleMetAlaSerIyGlnGlnIleuGlnAsnLeuProArgSerLeuThrTrpLeuAsn	575
QY	13704	CTTACTACAGATGACTTGTGCTTGATCTTGTAACACCAAGAGTTTCTCGAAATGAGTCAAG	13763
Db	576	LeuThrGlnAsnAlaPheAlaCysValCysGlnIyGlnSerPheLeuGlnTrpValIys	595
QY	13764	GACCAAGGCAAGCTTGTGGAGATTGAACGAATGAGATGTGCAACACTTCAGATTAAG	13823
Db	596	AspGlnArgGlnLeuLeuValGlyAlaGlnGlnMetCysAlaGlnProLeuAspMet	615
QY	13824	CAGGCAATGCTGTGCTGAGTTG--AAATACACTGTCCAGATGAATAGCCATCATT	13880
Db	616	GlnAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerIyThrIleIle	635
QY	13881	GGTGTGGGTGCTCAGTGTGTGTAGATGTGTGTAGAGCACTTGCTGATTAAGTTC	13940
Db	636	SerValSerValThrValLeuLeuValSerValGlyValLeuValIyTrpIysPhe	655
QY	13941	TATTTTCACTGATGCTTCTTGCTGCTGCAATTAAGTATGTAAGAGTGAACAATCTAT	14000
Db	656	TyrPheHisIleMetLeuLeuAlaGlyCysIyGlyGlyArgGlyIleIySerIleIy	675
QY	14001	GATGCTTTGTATTTACTCAAGCAAGATGAGACTGGGTGAAGATGACTAGTAAAG	14060
Db	676	AspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValIys	695
QY	14061	AATTTAGAAAGAGGGTGCTCCATTTGACGCTGCTCCTCACTACAGAGACTTTATGCC	14120
Db	696	AsnLeuGlnGlnGlyValProProPheGlnLeuCysIleHisIyTrpArgAspPheIlePro	715
QY	14121	GGTGTGGCATTTGCTGCCAACATCATCATGAGGTTTCCATTAAGGCCGAAGGTGATT	14180
Db	716	GlyValAlaIleAlaIleAsnIleIleGlnGlnGlyPheHisIyIysSerIyGlyValIle	735
QY	14181	GTGTGTGTGTCCAGCACTTCAACAGACCGCTGATCTTTGAAATATAGATGCT	14240
Db	736	ValIleValIleSerGlnHisPheIleIleGlnSerArgTrpCysIlePheGlnIyGlnIleAla	755
QY	14241	CAGACTTGCAATTTCTAGACAGTGTGTGTGTATCATCTTATATGTCTCGAAGAAAGTG	14300
Db	756	GlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIyIysLeu	775
QY	14301	GAGAAAGACCTTGTGAGCAGAGGATGTGAGCTGACCGCTTCTGACAGAAACTTAC	14360
Db	776	GlnIySerSerLeuAspArgGlnGlnIleAlaGlnLeuIyTrpArgLeuLeuSerIyArgAsnThrIy	795
QY	14361	CTGAGTGGAGAGACAGTGTCTTGAGGCGGCAATCTTTGAGAGAGACTCAAGAAAGCC	14420
Db	796	IeuGlnIyTrpGlnAspSerValIleuGlyArgHisValPheTrpArgIyLeuArgIyAla	815
QY	14421	CTGCTGAGATGTTAAATCATGGAATCCAGAAAGAAACAGTGGGATGACAGATGCAATTGGCAG	14480
Db	816	LeuIeuAlaGlyIyProGlnIySerProGlnGlyIyThrAlaAspAlaGlnIyThrAsnProGln	835

QY 14481 GAAGCAATCT 14492
 DB 836 GluAlaThrThr 839

RESULT 9
 Q6WCDS
 ID Q6WCDS PRELIMINARY; PRT; 841 AA.
 AC Q6WCDS;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL: AY297040; AAG62700.1;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:Citramembrane receptor activity; IEA.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003885; LRR_cyst.
 DR InterPro: IPR003591; LRR_typ.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF00560; LRR_1; 12.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00365; LRR_SD22; 6.
 DR SMART: SM00369; LRR_TYP; 13.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR Receptor.
 SQ SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;

Alignment Scores:
 Pred. No.: 3,14e-230 Length: 841
 Score: 2966.50 Matches: 582
 Percent Similarity: 84.06% Conservative: 77
 Best Local Similarity: 74.23% Mismatches: 114
 Query Match: 8.97% Indels: 11
 Gaps: 4

US-09-396-985b-47 (1-18989) x Q6WCDS (1-841)

QY 12165 CTGAGTAATATTC--TATTTAGTCTTATTCAGCAAAATATTAATCAATG 12221
 DB 59 LeuAspLeuSerPheAsnTyrLeuAlaArgHisLeuGlySerHisAsnPhe-----Ser 75

QY 12222 TCTTTTATTC-----TGTAGGTGAATTCAGCAATTAAGAT 12263
 DB 76 SerPheProGluLeuGlnValLeuAspLeuSerArgCysGluLeuIleIleGluAsp 95

QY 12264 GGGGCATATCAGAGCTTAAGCACTTCTTACCTTAATATTAAGCAAGAAATCCCATTCAG 12323
 DB 96 AspThrPheGlnGlyLeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGln 115

QY 12324 AGTTTACCTGGAGAGCTTTTCTTGACATCAAGTTTACAGAAAGCTGGCTGTGGAG 12383
 DB 116 SerLeuAlaTyrGlyAlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGlu 135

QY 12384 ACAATCTAGCATCTTACAGAACTTCCCATTCAGATCTCAAACTTTGAAGAAGCTT 12443

DB 136 ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGluLeu 155

QY 12444 AATGTGGCTCACAACTCTTATCCAACTTTCAATTCCTGACATTTTCTAATCGACC 12503
 DB 156 AsnValAlaHisAsnPheIleHisSerPheLysLeuProGluLysPheSerAsnLeuPro 175

QY 12504 AATCTAGACACTTGGACCTTTCAGCAACAAGATCAAGATTAATTAATTCAGACCTTG 12563
 DB 176 AsnLeuGlnHisLeuAspLeuSerAsnAsnLysIleGlnAsnIleTyrTyrGluAspVal 195

QY 12564 CGGGTTCTACATCAAAATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAACCTTAG 12623
 DB 196 LysValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu 215

QY 12624 AACTTTATCCAAACAGAGTGCATTTAAAGAAATTTAGCTCATAGCTGATTTAAGAAAT 12683
 DB 216 AspPheIleGluProGlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuArgSer 235

QY 12684 AATTTGATAGTTTAATGAATGAATGAACCTTGATTCAGAGTGTGGCTTGAAGTC 12743
 DB 236 AsnPheAsnSerSerHisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThr 255

QY 12744 CATCGTTTGGTTCTGGAGAAATTTAGAAATGAAGAACTTGGAAAGTTTGAACAATCT 12803
 DB 256 AsnArgLeuValLeuGlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSer 275

QY 12804 GCTCTAGAGGCGCTGTGCATTTGACCATTTGAAGAAATTCGATTAGCATTTAGACTAC 12863
 DB 276 PheLeuGlnGlyLeuLysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspLys 295

QY 12864 TACCTGATGATTAATTAATGATTAATTTGTTGACAAAGTTTCTTCATTTGCCCG 12923
 DB 296 PheSerGlyAspAspThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeu 315

QY 12924 GTGAGTGTACTATTTGAAGAGGTAAAGACTTTTCTTAATATTCGATGCGACAATTGA 12983
 DB 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgIleGlnHisLeu 335

QY 12984 GAATTGATTAATCTGTAATTTTGGACAGTTTCCACATTTGAACCTCAAAATCTCAAAAG 13043
 DB 336 GluIleAlaAsnLysAspPheAspLysPheProAlaLeuLysLeuSerLeuLysLys 355

QY 13044 CTTACTTCACTTCCAAACAAGGTGGAGATGCTTTTCAAGAGTTGATCTACCAACCTT 13103
 DB 356 PheValPheThrAspAsnLysAspIleSerThrPheThrGluPheGlnLeuProSerLeu 375

QY 13104 GAGTTTCTAGATCTCAGTAAGATGGCTTGAAGTTTCAAGTTTGTCTCAAAATGAT 13163
 DB 376 GlnTyrLeuAspLeuLysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAsp 395

QY 13164 TTTGGACAACAGCTTAAGATTTTGAATCTGAGCTTCAATGAGTTTATTAACATGAGT 13223
 DB 396 PheGlyThrThrAsnLeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGly 415

QY 13224 TCAAACTTGTGGCTTAAGAAACAACATTCGATTTCCAGATTTCCAAATTTGA 13283
 DB 416 SerAsnPheMetGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLys 435

QY 13284 CAATAGTAGAGTTTCAATATTCATATCTCAGAAACCTGATTAACCTTGCATTTCT 13343
 DB 436 GlnIleAsnAlaPheSerAlaPheLeuSerLeuAsnArgAsnLeuArgTyrLeuAspIleSer 455

QY 13344 CATACTCACACAGAGTGTCTTCAATGCAATCTTCAATGAGCTTGTCCAGTCCGAAGTC 13403
 DB 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475

QY 13404 TTGAAAATGGCTGGCAATCTTCTTCAAGAAATCTTCCGATTCCTTCCAGAGCTG 13463
 DB 476 LeuLysMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeu 495

QY 13464 AGAAACTTGAACCTTCTCGAGCTTCTCAGTGTCAACTGAGACAGATTTGCTCAACAGCA 13523

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Db      496 ThrAsnLeuThrValLeuAspLeuSerIysCysGlnLeuGlnValAlaGlnThrAla 515
Qy      13524 TTTAACTCACTGCTCCAGTCTTCAAGTACTGAATATATAGCAACAATTCTTTTCATTG 13583
Db      516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisValnIysLeuSerLeu 535
Qy      13584 GATACGTTTCCTTAATAAGTGTGAACTCCGCTCCAGTCTTCTGATTAACAGTCCATCAC 13643
Db      536 AspThrPheLeuTyrluProlLeuHisSerLeuArgIleLeuAspCysSerPheAsnArg 555
Qy      13644 ATAAAGACTTCCAAAAACAGAACTACAGCAATTTTCCAGTAGTCTAGCTTTCTTAAAT 13703
Db      556 IleMetAlaSerIysGlnGlnIleuGlnIleuGlnAsnLeuProArgSerIleuThrIleuAsn 575
Qy      13704 CTTAACTCAGAAATGACTTTGCTTTGCTTACTTTGTAACACCAAGATTCTCTGCAATGGATCAAG 13763
Db      576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnIlePValIys 595
Qy      13764 GACCAAGGAGGAGCTTGGTGGAAAGTTGAAGTAAGTAAGTAAGTAAGTAAGTAAG 13823
Db      596 AspGlnArgGlnLeuLeuValGlyAlaGlnIleMetCysAlaGlnProlLeuAspMet 615
Qy      13824 CAGGGACGCTGCTGCTGAGTTTG--AAATACCTGTCCAGTAGTAAGCAATCAAT 13880
Db      616 GlnAspMetProlValLeuSerPheArgAsnAlaThrCysGlnLeuSerIysThrIleIle 635
Qy      13881 GGTGTGTCGCTCCTCAAGTGTGCTTGAATGATCTGTTGTAGCAATTCTGGTCTTAAAGTTT 13940
Db      636 SerValSerValValThrValLeuLeuValSerValValGlyValLeuValTyrlsPhe 655
Qy      13941 TATTTTCACTGATGCTTCTGCTGCTGCTCATTAAGTAGTAGTAGTAAGTAAGTCAATCT 14000
Db      656 TyrPheHisLeuMetLeuLeuAlaGlyCysIysIleTyrlGlyArgIleuSerThrTyrl 675
Qy      14001 GATGCTTTGTATCTACTCAAGCCAGATGAGAGACTGGTAAAGATAGACTAGTAAG 14060
Db      676 AspAlaPheValIleTyrSerSerGlnAspGlnAspIleArgValArgGlnIleuValIys 695
Qy      14061 AATTAGAAAGAGGGGCTCCATTTCACTGCTGCTTCACTCACTCAAGACTTATTTCC 14120
Db      696 AsnLeuGlnIleGlyValAlaProlPheGlnLeuCysLeuHisTyrIleArgAspPheIlePro 715
Qy      14121 GGTGTGGCAATGCTGCGCAACATCATCATGAAGTTTCCATAAAGCCGAAAGGTGAT 14180
Db      716 GlyValAlaIleAlaAsnIleIleGlnGlnGlyPheHisIlysSerArgIysValIle 735
Qy      14181 GTTGTGGTGTCCAGCACTTCATCCAGAGCCGCTGTGATCTTTGAATAGAGATTGCT 14240
Db      736 ValValValSerGlnHisPheIleGlnSerArgIlePheGlnIleAla 755
Qy      14241 CAGACCTGGAGTTTCTGAGCAGTCCGCTGCTGATCATCTTCACTGCTGCGAAGGTG 14300
Db      756 GlnThrIlePheGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleu 775
Qy      14301 GAGAAAGCCCGCTCAGAGCAGAGTGGAGTGAACCGCTTCCAGCAGAAACACTTAC 14360
Db      776 GlnIysSerLeuLeuArgGlnIleValGlnLeuTyrlArgLeuLeuSerIleArgAsnThrTyrl 795
Qy      14361 CTGAGAGTGGAGGACAGTGTCTGTGGGCGGACACTTCTTGAGACGACTCAGAAAGCC 14420
Db      796 LeuGlnIlePheGlnPheSerValLeuGlyArgHisValAlaPheIleArgAlaGlyValAla 815
Qy      14421 CTGTGTGATGTGAATCATGGAATCCGAAAGAAACAGTGGGTACAGATGCATTTGGCAG 14480
Db      816 LeuLeuAlaGlyIysProlGlnSerProlGlnIleThrAlaAspAlaGlnThrAsnProlGln 835
Qy      14481 GAGCAACATCT 14492
Db      836 GlnAlaThrThr 839

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AC      06WCD4;
DT      05-JUL--2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Toll-Like receptor 4.
GN      Name=TLR4;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
RA      White S.N., Taylor K.H., Abbey C.A., Gill C.A., Mornack J.B.;
RT      "Haplotype variation in bovine Toll-like receptor 4 and computational
RT      prediction of a positively selected ligand-binding domain.";
RL      Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
DR      EMBL; AY297043; AA062701.1; JOINED.
DR      EMBL; AY297041; AA062701.1; JOINED.
DR      EMBL; AY297042; AA062701.1; JOINED.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0048888; F:transmembrane receptor activity; IEA.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003885; LRR_Cyst.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF01463; LRRCT; 1.
DR      Pfam; PF00560; LRR_1; 12.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00369; LRR_SD22; 6.
DR      SMART; SM00369; LRR_Typ; 13.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SEQUENCE. 841 AA; 95954 MW; AD6D06ACBF44C91 CRC64;

Alignment Scores:
Pred. No. 1.67e-229 Length: 841
Score: 2957.50 Matches: 591
Percent Similarity: 83.93% Conservative: 77
Best Local Similarity: 74.11% Mismatches: 115
Query Match: 8.94% Indels: 11
DB: 2 Gaps: 4

US-09-396-985B-47 (1-18989) x 06WCD4 (1-841)
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Db      59 LeuAspLeuSerPheAsnTyrlLeuArgHisIleGlySerHisAsnPhe-----Ser 75
Qy      12222 TCTTTTATTTCC-----TGTAGGTGGAATCCAGCAATTTGAAGAT 12263
Db      76 SerPheProlGlnLeuGlnValLeuAspLeuSerArgCysGlnIleIleIleGlnAsp 95
Qy      12264 GGGGCAATATCAGAGCTTAAGCCACTCTCTTACTTAATATTTGACAGAAACCCCATCCAG 12323
Db      96 AspThrPheGlnGlnIleuAsnHisIleuSerThrIleuIleLeuThrGlyAsnProlIleGln 115
Qy      12324 AGTTTACCCCTGGAGACCTTTCTGTGACATCAAGTTTACAGAAAGCTGTGGCTGTGGAG 12383
Db      116 SerLeuAlaIleTyrlAlaPheSerGlyLeuSerSerLeuGlnIysLeuValAlaValGln 135
Qy      12384 ACAATCTAGCATCTCTTAGAGACTTCCCATTTGACATCTCCAAAATTGAAAGAACTT 12443
Db      136 ThrAsnLeuValSerLeuAsnAspPheProlIleGlyHisIleuIysAsnLeuIysGlnLeu 155
Qy      12444 AATGTGGCTCACAACTTATCCAAATCTTTCAAATTAAGTGAAGTATTTTCTGAC 12503
Db      156 AsnValAlaHisAsnPheIleHisSerPheIysLeuPro*****PheSerAsnLeuPro 175

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QY 12504 AATCTAGACACTTGGAACCTTTCCAGACAAGATTCAAGTTATTTATGACAGACTTG 12563
 DB 176 AsnLeuGlnHisLeuAspLeuSerAsnAsnLysIleGlnAsnIleTyrGluAspVal 195
 QY 12564 CGGGTTTACATCAAAATGCCCCCTACTCAATCTCTTTAGACCTGCTCCAGACCTTAG 12623
 DB 196 LysValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu 215
 QY 12624 AACTTATCCAAACCGGTGCATTTAAGAATTTAGGCTTCATAGCTGACTTAAGAAT 12683
 DB 216 AspPheIleGluProGlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuAspSer 235
 QY 12684 AATTGTAGTATGTTATGATGAAGAACTGTATTCAGGCTGCTGGCTGTTTAGAATGC 12743
 DB 236 AsnPheAsnSerSerHisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThr 255
 QY 12744 CATGCTTTGGTTCTTGGAAGAAATTGAAGAAAGAACTTGAAAGATTTGACAAATCT 12803
 DB 256 AsnArgLeuValLeuGlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSer 275
 QY 12804 GCTCAGAGGGCCTGCAATTTGACCAATGGAAGAACTCCGATTGCACTACTAGACTAC 12863
 DB 276 PheLeuGluGlyLeuCysAsnLeuThrIleGluGlnPheArgIleAlaTyrLeuAspLys 295
 QY 12864 TACCTCGATGATATATGACTTATTTAATTGTTGACAAAGTTCTTCAATTTCCCTG 12923
 DB 296 PheSerGlyAspAspThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeu 315
 QY 12924 GTGAGTGTACTATTTGAAGGGTAAAGACTTTTCTTAATTTGCGATGGCACTTTA 12983
 DB 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgTrpGlnHisLeu 335
 QY 12984 GAATTAAGTAACTGTAAATTTGGACAGTTTCCACATTGAAACTAAATCTCTCAAG 13043
 DB 336 GluIleIleAsnCysAspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLys 355
 QY 13044 CTTACTTCACTTCCAAAGGTTGGAAGTCTTTTCAAGAACTTGATCTCAAGCCTT 13103
 DB 356 PheValPheThrAspAsnLysAspIleSerThrPheTrpGlnPheGlnLeuProSerLeu 375
 QY 13104 GAGTTTCTAGATCTCAGTAGAAATGGCTGATTCAAAGTGTGCTGTTCTCAAGATGAT 13163
 DB 376 GlnTyrLeuAspLeuLysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAsp 395
 QY 13164 TTTGGGACACCAAGCTTAAAGTATTTAATCTGAGCTTCATAGCTGTTATTTACCACTG 13223
 DB 396 PheGlyThrThrAsnLeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGly 415
 QY 13224 TCAAACTTCTGGGCTTAGAACAACTAGAACATTCGATTTCCAGATTTCCAAATTTGAA 13283
 DB 416 SerAsnPheMetGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLys 435
 QY 13284 CAATAGAGTGAATTTTCAGTATTCCTATCACTCAAGAACTCATTTTACCTTGACATTTCT 13343
 DB 436 GlnIleAsnAlaPheSerAlaPheLeuSerLeuArgAsnLeuArgTyrLeuAspIleSer 455
 QY 13344 CATACTCACACCAAGTTGCTTTCAATGCAATCTTCAATGCTGCTTCAGTCTGGAATGC 13403
 DB 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475
 QY 13404 TTGAAATGCTGGCAATTTCTTCCAGGAAAACTTCCAGATATCTTCCAGAGATG 13463
 DB 476 LeuLysPheValArgLysAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeu 495
 QY 13464 AGAAATTCGACTTCTGACCTCTCTCAGTGTCAACTGAGACAGTGTCTTCCACAGCA 13523
 DB 496 ThrAsnLeuThrValLeuAspLeuSerLysCysGlnLeuGluGlnValAlaGlnThrAla 515
 QY 13524 TTTAATCACTCTCAGTCTTCAAGTATTTAAATATAGCCCAACAACATCTTTTCATTG 13583
 DB 516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeu 535

QY 13584 GATACGTTTCTTAAAGTGTGAACTCCCTCCAGGTTCTTGATTAAGTGTCAATCAC 13643
 DB 536 AspThrPheLeuTyrGluProLeuHisSerLeuAsnArgIleLeuAspCysSerPheAsnArg 555
 QY 13644 ATTAATGACTTCCAAAACACAGAACTACAGCAATTTTCCAGTAGTCTTACTTTTAAT 13703
 DB 556 IleMetAlaSerLysGluGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsn 575
 QY 13704 CTTTACAGAAATGACTTTGCTTGACTTGATGAAACAGCAAGATTTCCGCAATGATGACAG 13763
 DB 576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnTrpValLys 595
 QY 13764 GACCAGAGCAGCTCTTGCTGGAAGTTGAAGCAATGGAATGGAACACTTCATGATAG 13823
 DB 596 AspGlnArgGlnLeuLeuValGlyAlaGluGlnMetMetCysAlaGluProLeuAspMet 615
 QY 13824 CAGGCAATGCTGCTGCTGAGTTG--AAATTCACCTGTCCAGATGAATGAACATTCAT 13880
 DB 616 GluAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleLe 635
 QY 13881 GGCTGTGCGGCTCCAGTGGCTTGATGTAATCTGTTGACGAGTCTGCTATAGTTC 13940
 DB 636 SerValSerValValThrValLeuValSerValValGlyValLeuValTyrLysPhe 655
 QY 13941 TATTTTCACTGATGCTTCTTGCTGCTGCTCAATAAGTATGAGTGAAGATCATCTAT 14000
 DB 656 TyrPheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyGluSerIleTyr 675
 QY 14001 GATGCTTTGTTATCTACAGCCAGATGAGATGAGATGAGTGAAGATGAGTGAAG 14060
 DB 676 AspAlaPheValIleTyrSerSerGlnAspGluAspTrpValArgAsnGluLeuValLys 695
 QY 14061 AATTGAAGAAGGGGCTCCCTCCATTTCACTGCTGCTTCACTACATGACTTAATCCC 14120
 DB 696 AsnLeuGluGluGlyAlaProProPheGlnLeuCysLeuHisTyrArgAspPheIlePro 715
 QY 14121 GGTGTGCACTTGCTGCAACATCATCATGAAGTTTCCATAAAGCCGAAGGTGATT 14180
 DB 716 GlyValAlaIleAlaAlaAsnIleIleGlnGluLysPheHisLysSerArgLysValIle 735
 QY 14181 GTTGTGTGCTCCAGCACTTCATCATCAGACCGGCTGTGTATCTTTGAATGAGATTGCT 14240
 DB 736 ValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGluTyrGluIleAla 755
 QY 14241 CAGACCTGGGAGTTTCTGAGAGTCGTGCTGATCTTCAATTCCTGCTCCAGAGGTG 14300
 DB 756 GlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeu 775
 QY 14301 GAGAAACCTGCTCAGAGCAGAGGTGAAGCTGTGACCGCTTCTCAGACGGAACATTCAC 14360
 DB 776 GluLysSerLeuLeuAlaGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyr 795
 QY 14361 CTGAGTGGAGAGCAGATGTTCTTGAGGCGGCACTTCTTGAGAGCACTCAAGAAAGCC 14420
 DB 796 LeuGluTrpGluAspSerValLeuGlyArgHisValAlaPheTrpArgLysLeuArgAla 815
 QY 14421 CTGCTGATGTTAATCATGGAATCCAGAAAGAAACATGGGTACAGATGCAATTTGCAG 14480
 DB 816 LeuLeuAlaGlyLysProGlnSerProGluGlyThrAlaAspAlaGluThrAsnProGln 835
 QY 14481 GAAGCAACATCT 14492
 DB 836 GluAlaThrThr 839

RESULT 11
 TLR4_FELCA STANDARD; PRT; 833 AA.
 ID TLR4_FELCA STANDARD; PRT; 833 AA.
 AC P58727;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;

OS Felis silvestris catus (Cat).
 OC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshida N., Kano R.;
 RT "Felis catus Toll like receptor 4."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MYD88, TRAF6 and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and TRAF4
 CC via their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AB060687; BAB43947.1; -.
 DR HSBP; O60603; 1FXY.
 DR GO; GO:0046666; F:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappa-B inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:detection of activation; ISS.
 DR GO; GO:0045576; P:mast cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KM Glycoprotein; Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 833 Toll-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 833 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.

FT REPEAT 310 334 LRR 9.
 FT REPEAT 350 372 LRR 10.
 FT REPEAT 373 398 LRR 11.
 FT REPEAT 399 421 LRR 12.
 FT REPEAT 422 445 LRR 13.
 FT REPEAT 447 469 LRR 14.
 FT REPEAT 470 494 LRR 15.
 FT REPEAT 495 518 LRR 16.
 FT REPEAT 520 542 LRR 17.
 FT REPEAT 544 566 LRR 18.
 FT REPEAT 568 592 LRR 19.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 570 570 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GLNAC. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GLNAC. . .) (Potential).
 SQ SEQUENCE 833 AA; 95592 MW; 3E3A84F2B5A55EA CRC64;
 Alignment Scores:
 Pred. No.: 7,58e-228 Length: 833
 Score: 2937.00 Matches: 587
 Percent Similarity: 81.33% Conservative: 88
 Best Local Similarity: 70.72% Mismatches: 115
 Query Match: 8.88% Indels: 40
 DB: 1 Gaps: 6
 US-09-396-985b-47 (1-18989) x TLR4_FELICA (1-833)
 QY 11992 TGCTTATCATGTATGCTTAACATGACAAAGAGCCCTATTCAGCCAGTATGATA 12051
 Db 29 CyeValGluValValProanillethryGlnCysMetAspLeuasn----- 44
 QY 12052 TACTCAGTCGTGGGCTTTATTGCTT-----ATTGATCATCA 12093
 Db 45 -----LeuHilylelleProAspAnilleProSerSer 55
 QY 12094 TCTGTCGCTGATGCTTTGCTTATGACAAATATGACCAATGATGAGGAT 12153
 Db 56 ThrIlysAspLeuAspMet-----SerPheAsnPro----- 65
 QY 12154 GAGCTGATGACTAGATTAATATTCTATTAGCTTCTATTCA--GCAGAAATATTA 12210
 Db 66 -----LeuArgAsnLeuGlySerHisSerPheSerAsnPro 78
 QY 12211 GATTAATGATGCTTTTATTCCGTAGTGTAATCCAGACAAATTGAAGATGGGCAT 12270
 Db 79 GlnLeuGlnValLeuAspLeu--SerArgCysGlnIleGlnIleleGluAspAspIle 98
 QY 12271 ATCAGAGCTTAAGCAACCTCTCTACCTTAATATTGACAGGAAACCCATCAGAGTTAG 12330
 Db 98 YrGlnGlyLeuAsnHisLeuSerIleleuIleuThrGlyAsnProIleGlnArgLeuP 118
 QY 12331 CCTGGAGCCTTTCTGACATTCAGAGTTTACAGAACTGGTGGCTGTGAGACAAATC 12390
 Db 118 heProGlyAlaPheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGlnThrAsn 138
 QY 12391 TAGATCTTACAGAACTCCATTCGATGCAATGCAAACTTTGAAGAACTTAATGTGG 12450
 Db 138 IeAlaSerLeuGlnAspPheProIleGlyHisLeuYsrThrLeuLysGlnLeuAsnAla 158
 QY 12451 CTCACATCTTATTCATCTTCAATTAATGATGATTTTCTATCTGACCAATGTAG 12510
 Db 158 IahIsaenLeuIleHisSerPheYsLeuProGlnYrPheSerAsnMetSerAsnLeuG 178
 QY 12511 AGCATTGAGCTTTCCAGACAAAGATTCAAGATATTATTGACAGACTTGGGGGTTG 12570
 Db 178 IuYrIleuAspLeuSerAsnAsnIleGlnIleIleYrHisIlyAspLeuGlnValL 198

QY 12571 TACATCAATGCCCTCAATCTCTTTAGACCTGTCCTGAAACCTTGAATCTTA 12630
 DB 198 EHHISGlnlyProleuEuhnsleuSerleuAbspheSerleuAhnProleuAhnPhel 218
 QY 12631 TCACACAGGTGCAATTAAGAAATTAAGCTTCAATAGCTGATTAAGAAATTAATTTG 12690
 DB 218 leGlnProGlyAlaPhelyeGluValIySleuAArgIuLeuThrlEuhAArgSerAhnPha 238
 QY 12691 ATACTTAATGATGAAGAACTTGTAATCAAGCTGCGCTGTTGAATCCATCGCT 12750
 DB 238 snSerThraSpValMetIySAlaSerIleGlnIySleuAglIyLeuGlnIleHISGlnL 258
 QY 12751 TGGTCTGGGAGATTAAGAACTTGAAGAAATTTGAAGAAATTTGACAAATCTGCTAG 12810
 DB 258 euValIeugIyGluPhelyeAhnIuAArgAhnleuGlyAArgPhaAbspheSerIleuG 278
 QY 12811 AGGCGCTGTCGAATTTGACATTAAGAATTCGATTAAGCACTTAAGCTTAAGCTTCG 12870
 DB 278 IuGlyLeuCyAhnleuIleIleGlyuSPhaArgIleAlaTyPhaAbspheSerG 298
 QY 12871 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 12930
 DB 298 IuAhpAlaIleAaspSerPhaAhnCySleuAAlaAhnValSerThrlleSerleuValHISL 318
 QY 12931 TGACTTAATTAAGGATTAAGAACTTTCTTAATTAATTTGCGATGCGAATTAAGATTA 12990
 DB 318 euTyRPhelyeGlyeuleuSglnleuProlyAhnleuGlyTrpGlnIuAArgSleuL 338
 QY 12991 TTAATCTTAATTTGACAGTTTCCACATTAAGAACTCAATCTCAAAAGCTTAATCT 13050
 DB 338 AlaAncySglnuPhelGlnIuPhelProThrlrplySleuAhpProleuIySglnleuValP 358
 QY 13051 TCACCTTCCACAAAGGTGGGAAATGCTTTTTCAGAAAGTTGATCTCAAGCTTGAATTC 13110
 DB 358 heSerAlaAhnGluValAArgAhnAlaPhelThrluValIySleuGlnSerleuGlnPhel 378
 QY 13111 TAGATCTAGTAAGAAATGCTTGAATTTCAAAAGGTGCTGTTCCAAAGTATTTGGGA 13170
 DB 378 euAhpLeuSerThraSpAhnAhpPhaSerleuIySerCySgSerGlnuAArgAhpSleuL 398
 QY 13171 CAACAGCTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13230
 DB 398 hrThraSglnuLHISleuAhpLeuSerPhaAhnAlaIleThrlleSerSerAhnP 418
 QY 13231 TCTTGGGCTTGAACAACTAGACATCTGATTTCCAGCATTTCCAAATTTGAACAAATGA 13290
 DB 418 heLeuGlyLeuGlnIuLeuGlnIyRleuAhpPhaGlnHISerSerleuIySglnValS 438
 QY 13291 GTGAGTTTTCAGTATCTCAATCACTCAGAAACCTCATTTACCTTGACATTTCTGATCTC 13350
 DB 438 eThraSpheSerValPhelEuhProleuIyAhnleuAArgIyRleuAhpIleSerTyThrl 458
 QY 13351 ACACAGAGTGTCTTCAATGGAATCTTCAATGAGCTTGTCCAGCTGCGAAATCTTGAAGA 13410
 DB 458 IeThrluGlnValAlaPhelHISgIyIlePhaAhnGlyLeuIleSerleuGlnIleuLysM 478
 QY 13411 TGGCTGGCAATTTCTTCCAGAAATCTTCTTCCAGATTTCTTCCAGAGCTGAGAAACT 13470
 DB 478 eAlaAglAhnSerPhaGlnAhpAhnPhaAhnProAhnIlePhaMetGlnleuThraAhnL 498
 QY 13471 TGAACCTTCCAGACCTCTCTCAGTGTCAATGAGAGAGCTTCCCAACAGCATTTTAACT 13530
 DB 498 euThrlIleAhpLeuSerAhpCySglnleuGlnIuValSerGlnValAlaPhaAhnS 518
 QY 13531 CACTCTCCAGTCTTCAAGTACTTAATTAAGAACAACAATCTTCTTCAATTTGATGATCGT 13590
 DB 518 eRleuProlyAhpGlnleuEuhAhnMetSerHISaHnHISleuLeuSerleuAhpThrl 538
 QY 13591 TTCTTTTAAGTGTCTGAATCTCCCTCAAGGTTCTTGAATTAAGTCTCAATCAATTAATGA 13650
 DB 538 euProTyRglnuProleuHISerleuGlnThrlEuhAhpCySerPhaAhnAArgIleValA 558

QY 13651 CTTCCAAAAACAGGAATCAAGATTTTCCAAAGTACTAGCTTTCTTAATCTTACTC 13710
 DB 558 IeSerIySglnuGlnleuAhnHISphelProSerAhnleuSerSerleuAhnleuThra 578
 QY 13711 AGAATGACTTTGCTTGTGATCTTGTGAACACAGAGTTTCTGCAATGATTAAGAACACAGA 13770
 DB 578 rGlnAhpPhaAlaCySAlaCySglnHISglnSerPhaEuhGlnIuThrlValIySArgIuA 598
 QY 13771 GGCAGCTCTTGGGGAATGTAACGAATGAATGTGCAACAACCTTCAAGAGGAGCA 13830
 DB 598 rGlnleuLeuValGluValGlnIuMetValCySAlaIySProleuAhpMetGlnIyM 618
 QY 13831 TGCCTGTCTGAGTTTG--AATATCACCTGTGACAGATTAAGCAATCAATTTGGTGT 13887
 DB 618 eTPrometleuAhnPhaAArgAhnAlaThrlCySglnIuValAArgIySThrlIleThrlGlyS 638
 QY 13888 CGGTCTCAGTGTGCTTGTGATCTGTGTGACAGATTTGCTGTCTAATTAAGTTTATTTTC 13947
 DB 638 eValIPhelThrlValleuLeuValPhelEuhValIuValIuValIyRlySPhelThrlPhen 658
 QY 13948 ACCCTGATGCTTCTGCTGCTGATTAAGATGATGATGATGATGATGATGATGATGCT 14007
 DB 658 ISleuMetleuLeuAglIyCySelyeTyRserAArgIyGlnuSerThrlTyRAspAlaP 678
 QY 14008 TTGTTATCTACTCAAGCAGATGAGAGTGGGATTAAGAAATTAAGCTTAAGAAATTTAG 14067
 DB 678 heValIleTyRserSerGlnAhpSlnuAhpThrlValAArgAhnGlnleuValIySleuG 698
 QY 14068 AAGAAAGGAGTCTCCATTTCAAGCTGCTGCTTCACTAACAAGATTTAATTTCCGCTG 14127
 DB 698 IuGlnIyValIProPhaGlnleuCySleuHISTyRArgAhpPhelIleProGlyValA 718
 QY 14128 CCAATGCTGCAACATCATCATCAAGCTTTCATTAACCCGAAGGATTTGCTG 14187
 DB 718 IAlaIleAlaAhnIleIleGlnIuIyPhelHISySserAArgIyValIleValIuVal 738
 QY 14188 TGTCACAGACTTCAATCAGAGCGCTGATGATCTTGAATTAAGATTTGCTGAGACT 14247
 DB 738 AlSerGlnHISphelIleGlnSerAArgIyRplySleuGlnIyRgIyIleAlaGlnThrl 758
 QY 14248 GGCAGTTTTCAGAGAGTGTGCTGTGATCAATTTCAATTTGCTGACAGAGGTTGAGAGA 14307
 DB 758 rGlnPhelEuhSerSerAArgIyIleIlePhelIleValleuGlnIySleuGlnIyS 778
 QY 14308 CCTGTCTCAGAGAGAGTGTGATGATCAATTTCAATTTGCTGACAGAGGATTTGAGAGT 14367
 DB 778 eRleuLeuAArgIuValGlnleuTyRArgleuLeuAhnAArgAhnThrlTyRleuGlnI 798
 QY 14368 GGGAGAGCAGTGTCTGAGGCGGAGCAATTTCTGAGAGAGACTCAGAAAGCCCTGCTG 14427
 DB 798 rGlnuAhpSerValleuGlyAArgHISleIlePhelThraAArgleuAArgIyAlaIleuLeuA 818
 QY 14428 ATGTAAATCATGGAATCCAGAAAGA 14453
 DB 818 spGlyuSProAArgCySProGlnIy 826
 RESULT 12
 TLR4_PIG STANDARD; PRT; 841 AA.
 AC 068Y56;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DS Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Alveolus;
 RA Shinkai H., Uemishi H.;

[illegible]

QY	14197	ACTGATCCAGAGCCGGTGGTATGATCTTTGAATAATGATTTGTGACCTGGAGTTTC	14256
Db	741	ispheileginserAagTgPQsillepnedlunYrIdullelaaglnnrttPglInpHeL	761
QY	14257	TGACAGCTCGTGGTGTATCATCTTATGTCCTCTCGAGAGGGTGGAGAACCTGTCTCA	14316
Db	761	euatgserthlSalaglyllellepHeLleValleuclnlnYleuglnYusserleuLeuA	781
QY	14317	GGCAGCAGGTGGAGCTGTACCGCTTCTCGACGAGAACCTTAAGCTGGAGTGGAGACAA	14376
Db	781	rgtnglnlnvalIguleuYrArgleuLeuSerArGshnThYrLeuglnutrtPgIuAsPs	801
QY	14377	GTGTCCTGGGGCGGCAATCTTGTGGAGACAGCTCGAGAAAGCCCTCGATGGTGAAT	14436
Db	801	erValleuuglnYaghsillepnedlunYrIdullelaaglnnrttPglInpHeL	821
QY	14437	CATGGAATCCAGAGGAACAGTGGGTACAGATGCATTTGGCAGGAGCAACATCT	14492
Db	821	roTtPserProglunYlThngIuAsPserGlnSerAnGlnhIsapThrThrAla	839
RESULT 13			
Q8MIQ2	PRELIMINARY;	PRT;	839 AA.
AC	Q8MIQ2;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)		
DS	Toll-like receptor 4.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kajikwa O., Frevort C.W., Goodman R.B., Wong V.A., Martin T.R.;		
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY101394; AAM50060.1; -.		
DR	HSSP; O60603; 1077.		
DR	GO; GO:0016020; C:membrane, IEA.		
DR	GO; GO:0004888; F:transmembrane receptor activity, IEA.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR003591; LRR_Typ.		
DR	InterPro; IPR000157; TIR.		
DR	pfam; PF00560; LRR_1; 11.		
DR	pfam; PF01582; TIR_1.		
DR	PRINTS; PR00019; LEURICHRPT.		
DR	SMART; SM00082; LRRCT; 1.		
DR	SMART; SM00369; LRR_Typ; 1.		
DR	SMART; SM00255; TIR_1.		
DR	PROSITE; PSS0104; TIR_1.		
KM	Receptor.		
SO	SEQUENCE	839 AA; 96338 MW; 09F7D401EC14B6A CRC64;	
Alignment Scores:			
Pred. No.:	5,16e-213	Length:	839
Score:	2753.50	Matches:	544
Percent Similarity:	82.65%	Conservative:	80
Best Local Similarity:	72.05%	Mismatches:	126
Query Match:	8.33%	Indels:	5
DB:	2	Gaps:	3
US-09-396-985B-47 (1-16989) x Q8MIQ2 (1-839)			
QY	12237	AGGTGTGAATCCAGACAATTTGAAGATGGGGCATATCAAGAGCCTTACGACCTCTTAC	12296
Db	87	ArGcYsAllylellhlsThrllleGlunspAspalatYrGlnGlyLeuLysAnleuSerThr	106
QY	12297	TTAAATTTGACGAGAAACCCCATCCAGATTAAAGCCCTGGGAGCCTTTCTGGACATCA	12356
Db	107	LeuIlleuThnGclYAnenProIleGlnSerLeuSerProGlnAlaPneSerGlyLeuSer	126

RESULT 13					
ID	Q8MIQ2	PRELIMINARY;	PRT;	839 AA.	
AC	Q8MIQ2;				
DT	01-OCT-2002 (TrEMBLrel. 22, Created)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	Toll-like receptor 4.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kajikawa O., Frevert C.W., Goodman R.B., Wong V.A., Martin T.R.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: AY101394; AAM50060.1; -.				
DR	HSP: O60603; I077.				
DR	GO: GO:0016020; C:membrane; IEA.				
DR	GO: GO:0004888; F:transmembrane receptor activity; IEA.				
DR	InterPro: IPRO01611; LRR.				
DR	InterPro: IPRO00483; LRR_Cterm.				
DR	InterPro: IPRO03591; LRR_typ.				
DR	InterPro: IPRO00157; TIR.				
DR	Pfam: PF00560; LRR_1; 11.				
DR	Pfam: PF01582; TIR; 1.				
DR	PRINTS: PRO0019; LEURICHRPT.				
DR	SMART: SMO0082; LRRC7; 1.				
DR	SMART: SMO0369; LRR_TYP; 1.				
DR	SMART: SMO0255; TIR; 1.				
DR	PROSITE: PS50104; TIR; 1.				
DR	KW Receptor.				
SQ	SEQUENCE	839 AA;	96338 MW;	09F7D401ECC14B6A CRC64;	
Alignment Scores:					
Pred. No.:	5.16e-213	Length:	839		
Score:	2753.50	Matches:	544		
Percent Similarity:	82.65%	Conservative:	80		
Best local Similarity:	72.05%	Mismatches:	126		
Query Match:	8.33%	Indels:	5		
DB:	2	Gaps:	3		
US-09-196-985B-47 (1-18989) x Q8MIQ2 (1-839)					
QY	12237 AGGTGGGAATCCAGCATTTGAAAGATGGGGCATATCAGAGCTTAAGCACTCTCTTACC	12236			
D8	87 ATGCySLysrIehIsThrILegISunSpaPalatTyrgInGIyLeuLyASnLeSerThr	106			
QY	12297 TTATATTTCAGAGAAACCCCATCCAGAGTTTAGCGCTTGAGACCTTTCTTGAGACTATCA	12356			
D8	107 LeuIIleuThrdGLyAnPrroIIedInSerLeuSerProGInnaIaphneSerGIyLeuSer	126			

Db	127	AsnLeuGlnIysLeuValAlaValGluThrHisLeuThrSerLeuGlyAspPheProIle	146
Qy	12417	GGACATCTCAAAACCTTGAAGAAGAACTTAATGTGGCTCACAACTCTTATCCAACTCTTCAAA	12476
Db	147	GlyHisLeuIysThrLeuLysGluLeuAsnValAlaHisAsnLeuLeuHisSerPheSer	166
Qy	12477	TTACCTGAGTATTTTCTTAACTTGACCAATCTAGACACTTGACCTTTCACGAACAAG	12536
Db	167	ILleProAspIyrPheSerAsnLeuSerSerLeuGluHisLeuAspLeuSerAsnLys	186
Qy	12537	ATTCAAAGTATTTATTTGACACAGACTGGGGGTTCTACATCAAAATGCCCTTACTCATCTC	12596
Db	187	ILleGlnSerIleIyrHisLysAspLeuArgValLeuHisGluMetProLeuGlyThrLeu	206
Qy	12597	TCTTTAAGACCTGTCCCTGGAACCCATTAATCTTATATCCACAGAGCTCATTTAAAGAAATT	12656
Db	207	SerLeuAspLeuAlaLeuAsnProIleAspPheIleProProGlyAlaPheGluAlaIle	226
Qy	12657	AGGCTCATTAAGCTGACTTAAAGAAATATTTGATAGTTAAATGAATGAACCTGT	12716
Db	227	ArgLeuHisGluLeuIleIleuLysSerAsnPheLysSerThrAsnIleMetLysIleCys	246
Qy	12717	ATTCAGGCTGTGCTGGTTTGAAGTCCATCGTTTGCTTGGGAGAAATTTGAAGAAATGA	12776
Db	247	ILleGlnIysLeuSerGlyLeuGluValHisArgLeuValLeuGlyGluPheLysAsnGlu	266
Qy	12777	GGAAACTTGGAAAAAGTTTGACAAAATCGCTCTAGAGGGCCCTGGCAATTTGACCAATTGA	12836
Db	267	ArgAsnMetLysAsnAspPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuAlaIleGlu	286
Qy	12837	GAATTCGATTAAGCATCTTAGACTACTGATGATATTTATGACTTATTTAATGT	12896
Db	287	GluPheArgLeuAlaIyrIleAspAspLeuGlnGlyAsnIleThrAspLeuPheAspCys	306
Qy	12897	TTGACAAATGTTTCTTCAATTTCCCTGTGAGGTGACATTTGAAGAGGTAAAGACTTT	12956
Db	307	LeuGluAsnValSerValMetAlaLeuValHisMetLysIleAspAsnGlnGluIlePhe	326
Qy	12957	TCTTATATATTTCCGATGCAACATTTGATTAAGTATTAATGCTAAATTTGAGACAG--T	13013
Db	327	ProLysAspPheSerTrpLysSerLeuGluPheIleAsnGlyGluPheSerGluAsnIle	346
Qy	13014	CCCACTTGAACATCAATCTCTCAAAAGGCTTACTTCTCTCCAAACAAGGTGGAGAT	13073
Db	347	PhePheLeuLysLeuSerSerLeuArgArgLeuIlePheThrAlaAsnLysGlyAlaArg	366
Qy	13074	GCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTCAGTGAAGAAATGGCTTG	13133
Db	367	ThrPheProGluLeuAsnThrProSerLeuGluPheLeuAspIleSerAsnAsnGlyLeu	386
Qy	13134	AGTTCAAGGTTGCTGTCTCCAAAGAGATTTTGGGCAACCGCTTAAGATTTTAAAT	13193
Db	387	SerLeuGlnSerCysCysSerValAsnSerLeuArgLeuThrGlnLeuLysHisLeuAsn	406
Qy	13194	CTGAGCTTCAATGAGTGTATTTACCATGATGTTCAAACTTCTTGGGCTTAGAACAATGAA	13253
Db	407	LeuSerPheAsnGlyValIleThrMetThrSerAsnPheValGlyLeuGlnGluLeuGlu	426
Qy	13254	CATCTGATTTCCGACGATTCGAATTTGAAACAATGAGTAGTTCAGTATTTCTATATCA	13313
Db	427	HisLeuIyrPheGlnHisSerSerAsnLeuArgAsnIleAsnGluPheSerIlePheLeuSer	446
Qy	13314	CTCGAAACCCATTTACCTTGAACATTTCTCACTACACCGAGAGTCGTTTCAATGGC	13373
Db	447	LeuAsnAsnLeuLeuIyrLeuAspIleSerTyrThrHisIleArgValAlaPheArgGly	466
Qy	13374	ATCTTCATAGGCTGTGTCCAGTCTCGAAGTCTTGAAGAAATGGCTGGCAATCTTTCAGGAA	13433
Db	467	ILlePheAspGlyLeuIyrSerLeuArgValLeuLysMetLysGlyAsnAlaPheGlnAsp	486
Qy	13434	AACCTTCTTCAGATATCTTCACAGAGCTGAGAAACTTGACCTTCTCGAAGCTTCTCGAG	13493

Dd	487	AsnAArgLeuAenAnIlePheThrGluMetHisSerLeuThrThrLeuAerLeuSerSer	506
Qy	13494	TGTCACTGGAGCGAGTGTGCTCCAAAGACATTTAACTCACTCCAGCTTTCAGTACTA	13555
Dd	507	CysGlnLeuGlnGlnValTyrGlnGlyAlaPheGlnSerLeuProArgLeuGlnSerLeu	526
Qy	13554	AATATGAGCCCAACAACCTCTTTTCAATTGGATACGTTTCCCTTAATAGTGTCAACTCC	1361
Dd	527	AsnMetSerHisAsnAsnLeuLeuValLeuAerPheThrLeuThrTyrLysCysLeuTyrSer	546
Qy	13614	CTCCAGGCTCTTGAATTACAGTCCCAATCAACATATGACTTCCAAAAACAAGAACTACAG	13677
Dd	547	LeuGlnValLeuAerLeuSerPheAsnHisIleGlyAenIleThrGluProGlnGlnGln	566
Qy	13674	CATTTTCCAGTACTAGACTTTTCTTAATCTTAATCTCAAGATGACTTTGCTTGTACTGT	13733
Dd	567	HisPheProSerAsnLeuThrLeuLeuHisIleuThrThrAsnAlaPheValCysAerCys	586
Qy	13734	GAACACCAAGATTTCCTGCAATGGATGACAGACCCAAAGCAGCTCTTGTTGAAAGTTGA	13799
Dd	587	GlnHisGlnIlePheMetGlnTyrIleLysAerGlnArgLeuLeuValGlnValGln	606
Qy	13794	CGAATGCAATCTGCAACCTTCAGATACGAGGCGCATGCTGGTGCAGAGTTTG--AAT	13855
Dd	607	GlnMetValCysIleThrProProAsn-----MetProValLeuSerPheThrAsn	623
Qy	13851	ATCACCTGTCAGATGAATTAAGACCATATTGGTGTGTCGGTCTCACTGTGCTTGATGA	13911
Dd	624	AlaThrCysGlnIleSerLysThrIleIleSerValSerValPheSerValLeuValVal	643
Qy	13911	TCTGTGTAGCAGTTCTGTGCTATTAAGTCTTAATTCACTGATGCTTTCTTGCTGGCTC	13977
Dd	644	SerPheAlaValValLeuValTyrLysPheTyrPheProLeuMetLeuValGlyArg	663
Qy	13971	ATAAAGTATGGTAAAGGTGAAGAAACATCAATGATCCCTTGTATTACTCAAGCCAGAT	14033
Dd	664	ArgLysTyrGlyArgGlyGlnSerValTyrAspAlaPheValIleTyrSerSerGlnAsp	683
Qy	14031	GAGCACTGGGTAAAGGAATGAGCTGTAAAGAATTTAAGAAGAGGGTGCCTCCATTTTCA	14099
Dd	684	GlnAerTyrValAlaGlnGlnLeuValLysAsnLeuGlnGlnGlyValProProPheArg	703
Qy	14091	CTTGCTCTTCACTAACAGACCTTTATTTCCGGTGGCCATTGCTGCCAACATCATTCAT	14155
Dd	704	LeuCysLeuHisTyrArgAspPheIleProGlyAlaIleAlaIleAsnIleIleGln	723
Qy	14151	GAAGTTTCCCTAAAGCCGAAGGTGATTTGTGTGCCCGCCAGCACTTCACTCAAGAC	14211
Dd	724	GlnGlyPheHisLysLysSerArgLysValIleValValValSerGlnHisPheIleGlnSer	743
Qy	14211	CGCTGGTGTATCTTTGAATATGAAATTTGCTCAGACCTGGCAGTTTTCAGACATCTGGTCT	14277
Dd	744	ArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeuSerHisAla	763
Qy	14271	GGATCATCTTCATTTGCTCTGACAGAGGTGAGAAGACCTGCTCAGACGACGTGGAG	14333
Dd	764	GlyIleIlePheIleValLeuGlnLysValGlnLysSerLeuLeuArgGlnArgValGln	783
Qy	14331	CTGTACCGCTTTCACAGAGAAACCTTACTCGAGTGGAGGACAGTTCCTGGGGCGG	14399
Dd	784	LeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAerThrValLeuGlnLysArg	803
Qy	14391	CACATCTTCTGGAGACGACTCAGAAAAAGCCCTGCTGATGGTGAATCATGGAATCCAGAA	14455
Dd	804	HisIlePheThrPheArgLeuArgLysAlaLeuLeuAerGlnGlyLysThrLeuSerProGln	823
Qy	14451	GGAAACAGTGGGTACAGATGCATTTGGCAGGAGAACCAATCTATTC	14495
Dd	824	GlyMetAlaArgAlaGlnAsnAsnGlnGlnGlnIleuAlaMetThrLeu	838
RESULT 14			
ID	TLR4	CRIGR	STANDARD; PRT; 838 AA.

AC Q9WU82; 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 NC NCBT_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=20148868; PubMed=10683379;
 RA Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,
 RA Ingalls R.R., Golenbock D.T.;
 RT "Toll-like receptor 4 impacts ligand-specific recognition of bacterial
 lipopolysaccharide.";
 RL J. Clin. Invest. 105:497-504(2000).
 CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 immune response to bacterial lipopolysaccharide (LPS). Acts via
 MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 secretion and the inflammatory response (By similarity).
 CC -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 multi-protein complex containing at least CD14, LY96 and TIRAP via
 binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 their respective TIR domains.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -I- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
 hamster ovary fibroblast cell line.
 CC -I- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -I- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -I- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF153676; AAD41891.1; -
 DR HSPB; Q15399; 1FV.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Tyr.
 DR InterPro: IPR000157; TIR.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SMO0082; LRRCT; 1.
 DR SMART; SMO0369; LRR_Tyr; 1.
 DR SMART; SMO0255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 838
 FT DOMAIN 26 629
 FT TRANSMEM 630 650
 FT DOMAIN 651 838
 FT REPEAT 31 52
 FT REPEAT 53 75
 FT REPEAT 76 99
 FT REPEAT 100 123
 FT REPEAT 127 148
 FT REPEAT 149 172
 FT REPEAT 173 196
 FT REPEAT 200 224
 FT REPEAT 227 251

FT REPEAT 305 330 LRR 10.
 FT REPEAT 351 370 LRR 11.
 FT REPEAT 371 393 LRR 12.
 FT REPEAT 396 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 448 468 LRR 15.
 FT REPEAT 494 516 LRR 16.
 FT REPEAT 517 538 LRR 17.
 FT REPEAT 541 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (GlcNAc...)
 FT CARBOHYD 115 115 N-linked (GlcNAc...)
 FT CARBOHYD 172 172 N-linked (GlcNAc...)
 FT CARBOHYD 204 204 N-linked (GlcNAc...)
 FT CARBOHYD 237 237 N-linked (GlcNAc...)
 FT CARBOHYD 307 307 N-linked (GlcNAc...)
 FT CARBOHYD 492 492 N-linked (GlcNAc...)
 FT CARBOHYD 495 495 N-linked (GlcNAc...)
 FT CARBOHYD 524 524 N-linked (GlcNAc...)
 FT CARBOHYD 572 572 N-linked (GlcNAc...)
 FT CARBOHYD 622 622 N-linked (GlcNAc...)
 SQ SEQUENCE 838 AA; 96277 MW; 129B33596E908B48 CRC64;
 Alignment Scores:
 Pred. No.: 9,236-212 Length: 838
 Score: 2738.00 Matches: 528
 Percent Similarity: 81.66% Conservative: 100
 Best Local Similarity: 68.66% Mismatches: 129
 Query Match: 8.28% Indels: 12
 DB: 1 Gaps: 4
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 QY 12216 TCAATGCTTTTATTC-----TGAGCTGGAATC 12248
 DB |||||
 QY 70 SerHisserPhepAenPheProGluLeuLysLeuLysSerArgGluIle 89
 DB |||||
 QY 12249 CAGCAATTTGAAGATGGGCAATATGACGCTTACTTAAATTTGACA 12308
 DB ::|||
 QY 90 GluThrIleGluAspLysAlaIleGlyGlnGlyLeuHisGlnLeuThrIleLeuThr 109
 DB ::|||
 QY 12309 GGAACCCCATCCAGAGCTTTAGACCTTTCTGAGCATGATGAGTTACAGAG 12368
 DB |||||
 QY 12369 CTGGTGGCTGTGAGACAAATCTATGACATCTCCCATGAGCATCTGAAA 12428
 DB |||||
 QY 130 LeuValAlaValGluIleLysLeuAlaSerLeuAspSerLeuProIleGluHisLeuVal 149
 DB |||||
 QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAAATCTTATCCAAATCTTTCAATTAAGTAT 12488
 DB ::|||
 QY 150 ThrIleuLysLysLeuAsnValAlaHisAsnLeuIleHisSerPheLysLeuProGluTyr 169
 DB |||||
 QY 12489 TTTTCTATCTGACCAATCTAGACCACTTGACCTTTCCCAAGCAAGATTTCAAGTAT 12548
 DB |||||
 QY 170 PheSerAsnLeuThrAsnLeuGluHisLysLeuAspLeuSerAsnIleGlnThrIle 189
 DB |||||
 QY 12549 TATTTGACAGACTTGGCGGTTCTACATCAATGCCCCCTACTCAATCTCTTTAGACCTG 12608
 DB |||||
 QY 190 TyrTyrThrAspLeuGlnThrLeuArgGluAsnProGlnLeuAsnLeuSerLeuGluLeu 209
 DB |||||
 QY 12609 TCCCTGAACCTTATGAACTTTATTCACACGCGTCAATTTAAAGAAATTTAGGCTTCAAG 12668
 DB |||||
 QY 210 SerLeuAsnProIleAspPheIleGlnProGluAlaPheGlnGlyIleArgLeuHisGlu 229
 DB |||||
 QY 12669 CTGACTTTAAGAAATTAATTTTGAATGTTAAATGTAATGAAGAACTTATTTCAAGGCTG 12728
 DB |||||
 QY 230 LeuThrIleuArgSerAsnPheAsnSerThrAsnValMetLysThrCysIleHisAsnLeu 249
 DB |||||
 QY 12729 GCTGGTTTGAAGTCCATCGTTTGTCTTGAGGAATTTGAAGAAATTTGAGAACTTGAA 12788
 DB |||||
 QY 250 AspGlyLeuGlnValHisArgLeuIleLeuGlyGluIlePheLysAsnGluArgAsnValGlu 269
 DB |||||

12789 AAGTTGCAAAATGCTGCTTAGAGGCGCTGCGCAATTGTCAGCAATTGTAAGAAATTCGAGTTA 12848
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Db ArgPheAspArgTyrValIleGluGlyLeuGlySerValThrIleGluGluPheArgPhe 289
12849 GCATACCTTAGAGTACTACCTCGATGATATATTGACTTATTTAATGTTTGCAGAAATGTT 12908
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Db ThrTyrIleAsnGluPheSerGluAspIleThrAsp---PheAspCysLeuAlaAsnVal 308
12909 TCTTCATTTTCCCTGGAGTGTGACATTTAGAAAGGGTAAAGCTTTTCTTAAATTTTC 12968
|||:::|||||
Db SerIleMetSerLeuAlaAsnValTyrLeuValSerGluAspIleProLysTyrPhe 328
12969 GGAATGGCAACTTTAGATTGACTTAATTTGGACAGCTTCCCACTGAAATCTC 13028
|||:::|||||
Db LysTyrGlnThrLeuAlaValIleArgGlySerGluLeuValPheProPheGluLeu 348
13029 AATATCTCAAAAGGCTTACTTCTTCACTTCACAAAGGAGTGGAAATGCTTTTTCAGAAAT 13088
|||:::|||||
Db ProPheLeuValSerGluLeuIlePheIleThrAsnLysGlyAlaThrSerPheProGluVal 368
13089 GATTCACCAAGCTTTGAGTTTCTAGATCTCAGTAAATGGCTTGAAGTTTCAAGTTTC 13148
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Db AsnLeuProSerLeuThrPheLeuAspLeuSerGlyAsnGlyMetSerPheArgGlyCys 388
13149 TGTTCCTCAAGTGAATTTGGGCAACAACAGCCTAAGATTAGATCTGAGCTTCAATGCT 13208
|||:::|||||
Db CysSerTyrThrAspLeuGlyAlaArgSerLeuLysIleLeuAspLeuSerPheAsnGly 408
13209 GTATATACCATGAGTTCAAACTTCTGGGCTTAGAACAACTAGAACATTCGATTTTCAG 13268
|||:::|||||
Db ValIleSerMetSerGluAsnPheMetGlyLeuGluGlnLeuGluTyrLeuAspPheGln 428
13269 CATTCGAATTTGAAACAATAGTGAAGTTTTCAGTATCTCATCTCAGAAATCTCAT 13328
|||:::|||||
Db HisSerThrLeuLysLysAlaThrGluPheSerMetPheLeuProLeuGluLysLeuLeu 448
13329 TACCTGACATTTCTCACTACTACACAGCAGAGTGGCTTCAATGACATCTTCAATGGCTTG 13388
|||:::|||||
Db TyrLeuAspIleSerTyrThrAsnThrLysIleAsnPheAsnGlyIlePhePheGlyLeu 468
13389 TCCAGTCTCGAAGTCTTGAAATGGCTGCGCAATCTTCTCCAGAAATCTTCTTCAGAT 13448
|||:::|||||
Db ThrSerLeuAsnThrLeuLysMetAlaGlyAsnSerPheLysAspAsnIleLeuSerAsn 488
13449 ATCTTCACAGAGCTGAGAAATCTTGAACCTTCTGCACTCTCTCAGTGTCAATGAGCAG 13508
:::|||||
Db ValPheThrAsnThrThrAsnLeuThrPheLeuAspIleSerLysCysGlnLeuGlnGln 508
13509 TTGCTCCAAAGCATTTAACTCCCTCCAGTCTTCAGTACGTAATTAATAGGCAAC 13568
|||:::|||||
Db ValSerTyrGlyValPheAspThrLeuIleValArgLeuGluLeuLeuAsnMetSerIleAsn 528
13569 AACTCTTTTTCATGATACCTTCTTAAAGTGTGAAGTCCCTCCAGAGTTCTTGAT 13628
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Db AsnLeuLeuLeuLeuAspLeuPheIleTyrLysGlnLeuIleAsnIleSerLeuLysThrLeuAsp 548
13629 TACAGTCTCAATCAATATATGATCTTCAAAAAACAGAACTAGACATTTTTCAGATGAT 13688
|||:::|||||
Db CysSerPheAsnIleIleGluThrSer---LysGlyIleMetGlnIleAspPheProLysSer 567
13689 CTACCTTTCTTAATCTTACTCAGAAATGACTTGTCTTACTTGTGACACAGAGTTTC 13748
|||:::|||||
Db LeuAlaPheLeuAsnLeuThrAsnAsnProPheAlaCysIleCysGlnIleGlnAsnIle 587
13749 CTGCAATGATCAAGAGCAAGAGGAGCTTGTGTAAGTTGAACGATGAATGTGCA 13808
|||:::|||||
Db LeuGlnThrValLysAspGlnArgLeuPheLeuValLysThrGlnGlnMetThrCysAla 607
13809 AACCTTCAGATTAAGCAGGAGGAGCTGCTGTGTAAGTTG---AATATCACTGTTCAGATG 13865
|||:::|||||
Db ThrProValGluMetLysAspSerLeuValLeuAspPheArgAsnAlaThrCysTyrVal 627

13866 AATAAGACCATCATTTGGTGTGCTGCTCAAGTGTCTTGTAGTATCTGTGTGAGCAGTT 13925
|||:::|||||
Db GlnLysThrIleIleLeuSerValIleSerValLeuValValSerThrIleAlaPhe 647
13926 CTGGCTTAATAGTTCTTATTTTCACTGATGCTTCTTGTGCTGTCGATTAAGTATGCTAG 13985
|||:::|||||
Db LeuValTyrLysPheTyrPheIleIleuIleAlaGlyCysLysLysTyrSerArg 667
13986 GGTGAAACAATCTATGATGCTTGTATCTTACTCAAGCGACAGATGAGGAGCTGGTAAAG 14045
|||:::|||||
Db GlyLysSerIleTyrAspIlePheValIleTyrSerSerGlnAspGluAspIleValArg 687
14046 AATGAGCTAGTAAGAATTAGAAAGAGGAGTGCCTTCATTTCAAGCTGTGCTTCACTAC 14105
|||:::|||||
Db AsnGluLeuValLysAsnLeuGluGluGlyValProProPheGlnLeuCysLeuIleTyr 707
14106 AGAGACTTATTTCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14165
|||:::|||||
Db ArgAspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleGlnGluGlyPheIleLys 727
14166 AGCGGAAGGATGATTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14225
|||:::|||||
Db SerArgLysValIleValValValSerArgHisPheIleGlnSerArgTyrCysIlePhe 747
14226 GAATATGAGATGCTGACACTGCTGAGTCTGAGCAGTGTGCTGAGTATCATCTTCAT 14285
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Db GluTyrGluLeuAlaGlnThrTyrGlnPheLeuSerHisSerGlyIleIlePheIle 767
14286 GTCTTCAGAAAGGTGAGAAAGACCTGCTGAGCAGCAGCAGCAGCAGTGTGACGCTTCTC 14345
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Db ValLeuGluLysValGluLysSerLeuLysGlnGlnValGluLeuTyrArgLeuLeu 787
14346 AGCAGAAACCTTACTGAGTGGAGGAGCAGAGTCTGCGGCGGAGCACTTCTTGAGA 14405
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Db SerArgAsnThrTyrLeuGluTyrGluAspAsnAlaLeuLysIleArgHisIlePheTyrArg 807
14406 CGACTCAGAAAGACCTGCTGATGATGTAATCATGAAATCCAGAAAGACAGTGGGTACA 14465
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Db ArgLeuLysLysValAlaLeuLeuAspGlyArgAlaThrAsnProGluGluAlaThrGluAla 827
14466 GGAATGCAATGGCAGGAAGCAACATCT 14492
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Db GluAsnAsnGlnGlnGluThrThrThr 836
RESULT 15
ID Q8K2T5 PRELIMINARY; PRT; 835 AA.
Q8K2T5;
AC Q8K2T5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Mammary tumor;
RX MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
RA Hopkins R.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA DiCicco L., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stedman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA	Whiting R.M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA	Krzywinski M.I., Skelton U., Smalins D.E., Scherch A., Schein J.E.,
RA	Jones S.J., Maira M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences",
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	STRAIN=C2CH 11; TISSUE=Mammary tumor;
RC	Strasbourg R.;
RA	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC029856; AAH29856.1; -
DR	HSSP; O60603.1077.
DR	MGD; MG136824; T174.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0004872; F:receptor activity; IDA.
DR	GO; GO:0007249; P:1-kappa kinase/NF-kappaB cascade; IDA.
DR	GO; GO:0008653; P:cell signaling pathway; IDA.
DR	InterPro; IPR000887; Aldose_KDPG_KHG.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR00157; TIR.
DR	Pfam; PF00560; LRR_1; 10.
DR	Pfam; PF01582; TIR_1.
DR	PRINTS; PRO0019; LEURICRPT.
DR	SMART; SM00082; LRCT; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS00159; ALDOLASE_KDPG_KHG_1; UNKNOWN_1.
DR	PROSITE; PS50104; TIR; 1.
KW	Receptor.
SO	SEQUENCE 835 AA; 95488 MW; A103C3997A59CF5B CRC64;
Alignment Scores:	
Pred. No.:	1.58e-200
Score:	2599.00
Percent Similarity:	76.00%
Best Local Similarity:	63.57%
Query Match:	7.86%
DB:	2 Gaps: 8
US-09-396-985B-47 (1-18989) x Q8K2T5 (1-835)	
QY	11992 TGCTATCATGATGATGCTTACATGACGAC-----AAAAGAGCCTATCATTCGAG 120399
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QY	12040 CCAATGATGATAATVACATGATGCTGGGGCTTCTTATTTGGTTATTCATCATCATCATGTC 120999
DB	48 ProAsp-----Asp116ProSer168ThrLys 56
QY	12100 CTGCTGATGCTCTTGGCTATGACAAATCATATGACCAATCATCATCTGATGAGAGCTG 121599
DB	57 Asn116AspLeu-----Ser168AsnPro----- 64
QY	12160 GATGACATGAGATTAATATTTCTATTTTATGTTCTTATTCACACGAAATATTAATAT 122166
DB	65 -----Leu151lle151Leu151Ser151Ser158Asn158Ser158Leu 79
QY	12217 CAATGCTTTTATTTCTGATGAGTGTCGAATTCAGACAAATGAGAGGAGCATATCAGA 122766
DB	80 Gln151Pro158AsnLeu-----Ser158Cys161Ile161Thr161Gln161Arg161Trp161His 99
QY	12277 GCCTAAGCCACCTCTCTACCTTAATATTTGACAGAGAAACCCATCCAGAGTTTACCCCTGG 123366
DB	99 Lys161His161Ser168Asn161Leu161Thr161Lys161Pro161Gln161Ser168Pro161G 119
QY	12337 GAGCGTTTCTGAGCATTCAGATTTCAGAGAGCTGGGCTGTGGAGCAATCTTACAT 123966
DB	119 Lys168Pro168Ser168Gln168Thr168Leu168Val168Ala168Gln168Trp168Leu168As 139

QY	12397	CTCAGAGAACTTCCCATTTGGACATCTGCAAACTTTGAAGAAGCTTAATGTGGCTCAC	12455
Dp	139	159
QY	12457	ATCTTAATTCGAACTTTCAAAATTAACCTGAGAAATTTTCTTAATCTGACCAATCTAGAGCACT	12516
Dp	159	179
QY	12517	TGACACTTTTCACAGCAACAGATTCGAAAGTAATTTATATGCAACAGACTTGGCGGTCTTAATCAT	12576
Dp	179	199
QY	12577	AAATGCCCTTACATCAATCTCTCTTTAGACCTGTGCTGCAACCTTAATGAACTTTATCCAA	12636
Dp	199	219
QY	12637	CAGGTGCAATTTAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATATATTTTGATAGTT	12696
Dp	219	239
QY	12697	TAAATGTAATGAAACTTGTATTCAGAGCTGTGGCTGGTTAGAACTCCAGCTTGGTTC	12756
Dp	239	259
QY	12757	TGGGCAATTTTAAAGAAATGAAAGAAATTTGGAAGAAAGTTTACAAATCTGCTTAGAGGGCC	12816
Dp	259	279
QY	12817	TGTGCAATTTGACCAATTTGAAGAAATTCGCAATTTGCAATCTTAACACTTAACCTCCAGATGATA	12876
Dp	279	299
QY	12877	TTATGCAATTTAAATTTGTTTGGACAAATGTTTCTTCAATTTCCCTGTAGCTGATGATCA	12936
Dp	299	318
QY	12937	TTGAAAGGTTAAAGCTTTTCTTAATTTGCGATGCGACATTTAGCAATTAAGTTAACT	12996
Dp	318	338
QY	12997	GTTAAATTTGGACAGTTTCCGCAATTTGAACCAATCTGCAAGGCTTAATCTTCACT	13056
Dp	338	358
QY	13057	CCAAACAAAGTGGGAATGCTTTTTCGACAGTTGATCTCAACGCTTGAAGTTCTAGATC	13116
Dp	358	378
QY	13117	TCAGTGAATGCGCTTGAAGTTTCAAGGCTGTCTTCAAGTGATATTTGGGACAAACA	13176
Dp	378	398
QY	13177	GCTTAAGATTTAAGTCTGAGCTTCAAGTGCTTATTAACAATGAGTTCAACCTTGG	13236
Dp	398	418
QY	13237	GCTTGAACAACTAGCAATCTGGAATTTCCACATTTCCAAATTTGAACAAATGAGTGAAGT	13296
Dp	418	438
QY	13297	TTTCAGATTTCTGATCTGACGAACCTCATTTTACCTTGACATTTCTCATACTACACA	13356
Dp	438	458
QY	13357	GAGTTCCTTCAATGTCATCTTCAATGCTTGTCCAGTCTGGAATCTTGAAGAAAGGCTG	13416
Dp	458	478
QY	13417	GCAATCTTTCCAGGAAATCTTCTTCCAGATATCTTCAAGAGCTGGAACCTTGAAGCT	13476
Dp	478	498
QY	13477	TCTCGAGCTCTTCTAGTGTCACTGAGACAGTGTCTTCCAAACAGATTTAACTCATCT	13536

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Db 498 heLeuAryLeuSerLysCysGlnLeuGlnIleSerTrpGlyValPheAspThrLeuH 518
QY 13537 CCAAGTCTTCAAGGTAATAATATAGCCACAACAATTCTTTCAATTGATATAGCTTTCCTT 13596
Db 518 iSArGLeuGlnLeuAsnMetSerHisAsnAsnLeuPheLeuAspSerHisIer 538
QY 13597 ATAAGTCTCGAAGTCCCTCCAGGTTCTTATTAACAAGTCTCAATCAATCAATATAGCTTCCA 13656
Db 538 yIraNGlnLeuTySerLeuSerThrLeuAspCysSerPheAsnArgIleGlnThrSer- 557
QY 13657 AAAAACAAGAACTTACAGACATTTTCCAAAGTACTAGCTTTCTTAATCTTACTACAGATG 13716
Db 558 --LysGlyIleLeuGlnHisPheProLysSerLeuAlaPhePheAsnLeuThrAsnAsn 577
QY 13717 ACTTGGCTGTACTGTGAACACCAAGATTCTCTGCAATGATCAGACCAAGGCAAGC 13776
Db 577 eValAlaCysIleCysGlnHisGlnLysPheLeuGlnTrpValLysAspGlnLysGlnP 597
QY 13777 TCTTGGTGAAGTGAAGATGGAATGGAACACCTTCAGATTAAGCAGGCAATGCGCTG 13836
Db 597 heLeuValAsnValGlnGlnMetThrCysAlaThrProValGlnMetAsnThrSerLeuV 617
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QY 13894 TCAAGTGTCTTATGATCTGTTGTTAGCAAGTCTGTCTATTAAGTCTTATTTTCACTGA 13953
Db 637 leSerValIleValValSerThrValAlaPheLeuIleTyHisPheTyPheHisIleuI 657
QY 13954 TGGTCTTGTGGTGGTGAATAAGTATGATGATGAGGTAAGCAATGATGATGCTTGTGA 14013
Db 657 leLeuIleAlaGlyCysValLysTySerArgGlyGlnSerIleTyAspAlaPheValI 677
QY 14014 TCTACTCAAGCCAGATGAGAGTGGTGAAGATGAAGTGAAGTGAAGATTTAGAAAG 14073
Db 677 leTySerSerGlnAsnGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnG 697
QY 14074 GGGTGCCTCCATTCAAGTCTGCTTCACTACAGAACTTATTCCTGGTGTGCGCATTG 14133
Db 697 LysAlaProArgPheHisIleuCysValHisIleTyArgAspPheIleProGlyValAlaIleA 717
QY 14134 CTGGCAACATCATCATGATGAAGGTTTCCATAAAGCCGAAAGGATGTTGTTGTGTTGCC 14193
Db 717 laAlaAsnIleIleGlnGlnIleuPheHisValSerArgLysValIleValValAlaSerA 737
QY 14194 AGCACTTCATCCAGAGCCGCTGATGATCTTTGAATATGAATTGTCTCAGACTTGCGAGT 14253
Db 737 rGHisPheIleGlnSerArgTrpCysIlePheGlnTyArgIleAlaGlnThrTrpGlnP 757
QY 14254 TTCTGAGCAGTCTGCTGGTATTCATCTTCATTTGCTGCAAGAGTGGAGAAACCTGCTGC 14313
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QY 14314 TCAGACAGCAGGTGAGGTGACGCTTCTCAGACGGAACACTTACTGGAGTGGAGG 14373
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QY 14374 ACAAGTCTCTGGGCGGAGCATTTCTTGAGACGACTCAGAAAGCCCTGCTGATGATA 14433
Db 797 sPAsnProLeuGlyArgHisIlePheTrpArgGlyLeuLysValAlaLeuLeuAspGlyL 817
QY 14434 AATCATGGAATCCGAAGAAACA 14456
Db 817 ysaIaSerAsnProGlnGlnThr 824
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Search completed: March 29, 2005, 19:41:11
Job time : 1213.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 2221.5 Seconds
(without alignments)
17409.875 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
Sequence: 1 ttccatcatcatgtagtc.....catttagtatttccaga 50000

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 8422768

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Geneseq_16Dec04 -QMT=fastran -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR=score=100 -THR_MTN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=ptco -NCR=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USER=US09396985 @CGN_1_1_4007 @runat_28032005_155742_21135 -NCPU=6 -ICPU=3
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2607	3.0	839	6	ABU04773 Human exp
2	2607	3.0	839	6	ABU04774 Human exp
3	2607	3.0	839	6	ABU04775 Human exp
4	2607	3.0	839	7	AD078785 Human PRO
5	2607	3.0	839	7	AD048826 Human PRO
6	2600.5	3.0	837	2	AAW86361 Human DNA
7	2600.5	3.0	837	6	AAE16102 Human DNA
8	2600.5	3.0	837	6	ABU04776 Human exp
9	2599	3.0	795	8	AD057791 Rheus mo
10	2596	3.0	808	8	AD057803 Chimpanze

11	2594	3.0	801	8	AD057797	AD057797 Squirrel
12	2593.5	3.0	837	5	AAE16116	AAE16116 Human DNA
13	2592	3.0	808	8	AD057782	AD057782 Chimpanze
14	2591	3.0	799	2	AAW86352	AAW86352 Human DNA
15	2591	3.0	799	5	AAE16093	AAE16093 Human DNA
16	2591	3.0	799	5	ABB83162	ABB83162 Human Tol
17	2591	3.0	799	6	ABR42963	ABR42963 Human Tol
18	2591	3.0	799	7	ADB39121	ADB39121 Human Tol
19	2591	3.0	799	8	ADP48597	ADP48597 Human Tol
20	2591	3.0	799	8	ADP48597	ADP48597 Human Tol
21	2582	3.0	795	8	AD057800	AD057800 Hamadryas
22	2574	3.0	808	8	AD057785	AD057785 Gorilla t
23	2558	2.9	801	8	AD057788	AD057788 Gibbon to
24	2548.5	2.9	745	8	AD057794	AD057794 White-fac
25	2547.5	2.9	738	8	ADP29455	ADP29455 Human sec
26	942	1.1	179	7	ADC42707	ADC42707 Murine To
27	886	1.0	208	3	AAW86059	AAW86059 Human Tol
28	748	0.9	178	8	ADN12270	ADN12270 IL-1R/TLR
29	727	0.8	1300	7	ADP63060	ADP63060 Rat Prote
30	701.5	0.8	1300	7	ADP63060	ADP63060 Rat Prote
31	598.5	0.7	1658	4	ABG06940	ABG06940 Novel hum
32	581.5	0.7	994	4	ABG14604	ABG14604 Novel hum
33	581.5	0.7	994	4	ABG07468	ABG07468 Novel hum
34	581.5	0.7	994	4	ABG19901	ABG19901 Novel hum
35	581.5	0.7	994	4	ABG14924	ABG14924 Novel hum
36	582	0.7	1318	7	ABG12875	ABG12875 Novel hum
37	568.5	0.7	513	7	ADP63833	ADP63833 Rat Prote
38	580	0.7	879	4	ABG12671	ABG12671 Novel hum
39	577.5	0.7	721	4	ABG13961	ABG13961 Novel hum
40	575.5	0.7	641	4	ABG08128	ABG08128 Novel hum
41	575.5	0.7	641	7	ADJ68375	ADJ68375 Human hea
42	575.5	0.7	1224	4	ABG03861	ABG03861 Novel hum
43	575.5	0.7	1284	4	ABG10795	ABG10795 Novel hum
44	575.5	0.7	1284	4	ABG06053	ABG06053 Novel hum
45	575.5	0.7	1284	4	ABG09636	ABG09636 Novel hum

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
AC	ABU04773;	
DT	29-JAN-2003	(first entry)
DE	Human expressed protein tag (EPT) #1439.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
XX	Homo sapiens.	
OS	W0200278524-A2.	
XX	10-OCT-2002.	
PD	28-MAR-2002; 2002WO-US009671.	
XX	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326780P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCOs INC.	
PA	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
PI		


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Db      497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPhe 516
Qy      39017 GAGACCCCTCCATAGCTTAAATATGATGTCACCAATCTATTCTTTGGAT 39076
Db      517 AsnSerLeuSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp 536
Qy      39077 TCATCCCATTTAAACAGCATGATTTCCCTCAGCATCTTGTGAGTTCAGTTCAGCAT 39136
Db      537 ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 556
Qy      39137 GAGACATCT--AAGAGAAATCTGCACATTTTCCAAAGATCTAGCCCTTCTCAATCTT 39193
Db      557 MetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
Qy      39194 ACTAACAATTCGTGCTGTGATATGATGACATCAAAATTCCTGCGAGTGGTCAAGAA 39253
Db      577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrPylLysAsp 596
Qy      39254 CAGAGAGATGTTCTTGTAATGTTGAACAATGACATGTGACACACCTGTGAGATGAT 39313
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Qy      39314 ACTCTCTTATGTTGATTTAAATTAATCTTACTGTTATGTAACAAGACATCATCAGT 39373
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Qy      39374 GTGTCAGTGTGATGATGATGTTGTTATCCACTGATGATTTCTGATATACACTTCAT 39433
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Qy      39434 TTTGACCTGATCTTATTTGCTGCTGTTAAAGATGACAGAGAGAGAAAGATCTATGAT 39493
Db      656 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlnArgGlnGlnAsnIleTyrAsp 675
Qy      39494 GCATTTGTGATCTACTGAGTCAAGATGAGAGATGAGATGAGAAATGAGCTGTAAGAT 39553
Db      676 AlaPheValIleTyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsn 695
Qy      39554 TTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39613
Db      696 LeuGlnGlnGlnValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGly 715
Qy      39614 GTAGCCATTTGCTGCAATCATCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39673
Db      716 ValAlaIleAlaAlaAsnIleIleHisGlnLysPheHisLysSerArgLysValIleVal 735
Qy      39674 GTAGTGTCTAGACATTTATTCAGAGCCGTTGGTGTATCTTGAATGAGATGCTCAA 39733
Db      736 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnLysGlnIleAlaGln 755
Qy      39734 ACATGGCAGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39793
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Qy      39854 GAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39913
Db      796 GlnTyrGlnAspSerValLeuGlnArgHisIleIlePheTrpArgLysValAlaLeu 815
Qy      39914 TTGGATGAGAAAGAGCTGAGATCTTCTGAGCAACA 39966
Db      816 LeuAspGlyLysSerTrpAsnProGlnLysThr 826

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RESULT 2
ABU04774
ID      ABU04774 standard; protein; 839 AA.
AC      ABU04774;
XX      29-JAN-2003 (first entry)
DT

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XX      XX      Human expressed protein tag (EPT) #1440.
DE      DE      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX      XX      protease; protease inhibitor; transporter; cytoskeletal protein;
XX      XX      receptor; transcription factor; cancer; MHC;
XX      XX      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX      XX      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS      OS      Homo sapiens.
PN      PN      MO200278524-A2.
PD      PD      10-OCT-2002.
PP      PP      28-MAR-2002; 2002MO-US009671.
PR      PR      28-MAR-2001; 2001US-0279495P.
PR      PR      21-MAY-2001; 2001US-0292544P.
PR      PR      08-AUG-2001; 2001US-0310801P.
PR      PR      01-OCT-2001; 2001US-0326370P.
PR      PR      04-DEC-2001; 2001US-0336780P.
PR      PR      20-FEB-2002; 2002US-0358985P.
PA      PA      (ZYCO-) ZYCOs INC.
PI      PI      Chicx RM, Tomlinson AJ, Urban RG;
XX      XX      WPI; 2003-040607/03.
PT      PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      PT      leukemia.
XX      XX      Example 2; SEQ ID NO 1440; 134pp; English.
PS      PS
XX      XX
XX      XX      The invention describes a purified polypeptide, which comprises a
CC      CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
CC      CC      transporter, cytoskeletal protein, receptor or transcription factor. The
CC      CC      polypeptide is useful as an immunogenic composition for eliciting in a
CC      CC      mammal an immunogenic response directed against any of the purified
CC      CC      polypeptides. The purified polypeptide, or the antibody that binds to this
CC      CC      polypeptide, is useful for treating cancer. The polypeptide is also
CC      CC      useful for identifying compounds that binds to a naturally processed
CC      CC      class I or class II MHC-binding polypeptide. The polypeptides and
CC      CC      polynucleotides are particularly useful for treating or preventing
CC      CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC      CC      lymphoma or leukaemia. These are also useful for screening agents for
CC      CC      treating the above mentioned diseases. This sequence represents an
CC      CC      expressed protein tag (EPT) isolated from human tissue for translational
CC      CC      profiling. Note: This sequence does not appear in the printed
CC      CC      specification but was obtained in electronic format directly from WIPO at
CC      CC      ftp.wipo.int/pub/published_pct_sequences
XX      XX
XX      XX      Sequence 839 AA:
XX      XX
XX      XX      Alignment Scores:
XX      XX      Pred. No.: 2.33e-234 Length: 839
XX      XX      Score: 2607.00 Matches: 526
XX      XX      Percent Similarity: 73.68% Conservative: 101
XX      XX      Best local Similarity: 61.81% Mismatches: 172
XX      XX      Query Match: 3.00% Indels: 52
XX      XX      DB: 6 Gaps: 8
XX      XX
XX      XX      US-09-396-985B-48 (1-5000) x ABU04774 (1-839)
Qy      Qy      37400 TGGAAAAAATGCAATTAATTAATCAAGATCAATCAATCTTATGATGACCCA 37459
Db      Db      26 TrpGlnProCysValGlnValValProAsnIleThrTyrGln----- 39
Qy      Qy      37460 GTTATGATCTTGAATGATTTTCTTATGATTTGCTGCTGACATAGTGATGATT 37519

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Db 40 CysMetGluLeuAsnPheTyrLysIleProAsnLeuPro----- 53
 Qy 37520 ATCATCACTGTAGCAAGTGTGAAATGACAAATCTGCAGAGTCTCTCTGCTCACACC 37579
 Db 54 -----PheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 68
 Qy 37580 ATCATCACTGTGTTTGTCTGTGTATCTCTTTTCAATTAACATGATGATATATCT 37639
 Db 69 -----LeuGlySerTyrSerPhe----- 74
 Qy 37640 GTTTGATCATATGATGTAGGAGCACTGTATGATTGATGAAAGGTTTTTTTTTCAGCAA 37699
 Db 75 -----PheSerPheProGlu 79
 Qy 37700 AAATACATAATGTGTATCTCTTTTGGCCATGATGTGATAATGAAACAATGAAAGACAG 37759
 Db 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 96
 Qy 37760 GCATGGCATGGCTTACACACACCTCTCAAACTTGATACGACGAGAAACCTATCCAGAGT 37819
 Db 97 AlaTyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSer 116
 Qy 37820 TTTTCCCAAGAACTTTCTCTGACTAACAAAGTTTAAAGAACTGTGGCTGTGAGACA 37879
 Db 117 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThr 136
 Qy 37880 AAATGGCTCTCTTCAAGAAAGTTCCTTATGACAGCTTAAACCTTAAAGAACTCAAT 37939
 Db 137 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsn 156
 Qy 37940 GTGGCTCAACATTTTATCATCTCTGTAAAGTTACCTGCATTTTCCAACTGACGAC 37999
 Db 157 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsn 176
 Qy 38000 CTAGTACATGTGATCTTTCTTAACTAATATCAAACTATTACTGTCAACGACTTACAG 38059
 Db 177 LeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArg 196
 Qy 38060 TTTTACGTGAATAATCCACAGTCAATCTCTTATGACAGTCTTTTGAACCCAAATGAC 38119
 Db 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsn 216
 Qy 38120 TTCAATTCAGACCAAGCTTTCAAGGAAATAGCTCCATGACACTGACACTTAAAGATTA 38179
 Db 217 PheIleGlnProGlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsn 236
 Qy 38180 TTTAATAGCTCAAAATATATATGAAAACTTGCCTTCAAACTGGCTGTATTACAGTCCAT 38239
 Db 237 PheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHis 256
 Qy 38240 CGGTGATCTGTGGAGAAATTTAAAGATGAAAGAACTGGAATTTTGAACCTCTATC 38299
 Db 257 ArgLeuValLeuGlyGluPheArgAsnGlnLysAsnLeuGlnLysPheAspLysSerIle 276
 Qy 38300 ATGAGAGCACTATGTGATGACCATGATGATGAGTTCAAGTAAATATACAAAGATTTT 38359
 Db 277 LeuGlnGlyLeuCysAsnLeuThrIleGlnLysPheArgLeuAlaTyrLeuAspTyrTyr 296
 Qy 38360 TCAGATGATATTGTTAG--TTCCATGCTTGGCGAAAGTTTGTGCAGATCTCTGGCA 38416
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 Qy 38417 GGTATATATATAAATATCTAAGAAATGTTCTTAAACCTTTCMAATGGCAATCCTTATCA 38476
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 Qy 38477 ATCATAGATGTCAACTTAAGCAAGTTTCAACTGATGATACCTTTCTTAAAGTTT 38536
 Db 337 LeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu 356
 Qy 38537 ACTTAACTATGAACAAAGGCTTATCAGTTTAAAAAGTGGCCCTTACCAAGTCTCAGC 38596
 Db 357 ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGln 376

Qy 38597 TATCTAGATCTTGTAGAAATGCACTGAGCTTTAGTGGTTGCTTATTCGATTTG 38656
 Db 377 PheLeuAspLeuSerTyrGlnGlyLysLeuSerPheLysGlyCysSerGlnSerAspPhe 396
 Qy 38657 GGAACAACACCTGTGACACTTATGACCTCAGCTTCAATGGTCCATCATTAATAGTCC 38716
 Db 397 GlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSer 416
 Qy 38717 AATTTCATGGGTCTAAGAAAGCTGCAGACCTTGGATTTTACAGACTTCACTTAAAAAG 38776
 Db 417 AsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGln 436
 Qy 38777 GTCAAGAAATTCACAGGTTCTTATCCCTTGAAGAAGCTTTTACCTTACCTCATCTCTAT 38836
 Db 437 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 456
 Qy 38837 ACTTACACCAAAATGACTTGTGATGTATATTTCTTGGCTTGAACAATCTTCAACATTA 38896
 Db 457 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 476
 Qy 38897 AAAATGGCTGGCAATCTTTCAAGACACACCTTCAAAATGCTTTTGCAAACACACA 38956
 Db 477 LysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArg 496
 Qy 38957 AACTTGACATTCCTGAGTCTTTCTTAAATGTCATTTGGAACAAATATCTGGGGGTATT 39016
 Db 497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPhe 516
 Qy 39017 GACACCTTCATAGACTTCAATATTAATATATGATGACACAAATCTATTTGTTTGAT 39076
 Db 517 AsnSerLeuSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp 536
 Qy 39077 TCATCCATTAATACACAGCTTATTCCTTACAGACTTATGAGTTTCAATCGATA 39136
 Db 537 ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 556
 Qy 39137 GAGACATCT---AAAGAAATATGCAACATTTTCCAAAGAGCTTACGCTTCAATCTT 39193
 Db 557 MetThrSerLysLysGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
 Qy 39194 ACTTACATTTCTGTGCTTATATATGTAACATCAGAAATCTTGCAGTGGCTCAAGAA 39253
 Db 577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAsp 596
 Qy 39254 CAGAGCACTTCTTGGTGAATGTGGAACAATGACATGTGCACACCTGTAGAGATAAT 39313
 Db 597 GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGln 616
 Qy 39314 ACCTCCTTAGTGTGATTTTAAATTAATTTACCTGTATATGTAACAGATCATCAGT 39373
 Db 617 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetCysAsnIleIleGly 635
 Qy 39374 GTGTCACTGTGCACTGTATGTGTGATTCACCTGTATATGATATACCACTTAT 39433
 Db 636 ValSerValLeuSerValLeuValIleSerValValAlaValLeuValTyrLysPheTyr 655
 Qy 39434 TTTTACCTGATCTTATTTGCTGTGCTGTTAAAAAGTACAGAGAAAGAAAGCTTATGAT 39493
 Db 656 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrIleLysArgGlyLysAsnIleTyrAsp 675
 Qy 39494 GCATTTGATCTTACCTGAGTCAAGTACAGAGAGAGCTGGGTGGAATGAGCTGTAAAGAT 39553
 Db 676 AlaPheValIleTyrSerSerGlnAspGlnAspTrpAlaArgAsnGlnLeuValLysAsn 695
 Qy 39554 TTAGAAAGAGAGTCCCGCTTTCACCTTGCCTTCACTACAGAGACTTATATCTGTGT 39613
 Db 696 LeuGlnLysGlyValProPhePheGlnLeuCysLeuHisLysTyrArgAspPheIleProGly 715
 Qy 39614 GTAGCCATTTGCTGCAACATCATCTCAGAAAGGCTTCCACAAAGAGCCGGAAGTTATGTG 39673
 Db 716 ValAlaIleIleAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal 735

QY 39674 GTAGTCTAGACATTATTCAGAGCCGCTGATCTTGAATATGAGATTCCTCAA 39733
 Db ValValSerGlnHisPheIleGlnSerIleArgTrpCysIlePheGluTrpGlnIleAlaGln 755
 QY 39734 ACATGACAGTTTCTGAGACGCCCTCTGACATCATCTTCATTTGCTTGAGAGGTTGAG 39793
 Db ThrTrpGlnPheLeuSerSerArgIleGlyIleIlePheIleValLeuGlnIleValGlu 775
 QY 39794 AAGTCCCTGAGGACAGGATGGAATTGATGCGCTTCTTGAAGAAACACCTACTG 39853
 Db LysThrLeuLeuArgGlnGlnValGlnLeuTrpArgLeuLeuSerArgAsnThrTrpLeu 795
 QY 39854 GAATGAGAGACAAATCTCTGAGGAGACATCTTCTGAGAAAGCTTAAATGCCCCA 39913
 Db GluTrpGlnAspSerValLeuGlnIleArgIleIlePheTrpArgLeuArgLeuAlaLeu 815
 QY 39914 TTGATGAGAAACCTCGAATCTCTGAGCAACA 39946
 Db LeuAspGlyLysSerTrpAsnProGluGlyThr 826
 RESULT 3
 ABU04775 standard; protein; 839 AA.
 AC ABU04775;
 XX 29-JAN-2003 (first entry)
 DT Human expressed protein tag (EPT) #1441.
 DE
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 KM
 XX Homo sapiens.
 OS
 XX WO200278524-A2.
 PN 10-OCT-2002;
 PD 28-MAR-2002; 2002WO-US009671.
 PF 28-MAR-2001; 2001US-0279495P.
 XX 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX (ZYCO-) ZYCO INC.
 PA
 XX Chicx RM, Tomlinson AJ, Urban RG;
 PI WPI; 2003-040607/03.
 DR
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 XX Example 2; SEQ ID NO 1441; 134pp; English.
 PS
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 2,33e-234 Length: 839
 Score: 2607.00 Matches: 526
 Percent Similarity: 73.68% Conservative: 101
 Best Local Similarity: 61.81% Mismatches: 172
 Query Match: 3.00% Indels: 52
 DB: Gaps: 8
 US-09-396-985b-48 (1-50000) x ABU04775 (1-839)
 QY 37400 TGGAAAAATGCAATTAATCTAAGACTATCATCTGCTTTATGACCCA 37459
 Db 26 TrpGluProCysValGluValAlaProAsnIleThrTrpGln----- 39
 QY 37460 GTTATGATCTTGAATGATTTTCTAATGATTTGCTGCGCTGACATAGTGATGATTT 37519
 Db 40 CysMetGluLeuAsnPheTrpLysIleProAspAsnLeuPro----- 53
 QY 37520 ATCATCACTGAGCAAGTGAAGTGAATCAATCTGCAAGATTCCTCTGTCACACC 37579
 Db 54 -----PheSerThrLysAsnLeuAspLeuPheAsnProLeuArgHis--- 68
 QY 37580 ATCATCACTGTTTGTCTGTCGACAGTTTCTCTTCAATATACATGATATATCT 37639
 Db 69 -----LeuGlySerTrpSerPhe----- 74
 QY 37640 GTTTGTATCATAGATGATGAGGACGTGTTATGCTTATGAAAGGTTTTCCTCAGCA 37699
 Db 75 -----PheSerPheProGlu 79
 QY 37700 AAATACATAATGATATCTCTTTTCCCATAGGTGAAATGAAACATTTGAAGACAG 37759
 Db 80 LeuGlnValLeuAsnLeuSer-----ArgCysGlnIleGlnThrIleGluAspGly 96
 QY 37760 GCATGCAATGCTTACACCACTCTCAACTGATCTGACAGAAACCTTATCAAGCT 37819
 Db 97 AlaTrpGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 116
 QY 37820 TTTTCCCAAGAAAGTTTCTCTGACCTAACAAGTTTGAAGATCGTGCGTGGAGACA 37879
 Db 117 LeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThr 136
 QY 37880 AAATGAGCTCTCTAGAAAGCTTCCCTATTGACAGCTTATTAACCTTAAAGAACTCAAT 37939
 Db 137 AsnLeuAlaSerLeuGlnLeuAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsn 156
 QY 37940 GTGGCTCACAATTTTATACATTCCTGTAAGTTACTGACATTTTTCATCTGACGAA 37999
 Db 157 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTrpPheSerAsnLeuThrAsn 176
 QY 38000 CTAGTACATGATGATCTTCTTATTAATATATTAATCAACTTATGTCACAGACTTACG 38059
 Db 177 LeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTrpCysThrAspLeuArg 196
 QY 38060 TTTTACGTGAATAATCCACAAGATCAATCTCTTATGACATGCTTTGAACCCATTTGAC 38119
 Db 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsn 216
 QY 38120 TTCAATCAAGACCAAGCTTTCAAGGGAATTAAGCTCCATGAACTGACTTGAAGGTAAT 38179
 Db 217 PheIleGlnProGlyAlaPheLysGluIleArgSerHisLysLeuThrLeuArgAsnAsn 236

QY	38180	TTTATATAGCTCAATATATATATGAAAACCTTGCTTCAAAACCTGGCTGGTTTACACGTCAT	382823
Db	237	PhenylserineLeuValMetIleThrCysIleGlnGlyLeuAlaGlyLeuAlaValHis	256
QY	38240	CGGTGATCTGGGAGAAATTTTAAAGATGAAAGAAATCTGGAAATTTTGACCCCTCTATC	382929
Db	257	ArgLeuValIleuGlyGluPheArgGluGlyAsnLeuGlyIlePheAspIysSerAla	276
QY	38300	ATGGAAGACATATGTGATGTGACCATTTGATGAGTTACAGTTTACATATCAAAATGATTTT	38359
Db	277	LeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeuAlaIleIleuAspTyrTyr	296
QY	38360	TCAAGTATATGTTAAAG---TTCATTTGCTTGGCCAAATGTTTCTGCAATGCTCTGGCA	38416
Db	297	LeuAspAspIleIleAspLeuPheAsnGlyLeuThrAsnValSerSerPheSerLeuVal	316
QY	38417	GGTGTATCTATAAATATCTAGAAAGATGTTCCATAATTTGACAAATGCAATCTTATCA	38476
Db	317	SerValThrIleGluArgValIysAspPheSerTyrAsnIleGlyTyrGlnIleuGlu	336
QY	38477	ATCATATGATGTCAATTAAGACAGTTTCCAACTCGGATCTACCCCTTTCTTAAAGTTTG	38536
Db	337	LeuValAsnGlyIysPheGlyGlnPheProThrLeuIleIleuIysSerLeuIysArgLeu	356
QY	38537	ACTTTAACTATGAACAAGAGCTATCAATTTTAAAAAGTGCCCTTACCAAGTCTCAC	38596
Db	357	ThrPheThrSerLeuIysGlyGlyAsnAlaPheSerGlyValAlaAspLeuProSerLeuGlu	376
QY	38597	TATCTAGATCTTATAGAAATGACCTGAGGTTTATAGTGTCGTCTTATCTGATTTG	38656
Db	377	PheLeuAspLeuSerAlaArgAsnGlyLeuSerPheIleGlyCysPheSerGlnSerAspPhe	396
QY	38657	GGAACAAACAGCCTGAGACACTTAGACCTTCAGCTTCAATGTGTCATTTATGAGTGCC	38716
Db	397	GlyThrThrSerLeuIysTyrIleAspLeuSerPheAsnGlyAlaIleThrMetSerSer	416
QY	38717	AATTTGATGGGTCTAGAAAGAGCTGACACCTGATTTTCAGACCTCTCATTTTAAAAAG	38776
Db	417	AsnPheLeuGlyLeuGluGlnIleuGlnIleuAspPheGlnIleSerAsnLeuIysGln	436
QY	38777	GTCACAGAAATCTCAGGGCTTATCCCTTGAAAGGTCATTTTACCTGACATCTCTAT	38836
Db	437	MetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis	456
QY	38837	ACTAACAACAATTAAGTCTTCGATGATATTTCTTGAGCTTGACAGCTCAACAACATTA	38896
Db	457	ThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeu	476
QY	38897	AAATGCTGGCAATCTTTCAAGACACACACCTTTCAATGTCTTTGCAAAACACACA	38956
Db	477	LysMetAlaGlyAsnSerPheGlnGlnIleAsnPheLeuProAspIlePheThrGluLeuArg	496
QY	38957	AACTTGACATTCCTGATCTTTCTTAATGTGCATTTGAAACAATATCTTGGGGGGATTT	39016
Db	497	AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGluIleuLeuSerProThrAlaPhe	516
QY	39017	GACACCCCTCAATACCTTCAATTTTAAATATGAGTCACACAACATCTATGTTGTTTGAT	39076
Db	517	AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp	536
QY	39077	TCATCCCATTTAAACAGCTGATTTCCCTGACACTTTGATTTGACAGTTTCAATGCGAT	39136
Db	537	ThrPheProTyrIysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle	556
QY	39137	GAGACATCT---AAAGAAATCTGCAACATTTTCCAAAGAGCTTACGCTTTCTTCAATCTT	39193
Db	557	MetThrSerIleIysGlnGluLeuGlnIlePheProSerSerLeuAlaPheLeuAsnLeu	576
QY	39194	ACTAACAATTCGTGGCTGTGATATATGACATCAGAAATTTCTGCGAGTGGGACGAAGA	39253
Db	577	ThrGlnAsnAspPheAlaCysThrCysGluHisIleSerPheLeuGlnIlePheIleIysAsp	596
QY	39254	CAGAAGCAGTCTCTGGTGAAATGTTGAACAATGACATGTGCAACACTGTAGATGAAT	39313

Db	597	GIhNrgSiLeuLeuValGIuValGIuAqMeGIuCyAlaThrProSerAerLysGln	616
QY	39314	ACSTCTTATGTGTGGATTTTAAATATCTACSTGTATATATATACAAAGCAATCACTACGT	39373
Db	617	GIuMeProValLeuSerLeu---AanILethrCyGlnMeAAsLysThrILethrLeuGI	635
QY	39374	GTCGCACTGTCAGTGTGATGTGGATGCACTGTAAGCACTTTCTGTATATACACTTCTAT	39433
Db	636	ValSerValLeuSerValLeuValValSerValValAlaValLeuValValLysPheTyr	655
QY	39434	TTTCACSTGTACTTATATGCTGGCTGTAAAGATACAGAGAGAGAAAGCACTTATGAT	39493
Db	656	PhehIvleuMeuSerLeuValaGIuCyvILeYrGIuAqGIuAAsnILeTyrAer	675
QY	39494	GCATTTTGTATCTACSTGATGCAATGAGATGAGACTGGGTGAGAAATGACCTGTAAAGAT	39553
Db	676	AlaPheValILeTyrSerSerGIuAerGIuAerTrValAlaAAsnILuLeuValLysAAsn	695
QY	39554	TTAGAAAGAGAGTGCCTCCGCTTTCACCTGTGCTTACATACAGACCTTATTTCTGTGT	39613
Db	696	LeuGIuGIuGIuValAlProPheGlnLeuCyvLeuILeTyrAqAerPheILeProGI	715
QY	39614	GTAGCCATTTCTGTGCGCAATCATCAAGCAAGAGCTTCCAAAGACCGGAAAGTTATGTG	39673
Db	716	ValAlaILeAlaILeAAsnILeILeILeAAsnILeGIuGIuPheILeLysSerTrGIuValILeVal	735
QY	39674	GTAGTGTCTACACACTTATATTCAGAGCCGTTGGTGTATCTTTGAATATGATGATGCTCA	39733
Db	736	ValValSerGIuILePheILeGlnSerAqTrGIuILePheGIuTyrGIuILeILeAAsn	755
QY	39734	ACATGCGAGTTTCTGAGACAGCCGCTGTGCAATCATCTTCAATTTGCTTGAAGAGTTGAG	39793
Db	756	ThrTrGIuILePheLysSerAqAlaGIuILeILePheILeValLeuGlnLysValGIu	775
QY	39794	AAGTCCCTGTGTGAGGAGAGGTGGAAATGTATGCGCTTCAAGCAAGCAACTACCTG	39853
Db	776	LysThrLeuLeuAqGIuGlnILeValGIuLeuTyrAqLeuLysSerAqAAsnILeTyrLeu	795
QY	39854	GAATGCGAGAGACACTCTGTGGGAGAGCAATCTTCTGGAAGAAAGATTAAATGCGCTTA	39913
Db	796	GIuTrGIuAerSerValLeuGIuAqAAsnILePheTrAqTrGIuAqLysValaLeu	815
QY	39914	TTGGATGAAAAAGCTCGAATCTCTGAGCAAAACA	39946
Db	816	LeuAerGIuLysSerTrPheAAsnProGIuGIuThr	826
RESULT 4			
ADCT8785	ID	ADCT8785 standard; protein; 839 AA.	
XX	AC	ADCT8785;	
XX	DT	01-JAN-2004 (first entry)	
XX	DE	Human PRO protein #7.	
XX	KW	human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;	
XX	OS	Crohn's disease.	
XX	PN	Homo sapiens.	
XX	PD	WO2003034984-A2.	
XX	PF	01-MAY-2003.	
XX	PR	15-OCT-2002; 2002WO-US030370.	
XX	PA	19-OCT-2001; 2001US-0340083P.	
XX	PI	(GETH) GENENTECH INC.	
XX		Goddard A, Gurney AL;	

[illegible]

Db	197	ValLeuHi seqlmetProLeuLeuAaenLeuSerLeuAaSpLeuSerLeuAaenProMetAaen	216
Qy	38120	TTCAATTCAGAACCAAGCCITTCAGGAGAAATTCAGCTCCATGAACCTGAAGAGCTA	38175
Db	217	PheIleGlnProGlyAlaPheLeuYsGluIleArgLeuHi sIbyleuThrLeuArgAaen	236
Qy	38180	TTTAAATGCTCAAAATATTAATGAAGAACTGGCTTCGCAAACTGGCTGGTTACACGTCCT	38233
Db	237	PheAspSerLeuAaenValMetIlysthrCyAlleGlnGlyLeuAlaGlyLeuGluValHis	256
Qy	38240	CGGTATCTTGGGAGAAATTTAAAGTAAGTAAGCACTGGAAATTTTGAACCCCTATAC	38299
Db	257	ArgLeuValIleuGlyGluPheArgAaenGluGlyAsnLeuGluIlySerpheAspIySeraIa	276
Qy	38300	ATGGAAGACATATGATGTGATGACCACTGATAGAGTTGAGGTAAACATATACAAATGATTT	38358
Db	277	LeuGluIlyLeuCyAsnLeuThrIleGluGluPheArgLeuAlaIyLeuAspTyrTyr	296
Qy	38360	TCAGATGATATGTTAAG--TTCCATGCTTGGCGAATGTTTTCGCAATGTCCTCGGCA	38418
Db	297	LeuAspAspIleIleAspLeuPheAsnCySyleuThrAsnValSerSerpheSerLeuVal	316
Qy	38417	GGGTATCTTAATAAATATCTAGAAGATGTTCCCAAACTTCGAAGGAATCCCTATATCA	38476
Db	317	SerAlaThrIleGluArgValIyAspSerpheSerTyrAsnPheIlyTyrGlnHisLeuGlu	336
Qy	38477	ATCATATGATGTCAACTTAAAGCAAGTTTCCAACTCGATCTACCCCTTTCTTAAAGTTTG	38536
Db	337	LeuValAsnCySylsSerpheGlyGlnPheProThrLeuIlyLeuIlySerLeuIyAsnGlu	356
Qy	38537	ACTTAACTATGAACAAAGGGCTATCAGTTTAAAAAGTGCCCTTCAACAGTCTCACG	38596
Db	357	ThrPheThrSerAaenIySglIyGluAaAlaPheSerGluValAspLeuProSerLeuGlu	376
Qy	38597	TATCTAGATCTTTAGTGAAGAAATGACCTGAGCTTTAGTGGTGGCTGTCTTATTTCTGATTG	38656
Db	377	PheLeuAspLeuSerAArgAaenGlyLeuSerPheIySglIyCyAsSerGlnSerAspPhe	396
Qy	38657	GGAACAAACAGCCTGAGACACTTGAACCTTCAGCTTCAAATGGTGGCCATCTTATGAGTGC	38716
Db	397	GlyThrThrSerLeuIyStryIleAaAspLeuSerPheAsnGlyValIleThrMetSerSer	416
Qy	38717	AATTCATGGGCTTAGAAGAGCTGACGACCTGGATTTTCACAGCTCTTCTTAAAGAG	38776
Db	417	AsnPheLeuIlyLeuGluGlnLeuGluHisIleAspPheGlnHisSerAaenLeuIySgl	436
Qy	38777	GTCACAGAAATTCACAGGTTCTTATCCCTTGAAAGCTACTTACCTGACATCTTCTAT	38836
Db	437	MetSerGluPheSerValPheLeuSerLeuAArgAsnLeuIleTyrLeuAspIleSerHis	456
Qy	38837	ACTAACAACCAAAATGACATCTGCATGATATTTCTTGGCTGACACAGTCCACACATTA	38896
Db	457	ThrHisThrArgValAlaPheAaenGlyIlePheAaenGlyLeuSerSerLeuGluValLeu	476
Qy	38897	AAATGGCTGGCAATCTTTCAAGACCAACAACCTTTCAAATGTCCTTGCAACAACA	38956
Db	477	IyMetAlaGlyAsnSerPheGlnGluAaenPheLeuProAspIlePheThrGluAaArg	496
Qy	38957	AACTGACATCTCTGGATCTTCTGTAATATGTCATTTGGAACAAATCTTGGGGGATTT	39016
Db	497	AsnLeuThrPheLeuAspLeuSerGlnCySglLeuGluGlnLeuSerProThrAlaPhe	516
Qy	39017	GACACCTGCATGACCTTCAATTAATTAATGAGCACAACAATGATATGTTTGGAT	39076
Db	517	AsnSerLeuSerSerLeuGlnValIleAaenMetSerHisAsnAsnPheSerpheSerLeuAsp	536
Qy	39077	TCATCCATATATACAGCTGATATCCCTCACACACTCTGATTTGAGAGTTCAATGCGCAT	39136
Db	537	ThrPheProTyrIySylsLeuAaenSerLeuGlnValIleAspTyrSerLeuAaHisIle	556
Qy	39137	GAGACATCT--AAAGGAATTACTGCAACATTTTCCAAAGAGTCTAGCCCTTCTCAATCTT	39193

Db	557	MethionylserineValylserineGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuHisLeu	576
QY	39194	ACTAACAATTCCTGCTGCTGCTGATATATGTAACATCAGAAATTCCTGCACTGGGTCAAGAA	39253
Db	577	ThrGlnHisMetPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIrrPheLeuSer	596
QY	39254	CAGAAAGCATTCCTGGTGGTGAATGTTTGAACAAATGACATGTGGCAACACCTGTAAAGATGAAT	39313
Db	597	GlnArgGlnLeuLeuValGluValGluArgMetGluCysValaThrProSerMetPylGln	616
QY	39314	ACCCCTTAGTGGTGAATTTTAATTAATTTTAACTCTGTATATGTATGACAAAGCAATTCATCACT	39373
Db	617	GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnHisThrIleIleGly	635
QY	39374	GTCCTCACTGCTCACTGATGTGATGTGGATATCCACATGACATTTCTGATATACACTTTGAT	39433
Db	636	ValSerValLeuSerValLeuValValSerValAlaValLeuValIrrLysPheTyr	655
QY	39434	TTTCACTGATATCTTATTCCTGGCTGGTAAAAAGTACAGCAGAGAGAAAGCATCTTGAT	39493
Db	656	PheHisLeuMetLeuLeuAlaGlyCysIleTyrGlyAlaGlyGlnAsnIleTyrAsp	675
QY	39494	GCATTGTGATCTCACTGAGTCAGATCAGAGAGACATGGGTGAGAAATGACCTGGTAAAGAT	39553
Db	676	AlaPheValIleIrrYrSerSerGlnAspValAspIrrValAlaArgMetLeuLeuValIrrAsn	695
QY	39554	TTAGAGAAGAGAGTCCGCCGCTTCACTCTGCTTCACTACAGACCTTTATTCCTGCT	39613
Db	696	LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisIrrLysArgMetPheIrrGly	715
QY	39614	GTACCCATTCCTGCCAATCATATCCAGAAAGCTTCACAAAGCCGGAAGGTTATTGTC	39673
Db	716	ValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal	735
QY	39674	GTACTGTCTGACACCTTATTCAGAGCCGCTTGATATCTTTGAATATGAGATTGCTCA	39733
Db	736	ValValSerGlnHisPheIleGlnSerArgIrrCysIlePheGlnIrrGlnIleAlaGln	755
QY	39734	ACATGAGAGATTCTCGACAGCCGCTGAGCATATCTTCACTTCTCTGAGAAAGTTTGAG	39793
Db	756	ThrIrrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln	775
QY	39794	AAGTCCCTGCTGAGGACAGCAGTGAATTTGATGCCCTTTAGCAAAACACTTACTTG	39853
Db	776	LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu	795
QY	39854	GAATGGAGAGACATCTCTCGAGGAGGACATCTTCTCGAAGAGACTTAAAAATGCCCTA	39913
Db	796	GlnIrrGlnAspSerValLeuGlyArgHisIlePheThrIrrArgLeuArgLysValAlaLeu	815
QY	39914	TTGATGAGAAAGCCTCGAATCTCGAGACAACA 39946	
Db	816	LeuAspGlyLysSerTrrAsnProGlnGlyThr 826	
RESULT 5			
ADD48826			
ADD48826		standard; protein; 839 AA.	
AC	ADD48826;		
XX	02-DEC-2004 (revised)		
DT	29-JAN-2004 (first entry)		
XX			
XX	Human Protein AAF05316, SEQ ID NO 14536.		
DE			
XX	Human; pain; neuronal tissue; gene therapy;		
KW	spinal segmental nerve injury; chronic constriction injury; CCI;		
KW	spared nerve injury; SNI; Chung.		
XX			
OS	Homo sapiens.		
XX	Unidentified.		
PN	W03003016475-A2.		

```

XX XX 27-FEB-2003.
XX PD
XX PF 14-AUG-2002; 2002WMO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX RR 01-NOV-2001; 2001US-0346382P.
XX RR 26-NOV-2001; 2001US-0333347P.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; AAF05316.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Example 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 839 AA;

Alignment Scores:
Pred. No.:      2.33e-234          Length:      839
Score:           2607.00            Matches:       526
Percent Similarity: 73.68%         Conservative:   101
Best Local Similarity: 61.81%        Mismatches:    172
Query Match:     3.00%             Indels:         52
DB:              7                 Gaps:           8
US-09-396-985B-48 (1-50000) x ADDA8826 (1-839)

QY 37400 TGGAAAGATGCAATAATTATCTAAGACACTACATCACTGCTTATGTACCACA 37459
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 37460 GTTAATGCTTGGAATTGTTTTCCTAATGATTTCTGCCTGACATGATGATATT 37519
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
QY 40 CysMetGlueuLenPhenTyrlYslleProAspAnLeuPro----- 53
Db ATCATCTAGTAGCAATGTGAAAATGACAAATCTGCAGAGTTCTCTCTGCTCACACC 37579
QY 54 -----PhesrThrlIlyValnLeuLseArPhesAnsProLeuArgHis--- 68

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QY 37580 ATCATACCTGTTTGTCTCTGACAGTTTCTTTACAAATACATGATATCATATCT 37639
Db 69 -----LeuGlySerTyrSerPhe----- 74
QY 37640 GTTTGTATCATATGATGTAGGAGCTGTATGTACTATTGAAGAGGTTTTTTTTTCAGCAA 37699
Db 75 -----PheSerPheProGlu 79
QY 37700 AAATACATATATGGTATCTCTTTTGGCCATGAGTGTAATTTGAACAAATGGAAGACAG 37759
Db 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspIly 96
QY 37760 GCATGCGCATGTCCTACACACCTCTCAAACTGTACTGACAGAAACCTTACAGAGT 37819
Db 97 AlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 116
QY 37820 TTTTCCCGAGAGTTTCTCTGACTAAACAGTTTAGAAATCTGCTGGCTGGAGACA 37879
Db 117 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGlnThr 136
QY 37880 AAATGGCTCTCTAGAAAGCTTCCCTATTTGGACAGCTTATAACCTTAAAGAACTCAAT 37939
Db 137 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuIlyThrLeuIlyGlnLeuAsn 156
QY 37940 GTGGCTCAATTTTATCATCTTCTGTAAGTACCTGCATATTTTTCATCTGACGAC 37999
Db 157 ValAlaHisAsnLeuIleGlnSerPheIlyLeuProGlyTyrPheSerAsnLeuThrAsn 176
QY 38000 CTAGTACATGTGATCTTTCTTAACTAATATTCAACTATTACTGTCAACAGACTTACAG 38059
Db 177 LeuGlnHisLeuAspLeuSerSerAsnIlyIleGlnSerIleTyrCysThrAspLeuArg 196
QY 38060 TTTTACGTGAATAATCCACAAGTCAATCTCTTAAACATGTCTTTGAACCCATTTGAC 38119
Db 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuLeuPheLeuSerLeuAsnProMetAsn 216
QY 38120 TTCAATTCAGACCAAGCTTTCAGGAGAAATTAAGCTCCATGACAGTCTGAGAGGTAT 38179
Db 217 PheIleGlnProGlyAlaPheIlyGlnIleArgLeuHisIlyLeuThrLeuArgAsnAsn 236
QY 38180 TTTAATAGCTCAATATATATGAATAAATTCCTTCAAACTGGCTGTTTACAGTCCAT 38239
Db 237 PheAspSerLeuAsnValMetIlyThrCysIleGlnIlyLeuAlaGlyLeuGlnValHis 256
QY 38240 CCGTTGATCTTGGAGAAATTTAAAGATGAAGAATCTGGAATTTTGAACCTCTATC 38299
Db 257 ArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGlnIlyPheAspIlySerIla 276
QY 38300 ATGGAAGACTATGATGATGACCATTTGATGAGTTTCAAGTATACAAATGATTTT 38359
Db 277 LeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuAlaTyrLeuAspIlyTyr 296
QY 38360 TCAGATGATATTTGTAAG---TTCCATTTCTTGGCGATGTTTCTGCAATGCTCTGCA 38416
Db 297 LeuAspIlyIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal 316
QY 38417 GGTATATCTATTAATATCTGAAGAATGTTCTTAACATTTCAAAATGGCAATCTTATCA 38476
Db 317 SerValThrIleGlnArgValIlyAspSerSerTyrAsnPheGlyTyrGlnHisLeuGln 336
QY 38477 ATCATGATGTCACTTAACAGATTTCCATCTGATCTGATCAACCTTTCTTAAAGTTTG 38536
Db 337 LeuValIleAsnCysIlyPheGlyIlePheProThrLeuIlySerIlySerLeuIlyArgLeu 356
QY 38537 ACTTATCATGACAAAGGCTCTATCATCTTATTAATAAAGTGGCTTACAGTCTGAC 38596
Db 357 ThrPheThrSerAsnIlyGlyAlaAsnAlaPheSerGlnValAspLeuProSerLeuGln 376
QY 38597 TATCTAGTCTTGTAGAAATGACAGCTTATGAGTGTCTGTTTATTTCTGATTTG 38656
Db 377 PheLeuAspLeuSerArgAsnGlyLeuSerPheIlyGlyCysCysSerGlnSerAspPhe 396

QY 38657 GGAACAAACAGCTTGAGACATTAAGACCTGACCTTCAATGAGTGCATCATTAATGAGCC 38716
Db 397 GlyThrThrSerLeuIlyTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSer 416
QY 38717 AATTTCATGGGTCTAGAAAGCTGCAGACCTTGAAATTTTCAAGCACTCTCATTTTAAAAAG 38776
Db 417 AsnPheLeuGlyLeuGlnIleGlnHisLeuAspPheGlnHisAsnLeuIlyGln 436
QY 38777 GTCAACAAATCTCAGGCTTCTTATCCCTGAAAGACTTTTACCTTACATCTCTAT 38836
Db 437 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 456
QY 38837 ACTAACAACAAATGACCTTGATGTATATTTCTGCTTGCACAGTCTTCAACATTA 38896
Db 457 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 476
QY 38897 AAAATGGCTGGCAATTTCTTTCAAGAACACACCTTTCAATGTCTTTGCAACACACA 38956
Db 477 LysMetAlaGlyAsnSerPheGlnIleAsnPheLeuProAspIlePheThrGlnLeuArg 496
QY 38957 AACTTGACATTTCCGTGATCTTTCAATGTCAATTTGAACAAATATCTTGGGGGTATTT 39016
Db 497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnIleGlnIleuLeuSerProThrAlaPhe 516
QY 39017 GACACCTCCATAGACTTCAATTTAATATGATGACACAACAAATCTATTGTTTGGAT 39076
Db 517 AsnSerLeuSerSerLeuGlnIleValLeuAsnMetSerHisAsnAsnPheSerLeuAsp 536
QY 39077 TCATCCCATTAATACAGAGTGTATTCCTGACAGACCTGTGATGACGTTTCAATGCA 39136
Db 537 ThrPheProTyrIlyCysLeuAsnSerLeuGlnIleValLeuAspTyrSerLeuAsnHisIle 556
QY 39137 GAGACATCT---AAGAAATATCTGCACATTTTCCAAAGTCTTACGCTTCTTCAATCT 39193
Db 557 MetThrSerIlyIlyGlnIleGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
QY 39194 ACTAACAATCTGTGCTGTGATATGATGACATGAGAAATTCCTGACAGTGGTCAAGGAA 39253
Db 577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrIlyAsp 596
QY 39254 CAGAGAGAGTTCTTGTGAATGTTGAACAATGACATGTCGACACCTGTAGAGATGAT 39313
Db 597 GlnArgIleLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspIlyGln 616
QY 39314 ACCCTCTTATGTTGATTTTAATATTTCACTGTTATATGTACAGACAAATGATCAGT 39373
Db 617 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnIlyThrIleIleGly 635
QY 39374 GTGTCAGTGGTCACTGATGTGATGTGATTCACATGATGATTTCTGATATACCATCTCAT 39433
Db 636 ValSerValLeuSerValLeuValSerValValAlaValLeuValIlyIlyPheTyr 655
QY 39434 TTTCACTGATCTTATTTGCTGTGCTGTAATAAAGTACAGACAGAGAGAAAGCATCTATGAT 39493
Db 656 PheHisLeuMetLeuLeuAlaGlyCysIleIlySerGlyIlyArgIlyGlnAsnIleTyrAsp 675
QY 39494 GCATTTGTATCTTACAGTACAGATGAGAGCTGGGTGAGAAATGACCTGTGTAAGAT 39553
Db 676 AlaPheValIleTyrSerSerGlnAspGlnAspThrValArgAsnGlyLeuValIlyAsn 695
QY 39554 TTGAAGAGAGAGGCGCTTACCTGACCTGACCTGACATGACAGACTTATCTCCGGT 39613
Db 696 LeuGlnIleGlyValProPheGlnIleCysLeuHisTyrIlyArgAspPheIleProGly 715
QY 39614 GTAGCCATTTCTGCAACATCATCTCAGAGAGGCTTCCACAAGAGCCGGAAGTTATTTG 39673
Db 716 ValAlaIleAlaIleAsnIleIleHisGlnIlyPheHisIlySerIlyGlyValIleVal 735
QY 39674 GTAGTCTTACAGACTTTATTCAGAGCGTGTGGTATCTTTGAATATGAGATGCTGCA 39733
Db 736 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnIlyTyrGlnIleAlaGln 755
QY 39734 ACATGGAGTTTCTGAGACAGCCGCTGAGCATATCTTCAATTTGCTTGAAGGTTGAG 39793

|||||
Db ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIyValGlu 775
QY 39794 AAGTCCCTGCTGAGGAGGAGGTGGAATTGATGCTTCTTACAGAAACACCTACTG 39853
|||:::|||||
Db LysThrLeuLeuArgGlnGlnValGlnLeuTyArgLeuLeuSerArgAsnThrTyLeu 795
QY 39854 GAATGGAGGAGCAATCTCTGGGAGGACACATCTTCTGAGAAAGCTTAAATGCCCTA 39913
|||||
Db GluTrpGlnAspSerValLeuGlyArgHisIlePheThrPArgLeuArgIyValLeu 815
QY 39914 TTGGATGAAAAGCCTCGAATCTCTGAGCAACA 39946
|||||
Db LeuAspGlyLysSerTrpAsnProGluGlyThr 826
RESULT 6
ID AAM86361 standard; protein; 837 AA.
AC AAM86361;
XX
XX 15-MAR-1999 (first entry)
XX
XX Human DNAX toll-like receptor DTLR4.
XX
XX DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
XX interleukin 1 receptor; phosphate metabolism; innate immunity response;
XX modulate inflammatory function; morphological effect;
XX immunological disorder.
XX
XX Homo sapiens.
XX
XX WO9850547-A2.
XX
XX 12-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US008979.
XX
XX 07-MAY-1997; 97US-0044293P.
XX 22-JAN-1998; 98US-0072212P.
XX 05-MAR-1998; 98US-0076947P.
XX
XX (SCHE) SCHERING CORP.
XX
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
XX WPI; 1999-059670/05.
XX
XX N-PSDB; AAV80675.
XX
XX Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
XX metabolism, modulate inflammatory function or innate immunity responses.
XX
XX Claim 3; Page 147-149; 171pp; English.
XX
XX The present invention specifically describes human DNAX toll-like
XX receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
XX in the present invention. Also described are: (1) a fusion protein
XX comprising a DTLR protein or peptide; (2) a binding compound, preferably
XX an antibody or antibody fragment which specifically binds to a DTLR
XX protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
XX; (4) an expression vector comprising the nucleic acid of (3); and (5) a
XX host cell comprising the vector of (4). The host cell of (5) can be used
XX to produce the DTLR proteins. The DTLR proteins can be used to alter
XX phosphate metabolism, to modulate inflammatory function, innate immunity
XX responses or morphological effects. The DTLR proteins can be used in the
XX treatment of conditions exhibiting abnormal expression of the receptors
XX of their ligands. These abnormalities are typically manifested by
XX immunological disorders
XX
SQ Sequence 837 AA;
Alignment Scores: 9.5e-234 Length: 837
Pred. No.:

Score: 2600.50 Matches: 526
Percent Similarity: 73.68% Conservative: 101
Best Local Similarity: 61.81% Mismatches: 171
Query Match: 2.99% Indels: 53
DB: 2 Gaps: 9
US-09-396-985b-48 (1-50000) x AAM86361 (1-837)
QY 37400 TGGAAAAATGCAATTAATATCACTACTACATCACTGCTTATGACCCA 37459
|||:::|||||
Db TrpGlnProCysValGlu---ValProAsnIleThrTyLeu----- 37
QY 37460 GTTATGATCTTGAATTTGATTTTCTAATGATTTCTGCTGACATAGTGATGTT 37519
||| ||||| :::: ||| |||||
Db CysMetGlnLeuAsnIlePheTyLysIleProAspAsnLeuPro----- 51
QY 37520 ATCATCATCTGACAAAGTGTGAAAATGACAAATCTGCAGATTCCTCTGCTCACACC 37579
||| ||||| :::: ||| |||||
Db 52 -----PheSerThrLysAsnLeuAspLysSerPheAsnProLeuArgHis--- 66
QY 37580 ATCATCACCTGTTTGTCTGTCACAGTTTCTCTTACAAATACATGATATCATATCT 37639
||| ||||| |||||
Db 67 -----LeuGlySerTySerPhe----- 72
QY 37640 GTTGTGATCATAGTATGATGAGGACTGTATGTCATTAGAAAGGTTTTTTTTCAGCAA 37699
||| ||||| |||||
Db 73 -----PheSerPheProGlu 77
QY 37700 AAATPACATATGATGATCTTTTGGCCATAGTGGAATTTGAAACATTTGAAAGCAAG 37759
::: ||||| :::: ||| |||||
Db 78 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGluAspGly 94
QY 37760 GCATGGCATGCTTATGACACCACTCTCAACCTTATCTGACAGAAACCTATCCAGAGT 37819
|||:::||||| ||||| |||||
Db 95 AlatyreIleSerLeuSerHisLeuSerThrIleuIleuThrIleuAsnProIleGlnSer 114
QY 37820 TTTTCCCGAGAAATTTCTCTGAGCTTACAGATTTAGAGATGTGCTGCTGAGACA 37879
::: ||||| :::: ||| |||||
Db 115 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIyLeuValAlaValGluThr 134
QY 37880 AAATTTGGCTCTCTAGAAAGCTTCCCTATTTGACAGCTTATACCTTTAAAGAACTCAT 37939
||| ||||| :::: ||| |||||
Db 135 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsn 154
QY 37940 GTGGCTCAGCAATTTTATCATCTCTGATGTTTCTGCAATTTTCCCATTCGACGAAAC 37999
||| ||||| ||||| |||||
Db 155 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluIyTrpPheSerAsnLeuThrAsn 174
QY 38000 CTAGTACATGTGATCTTCTTATTAATCTATATTCAAACTATTACTGTCACGACTTACAG 38059
||| ||||| :::: ||| |||||
Db 175 LeuGlnHisLeuAsnLeuSerSerAsnIyIleGlnSerIleTyCysThrAspLeuArg 194
QY 38060 TTTCTACGTGAATAATCCACAAATCTCTCTTTAGACATGTCTTTGAACCCAAATTGAC 38119
||| :::: ||| ||||| :::: ||| |||||
Db 195 ValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsn 214
QY 38120 TTGATTCAGAACCAAGCCTTTCAGGGAATTAATCACTCCATGCACTCAAGAGGTAAT 38179
||| ||||| ||||| |||||
Db 215 PheIleIleIleProGlyAlaPheLysGluIleArgLeuHisIleLysLeuThrLeuAlaGlnAsn 234
QY 38180 TTTTAATAGCTCAATATTAATGAAGAACTGTGCTTCAAAACCTGCTGTTTACAGTTCAT 38239
|||:::||||| ||||| ||||| |||||
Db 235 PheAspSerLeuAsnValMetLysTrpCysIleGlnGlyLeuAlaGlyLeuGluValHis 254
QY 38240 CGGTGATCTTGGAGAGATTTAAAGATGAAGAAATCTGGAATTTTGAACCTCTATC 38299
||| ||||| :::: ||| |||||
Db 255 ArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAla 274
QY 38300 ATGGAAGGACTATGTGATGACCATTTGATGATGATGATGATTAATCAATTAACGATTT 38359
::: ||||| ||||| ||||| |||||
Db 275 LeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyTrLeuAspTyTrTy 294
QY 38360 TCAGATGATATGTTGTAAG--TTCCATGTGCTTGCGAATGTTTCTGCAATGTCTGCGCA 38416


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QY 39137 GAGACATCT---AAGAGATACGCAACATTTCCAAAGACTGACCTTCTTCAATCTT 39193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 555 MetHisSerIySlyBngIngluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 574
QY 39194 ACTAACATTTCTGTTGCTTGTATATGTAACATCAAGAAATTCCTGCAGTGGCTCAAGAA 39253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 575 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleIysAsp 594
QY 39254 CAGAGAGACTCTTGGAATGTTGAACAAATGACATGTGACACCGTGAAGATGAT 39313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 GlnArgGlnLeuLeuValGlnValGlnArgMetGlnSalatThrProSerAspIySlyGln 614
QY 39314 ACCTCTAGTGTGATTTAAATTAATCTTACCTGTTTATGTCACAGACATCATCAGT 39373
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 615 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAnlyThrIleIleGly 633
QY 39374 GTGTACGTGTGATGTGATGTGATTCACCTGATGATTTGTGATATACACTTCTAT 39433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 634 ValSerValLeuSerValLeuValValSerValValAlaValLeuValTyrIySlyPheTyr 653
QY 39434 TTTGACCTGATCTATTTATGCTGCTGCTGTAAGTAACAGACAGAGAAAGATCTATGAT 39493
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 654 PheHisLeuMetLeuLeuAlaGlyCysIleIySlyTyrGlyArgGlyGlnAsnIleTyrAsp 673
QY 39494 GCATTTGTATCTACTCGAGTCAGATGAGAGACTGGTGAGAAATGAGCTGTAAAGAT 39553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 674 AlaPheValIleTyrSerSerGlnAspGlnAspTyrPValAlaGlnGlnLeuValIySlyAsn 693
QY 39554 TTGAGAGAGAGAGTGCCTGCTTCACTCTGCTTCACTGACAGAGACTTATTTCTGCTGT 39613
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 694 LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGly 713
QY 39614 GTACCATGCTGCTGCAATCATCATCAGAGAGGCTTCCACAGAGCCGGAAGCTTATGTG 39673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 ValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisIySlySerArgIyValIleVal 733
QY 39674 GTAGTGTCTAGACACTTATTCACAGAGCCGTTGATGCTTCTTGAATATGAGATGCTCA 39733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 734 ValIleSerGlnHisPheIleGlnSerArgTyrPyrSyllePheGlnTyrGlnIleAlaGln 753
QY 39734 ACATGGCAGTTTCTGAGAGCCGCTTGACATCATCTTCAATGCTTCTTGAAGAGTTGAG 39793
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 754 ThrTyrGlnPheLeuSerSerArgIleGlyIleIlePheIleValLeuGlnIyValGln 773
QY 39794 AAGTCCCTGCTGAGGACAGCTGGAATGTATGCTTCTTGAAGAAACCTACTGCTG 39853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrIleu 793
QY 39854 GAATGGAGAGACATCTCTGAGGAGACATCTTCTGAGAAAGCTTAAATGACCTCA 39913
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 794 GlnTyrGlnAspSerValLeuGlnArgHisIlePheTyrArgIyValGlnIyAlaLeu 813
QY 39914 TTGATGAGAAAGACCTCGAATCTGAGCAACA 39946
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 LeuAspGlyIySerTyrAsnProGlnGlyThr 824

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XX XX MO200278524-A2.
XX XX
XX XX 10-OCT-2002.
XX XX
XX XX 28-MAR-2002, 2002MO-US009671.
XX XX
XX XX 28-MAR-2001, 2001US-0279495P.
XX XX 21-MAY-2001, 2001US-0292544P.
XX XX 06-AUG-2001, 2001US-0310801P.
XX XX 01-OCT-2001, 2001US-0326370P.
XX XX 04-DEC-2001, 2001US-0336780P.
XX XX 20-FEB-2002, 2002US-0358985P.
XX XX
XX XX (ZYCO-) ZYCOS INC.
XX XX
XX XX Chicz RM, Tomlinson AJ, Urban RG;
XX XX WPI; 2003-040607/03.
XX XX
XX XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX XX cytoskeletal proteins, receptors or transcription factors), useful for
XX XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX XX leukemia.
XX XX
XX XX Example 2; SEQ ID NO 1442; 134pp; English.
XX XX
XX XX The invention describes a purified polypeptide, which comprises a
XX XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX XX polypeptide is useful as an immunogenic composition for eliciting in a
XX XX mammal an immunogenic response directed against any of the purified
XX XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX XX polypeptide, is useful for treating cancer. The polypeptide is also
XX XX useful for identifying compounds that binds to a naturally processed
XX XX class I or class II MHC-binding polypeptide. The polypeptides and
XX XX polynucleotides are particularly useful for treating or preventing
XX XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX XX lymphoma or leukaemia. These are also useful for screening agents for
XX XX treating the above mentioned diseases. This sequence represents an
XX XX expressed protein tag (EPT) isolated from human tissue for translational
XX XX profiling. Note: This sequence does not appear in the printed
XX XX specification but was obtained in electronic format directly from WIPO at
XX XX ftp.wipo.int/pub/published_pot_sequences
XX XX
XX XX Sequence 837 AA;
XX XX
XX XX Alignment Scores:
XX XX Pred. No.: 9.5e-234 Length: 837
XX XX Score: 2600.50 Matches: 526
XX XX Percent Similarity: 73.68% Conserved: 101
XX XX Best Local Similarity: 61.81% Mismatches: 171
XX XX Query Match: 2.99% Indels: 53
XX XX DB: Gaps: 9
XX XX
XX XX US-09-396-985B-48 (1-50000) x ABU04776 (1-837)
QY 37400 TGGAAAAATGCATTAATTAATCTAAGACTACTCATCATGCTGCTTATGTACCCCA 37459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 TrrpGlnProCysValGlu---ValProAsnIleThrTyrGln----- 37
QY 37460 GTTATGATCTTGAATGATTTTCTAATGAGATTTGCTGCTGACATAGTGTATGTTT 37519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 38 CysMetGlnLeuAsnPheTyrIySylleProAspAsnLeuPro----- 51
QY 37520 ATCATCACTGACAGTGTGAAGAAATGACAAATGTGACAGATTCTCTGCTACACACC 37579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 52 -----PheSerThrIySlyAsnLeuAspLeuSerPheAsnProLeuArgHis--- 66
QY 37580 ATCATCACTGTTTGTCTGTCAGATTTTCTTTTCAATATACATGATATATCT 37639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 -----LeuGlySerTyrSerPhe----- 72

```

RESULT 8
 ABU04776
 ID ABU04776 standard; protein; 837 AA.
 AC ABU04776;
 XX 29-JAN-2003 (first entry)
 XX
 XX Human expressed protein tag (EPT) #1442.
 DB
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.

QY 37640 GTTGTATCATAGTAGTAGGAGCTGTATATGTCATTAGAAAGGCTTTTTCACGAA 37699
 Db 73 -----PheSerPheProGlu 77
 QY 37700 AAATACATAATTGGTATCTCTTTTCCCATAGGTGTGAAATGGAACAATTTGAAGACAG 37759
 Db 78 LeuGlnValLeuSerLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 94
 QY 37760 GCATGAGCATGGCTTACACCAACCTCTCAACCTGTACTGACAGGAAACCCATCCAGAT 37819
 Db 95 AlaIyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlnAsnProIleGlnSer 114
 QY 37820 TTTTCCCAAGAAAGTTCTCTGACACTAACAGTTTAGAGATCTGTGCTGTGAGACA 37879
 Db 115 LeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIlyAsnValAlaValGlnThr 134
 QY 37880 AAATGGCTCTCTTGAAGAGCTTCCATTTAGACAGCTTATACCTTAAAGAACTCAAT 37939
 Db 135 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuIlySerThrLeuIlyGlnLeuAsn 154
 QY 37940 GTGGCTCACAATTTTATACATCTCTGTAAAGTTACTGTCACATTTTTCATTCAGACGAA 37999
 Db 155 ValAlaHisAsnLeuIleGlnSerPheIlyLeuProGluIyrPheSerAsnLeuThrAsn 174
 QY 38000 CTAGTACATGTCATCTCTTTTATTAATACTATATTCAACTATTAATCTGACAGACTTACAG 38059
 Db 175 LeuGlnHisLeuAsnLeuSerSerAsnIlyIleGlnSerIleIyrCysThrAspLeuArg 194
 QY 38060 TTTTTCAGTGAAATCCACAGATCATCTCTCTTTAGACATGCTTTTGAACCCATTTGAC 38119
 Db 195 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnProMetAsn 214
 QY 38120 TTCAATCAAGCAAGAGCTTTTCAAGGAAATTAAGCTTCATGACAGCTTGAAGGTAAAT 38179
 Db 215 PheIleGlnProGlyAlaPheIlyGlnIleArgLeuHisIlyAsnThrLeuArgAsnAsn 234
 QY 38180 TTTATAGCTCAAAATATATATGAAGAACTTGCCTTCAAAACCTGGCTGTTTACAGTCCAT 38239
 Db 235 PheAspSerLeuAsnValMetIlyThrCysIleGlnIlyLeuAlaGlyLeuGlnValHis 254
 QY 38240 CGGTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGGAATTTTGAACCTCTATC 38299
 Db 255 ArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGlnIlyPheAspIlySerAla 274
 QY 38300 ATGGAAGCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38359
 Db 275 LeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuAlaIlyrLeuAspIlyTyr 294
 QY 38360 TCAGATGATATTGTTAAG---TTCCATTTGCTTGGCGAATGTTTCTGCAATGCTCTGGCA 38416
 Db 295 LeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal 314
 QY 38417 GGTGTATCTATAAATATCTAGAAAGATGTTCTTAAACATTTCAAAATGGCAATCCTTATCA 38476
 Db 315 SerValThrIleGlnArgValIlyAspSerSerIyrAsnPheGlyTyrGlnHisLeuGln 334
 QY 38477 ATCATATAGATTCACATTAACAGATTTCCAGATCTGATCTACCTTTCTTAAAGTTTG 38536
 Db 335 LeuValAsnCysIlyPheGlyGlnPheProThrLeuIlySerLeuIlyArgLeu 354
 QY 38537 ACTTTAATCTATGAGCAAGAGGCTCATCAGTTTAAATAAGTGGCTTCAAGAGTCTCAGC 38596
 Db 355 ThrPheThrSerAsnIlyGlyAlaAsnAlaPheSerGlyValAspLeuProSerLeuGln 374
 QY 38597 TATCTAGATCTTGAAGAAATGACCTGAGCTTTAGTGCTGTCTGTTTATTTCTGATTTG 38656
 Db 375 PheLeuAspLeuSerArgAsnGlyLeuSerPheIlyGlyCysCysSerGlnSerAspPhe 394
 QY 38657 GGAGCAAAACAGCTGAGACACTTGAAGCTTCAATGTCATATGTCATATTAAGAGCC 38716
 Db 395 GlyThrThrSerLeuIlySerIlyLeuAsnLeuSerPheAsnGlyValIleThrMetSerSer 414
 QY 38717 AATTTCATGGGTCTAGAAAGACTGACAGCTGATTTTTCAGACTTACTTAAAGAG 38776

Db 415 AsnPheLeuGlyLeuGlnIlyLeuGlnHisLeuAspPheGlnHisSerAsnLeuIlyGln 434
 QY 38777 GTACAGAAATTCCTCAGCGTCTTATCCCTTGAAGAAAGCTATTCATCTGATACATCTCTAT 38836
 Db 435 MetSerGlnPheSerValPheLeuSerLeuAspAsnLeuIleIyrLeuAspIleSerHis 454
 QY 38837 ACTAACACCAAAATTAATCACTCGATGATATTTCTTGGCTTGAACAGTCTCAACATTA 38896
 Db 455 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 474
 QY 38897 AAAATGGCTGGCAATCTTTCAAGACACACCTTTCAATGCTTTTGCACAAACACACA 38956
 Db 475 LysMetAlaGlyAsnSerPheGlnIlyAsnPheLeuProAspIlePheThrGlnLeuArg 494
 QY 38957 AACTTGACATCTCGATGCTTCTTAAATGTCATTTGGAACAAATATCTGGGGGATTTT 39016
 Db 495 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIlyLeuSerProThrAlaPhe 514
 QY 39017 GACACCTCCATGACTTCAATATTAATATGATGACACAAACATCTATTTGTTTGAT 39076
 Db 515 AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnThrPheSerLeuAsp 534
 QY 39077 TCATCCCATTAATACAGCTGATTCCTCAGACCTTTGATTTGACGTTTCAATCCGATA 39136
 Db 535 ThrPheProIlyIyrCysLeuAsnSerLeuGlnValLeuAspIlyrSerLeuAsnHisIle 554
 QY 39137 GAGACATCT---AAAGAAATACAGCAAACTTTCCAAAGCTGATAGCTTCAATCTT 39193
 Db 555 MetThrSerIlyIyGlnIlyLeuGlnHisPheProSerSerLeuAlaPheLeuLeu 574
 QY 39194 ACTAACAAATCTGTGCTGTATATGATGACATCAGAAATTCCTGACAGTGGTCAAGAA 39253
 Db 575 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIlyrIleAsp 594
 QY 39254 CAGAGCAAGTTCTTGGTGAATGTTGAACAATGACATGTGCAACACCTGTAGAGATGAT 39313
 Db 595 GlnArgGlnLeuLeuValGlnValGlnArgMetGlyCysAlaThrProSerAspIlyGln 614
 QY 39314 ACCTCTCTAGTGTGATTTTAAATTTTCAACCTGATATGACAAAGACATCATCAGT 39373
 Db 615 GlyMetProAlaLeuSerLeu---AsnIleThrCysGlnMetAsnIlyThrIleGly 633
 QY 39374 GTGTCAGTGTGTCAGTGTATGTGATATCCATGTAGCATTTTGCATATACCATCTTAT 39433
 Db 634 ValSerValLeuSerValLeuValSerValValAlaValLeuValIlyrIlyPheTyr 653
 QY 39434 TTTCACTGATCTTATTTGCTGTGCTGTTAAAGTACAGACAGAGACAAACATCTATGAT 39493
 Db 654 PheHisLeuMetLeuLeuAlaGlyCysIleIlyTyrGlyArgGlyGlnAsnIleIyrAsp 673
 QY 39494 GCATTTGTATCTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39553
 Db 674 AlaPheValIleIyrSerSerGlnAspGlnAspIlyrAlaArgAsnGlnLeuValIlyAsn 693
 QY 39554 TTGAAGAGAGAGGCGCCCTTCACTCTGCTTCACTACAGAGAGCTTATTTCTGCT 39613
 Db 694 LeuGlnIlyValIlyProPheGlnIlyCysLeuHisIlyrIyrArgAspPheIleProGly 713
 QY 39614 GTAGCCATTTCTGCAACATCATTCAGAAAGGCTTCCACAAAGAGCGGAAGTTATTTG 39673
 Db 714 ValAlaIleAlaAsnIleIleHisGlnIlyPheHisIlySerArgIlyValIleVal 733
 QY 39674 GTAGTCTAGACACTTATTAAGAGCGGTGGGTATCTTTGAATATGAGATTTGCTCAA 39733
 Db 734 ValValSerGlnHisPheIleGlnSerArgIlyrCysIlePheGlnIlyrGlnIleAlaGln 753
 QY 39734 ACATGCAAGTTTTCAGACAGCGCTGTGACATCATCTTATGCTTCTTGAAGAGTTGAG 39793
 Db 754 ThrIyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIlyValGln 773
 QY 39794 AAGTCCCTGTGAGACAGAGTGAATGTATGCTTTTTCAGACACTTAAAGAG 39853

Db 774 LysThrlLeuLeuArgGlnGlnValGluLeuTyraGluLeuSerArgAsnThrTyrlLeu 793
 QY 39854 GAATGGAGAGCAATCTCTGGGAGAGACATCTTCTGAGAGACCTTAAATAAGCCCTA 39913
 Db 794 GlutpGluAspSerValLeuGlyArgGhiSilePheTrpArgArgLeuArgValLeu 813
 QY 39914 TTGGATGGAAAAAGCCCTCAATCTCTGAGCAACA 39946
 Db 814 LeuAspGlyLysSerTrpAsnProGluGlyThr 824

RESULT 9
 ADO57791
 ID ADO57791 standard; protein; 795 AA.
 XX ADO57791;
 XX AC
 XX 12-AUG-2004 (first entry)
 XX DT
 XX Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
 XX DE
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
 XX OS
 XX Macaca mulatta.
 XX FH
 XX Key location/Qualifiers
 FT Misc-difference 635
 FT /label= Lys, Asn
 XX
 XX MO2004042365-A2.
 XX PN
 XX 21-MAY-2004.
 XX PD
 XX 03-NOV-2003; 2003WO-US036247.
 XX PR
 XX 01-NOV-2002; 2002US-0423113P.
 XX
 XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX PA
 XX Messier W;
 XX PI
 XX
 XX WPI; 2004-400726/37.
 DR N-PSDB; ADO57789, ADO57790.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 12; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents rhesus monkey TLR4.
 XX
 XX Sequence 795 AA;
 SO

Alignment Scores:
 Pred. No.: 1,28e-233 Length: 795
 Score: 2599.00 Matches: 524
 Percent Similarity: 74.26% Conservative: 99
 Best Local Similarity: 62.46% Mismatches: 164
 Query Match: 2.99% Indels: 52
 DB: 8 Gaps: 8

US-09-396-985B-48 (1-50000) x ADO57791 (1-795)
 QY 37433 ACATATCAACGCTTTATATGATACCCGTTATGATCTTGAATGATTTTCTAATGAT 37492
 Db 6 ThrTyrlGln-----CysMetGluLeuAsnPheTyrlLysIleProasp 19
 QY 37493 TTGCTGCTTGACATATGATGTATGATTTATCATCTGATGAGATGTTGAAATGCAAT 37552
 Db 20 AsnLeuPro-----PheSerThrLysAsnLeuasp 29
 QY 37553 CTGCAAGATTCCTCTCTCTGCTACACATCATCACCTGTTTGTCTGTATACATTTTCTC 37612
 Db 30 LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 43
 QY 37613 TTTACATATACATGATATCATATCTGTTGATCATAGTATGATGAGACTGTATGCT 37672
 Db 43 ----- 43
 QY 37673 CATTAGAAAGGTTTTTTTTTTCAGCAAAAATACATAATGGTATCTTTTGGCCATAGG 37732
 Db 44 -----PheSerPheProGluLeuGlnValLeuAspLeuSer-----Arg 56
 QY 37733 TGTGAATTTGAACAATTTGAAGACAGACATGAGCATGAGCTTTACACCACTCTCAAACTTG 37792
 Db 57 CysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrIle 76
 QY 37793 ATACTGACAGAAACCTTATCCAGATGTTTCCCGAGAAATTTCTCTGATCAATCAAGT 37852
 Db 77 IleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
 QY 37853 TTAGAGATCTGAGGCTGTGAGACAAAATGGCCTCTGAGAAAGCTTCCCTATTGGA 37912
 Db 97 LeuGlnLysLeuValAlaValGluThrAsnLeuAlaSerLeuGlnAsnPheProIleGly 116
 QY 37913 CAGCTTATTAACCTTAAAGAAATCAATGAGGCTCAACAATTTATATCAATTCCTGTAAGTTA 37972
 Db 117 HisLeuThrLeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeu 136
 QY 37973 CCTGCATATTTTCCATCTGACGAACTAGTACATGATGATCTTTCTTATTAATCATAT 38032
 Db 137 ProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIle 156
 QY 38033 CAACCTATTACTGTCAACGACTTCAAGCTTCTACGTGAATAATCAACAAGTCAATCTCTCT 38092
 Db 157 GlnAsnIleTyrCysLysAspLeuGlnValLeuHisGlnMetProLeuSerAsnLeuSer 176
 QY 38093 TTAGACATGCTTTGAAACCAATGACTTCAATTCAGACCAAGCTTTCAGAGGAATTAAG 38152
 Db 177 LeuAspLeuSerLeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArg 196
 QY 38153 CTGCATGAACGACTCTTAAGAGTAAATTTTAATAGCTCAAAATTAATGAATACTGCTT 38212
 Db 197 LeuHisLysLeuThrLeuAspGlySerAsnAspAsnLeuAsnValMetLysThrCysIle 216
 QY 38213 CAAAACCTGGCTGTGTTACAGCTCCATCGGTGATCTTGGAGAAATTTAAAGATGAAG 38272
 Db 217 GlnIleLeuAlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheAsnGlnArg 236
 QY 38273 AATCTGAATTTTGAACCCCTATCATGAGAAAGACTATGATGATGACCATTTGATGAG 38332
 Db 237 AsnLeuGlnGluPheAspLysSerSerLeuGlnGlyLeuCysAsnLeuThrIleGluGln 256
 QY 38333 TTACGTTAATCATATCAATAATGATTTTTCAGATGATTTGTTAAG---TTCATGCTGTTG 38389
 Db 257 PheArgLeuThrTyrlLeuAspTyrlTyrlLeuAspAsnIleIleAspLeuPheAsnCysLeu 276
 QY 38390 GCGAATTTCTGCAATGCTCTGGAGGAGTGATCTTAATAATATCTAGAAAGATGTCCT 38449
 Db 277 AlaAsnValSerSerPheSerLeuValSerValSerIleLysArgValGluAspPheSer 296
 QY 38450 AAACATTTCAATGAGCAATCTTATCAATCATTAAGATGTCACATTAAGCAATTTCAACT 38509
 Db 297 TyrAsnPheArgTrpGlnHisLeuGluLeuValAsnCysLysPheGlnGlnPheProThr 316


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QY 38510 CTGGATCTACCCCTTTCTTAAAGTTTGAATTAATGAAACAAGGGTCTACGTTT 38569
DB 317 LeuDIuLeuGIuSerLysArgLeuThrPheThrAlaAsnLysGlyValAsnAlaPhe 336
QY 38570 AAAAAGTGGCCCTTACCAAGCTTCAGCTATCTAGATCTTAGTAAATGACATGAGCTTT 38629
DB 337 SerGIuValAspLeuProSerLeuGIuPheLeuAspLeuSerArgAsnGlyLeuSerPhe 356
QY 38630 AGTGGTTCCTGTTCTTATTTGATTTGGGAAACAACGCTGAGACCTTAGACCTTAGC 38689
DB 357 LysGIuCySersGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSer 376
QY 38690 TTCAATGGTGCACATTAATGAGTCCAAATTTGAGTGTAGAAAGGCTGACACACTG 38749
DB 377 PheAsnAspValIleThrMetSerSerAsnPheLeuGIuLysGlyValGlnIleLeu 396
QY 38750 GATTTTCAGACCTCTACTTTAAAAAGGGTCAACAATTTCTCAGGCTTATCCCTTGA 38809
DB 397 AspPheGlnIleSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArg 416
QY 38810 AAGTCTATTACCTTGAATCTTCTTATACCTAACCCAAATTTGATGCTGATATTT 38869
DB 417 AsnLeuIleTyrLeuAspIleSerThrIleThrArgValAlaPheAsnGlyIlePhe 436
QY 38870 CTTCGCTTACGACCTTCAACACATTAATAATGGCTGGCAATCTTCCAAAGACACAC 38929
DB 437 AspGIuLeuLeuSerLeuLysValLeuLysMetArgLysAsnSerPheGlnGlnAspPhe 456
QY 38930 CTTCGAATGTCTTTGGAAACAACAACAACTTGAATTTCTGATCTTTCTTAATGTCAA 38989
DB 457 LeuProAspIlePheThrIleAspLeuLysAsnLeuThrPheLeuAspLeuSerGlnCyGln 476
QY 38990 TTGGAACAATATTTGGGGGGGTATTGACACCTCCATGACATTCATTAATTAATG 39049
DB 477 LeuDIuGlnLeuSerProThrAlaPheAspThrLeuAsnLysLeuGIuValLeuAsnMet 496
QY 39050 AGTCACAACATCTAATGTTTGGATTCCCATTAACAACAGCTGTATTCCTCAGC 39109
DB 497 SerIleAsnAsnPhePheSerLeuAsnSprThrPheProTyrLysCySLeuProSerLeuGln 516
QY 39110 ACTCTGATTGCACTTTCATGCAATGCAATGACATCTAAGAA--ATACTGCAACATTTT 39166
DB 517 ValLeuAspTyrSerLeuAsnIleIleMetThrSerAsnAsnGlnIuLeuGlnIlePhe 536
QY 39167 CCAAGAGCTAGGCTTTCTAATCTTAACAATTTCTGCTGTTGATATGTGAACAT 39226
DB 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCyThrCySLeuIleHis 556
QY 39227 CAGAAATTCCTGCAAGGCTCAAGAAACAAGAGTCTTGAGTGAATGTTGAACAATG 39286
DB 557 GlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeuValGlnAlaGlnAsnMet 576
QY 39287 ACATGTGCACACCTTAGAGATGAATACCTCTTAGTGTGATTTTAATTAATCTAAC 39346
DB 577 GluCySAlaThrProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThr 595
QY 39347 TGTATATGTACAAGACATATATCAGTGTGTCAGTGTGTCAGTGTGATTTGCTCACT 39406
DB 596 CysGlnMetAsnLysThrIleIleGlyValSerValPheSerValLeuValValSerVal 615
QY 39407 GTACATTTCTGATATACCACTTCTAATTTTCAACCGTAACTTATTTAGGCGGTGAAAAAG 39466
DB 616 ValAlaValIleValIleTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIle*** 635
QY 39467 TACAGCAGAGGAGAAAGCATATGATGATCTTGTGATCTTCTGAGTCAAGATGAGAGAC 39526
DB 636 TyrGIuArgGIuLysAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAsp 655
QY 39527 TGGGTGAGAAATGAGCTGTGTAAGAAATTTAGAAGAGAGTCCCGCTTTCACCTCTGC 39586
DB 656 TrpValIArgAsnGIuLeuValLysAsnLeuGIuGlnGlyValProProPheGlnLeuCyS 675

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QY 39587 CTTCACATGACAGACTTTATTTCCGTGTAGACCATTTGCTGCCCAATCATCATCAGAAAGC 39646
DB 676 LeuHisTyrArgAspPheIlePheProGlyValAlaIleAlaIleAsnIleIleHisGlnGly 695
QY 39647 TTCCACAAGAGCCGGAAGGTTATGTGTGTAGTGTCTAGACACTTTATTCAGACCCGTTG 39706
DB 696 PheIleLysSerArgLysValIleValAlValSerGlnHisPheIleGlnSerArgTyr 715
QY 39707 TGTATCTTGAATATATGATGTTGCTCAACATGCGACTTTCTGAGCAGCGCTGCGCATC 39766
DB 716 CysIlePheGlnTyrGIuIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIle 735
QY 39767 ATCTTATGCTCTTGAAGAGTTTGAAGTCCCTGCTGAGCAGCAGGTGTAATGTAT 39826
DB 736 IlePheIleValLeuGlnLysValGlnLysThrLeuLeuArgGlnGlnIuLeuTyr 755
QY 39827 CGCCTTTTACGAAACACCTTACCTGGAATGGAGAGACAACTCTTGGGAGGCAATC 39886
DB 756 ArgLeuLeuSerArgAsnThrTyrLeuGIuTrpGlnAspSerValLeuGIuGlnHisIle 775
QY 39887 TTCTGAGAAAGACTTAAAAATGCCCTAATTTGATGAGAAAAAGCCTCGAATCCTGAGCA 39943
DB 776 PheTrpArgArgLeuArgLysAlaLeuLeuAspGlyArgSerTrpAsnProGlnGlu 794

RESULT 10
AD057803
ID AD057803 standard; protein; 808 AA.
AC AD057803;
XX 12-AUG-2004 (first entry)
DT 12-AUG-2004 (first entry)
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX Pan troglodytes.
XX WO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003MO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Mesnier W;
XX WPI; 2004-400726/37.
XX N-PSDB; AD057801, AD057802.
XX DR Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX PT sequence of the Old World monkey with that of a human.
XX PS Disclosure; SEQ ID NO 24; 11pp; English.
XX XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and compositions are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX

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SQ Sequence 808 AA;
 Alignment Scores:
 Pred. No.: 2 47e-233 Length: 808
 Score: 2596.00 Matches: 524
 Percent Similarity: 74.29% Conservative: 100
 Best Local Similarity: 62.38% Mismatches: 164
 Query Match: 2.99% Indels: 52
 Gaps: 8
 DB: 8
 US-09-396-985b-48 (1-50000) x ADOS7803 (1-808)

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QY 37433 ACATATCAACTGCTTTATGATACCCAGTTATGATCTTGAATGATTTTCTAATGGAT 37492
Db 6 Thyrgrin-----CysMetGluLeuAsnPhenylLysIleProasp 19
QY 37493 TTGTCCTGACATAGTGTGATGATTATCATCACTGATAGCAAGTGTGAAAATGACAAAT 37552
Db 20 AsnLeuPro-----PheSerThrLysAsnLeuasp 29
QY 37553 CTGCAAGACTTCCTCCTGCTCAACACATCATCACTGTTTGGCTGTAGAGTTTCTC 37612
Db 30 LeuSerPheAsnProLeuaspArgHis-----LeuGlySerTyrSerPhe--- 43
QY 37613 TTACAAATACATGATATATATATCTGTTGATCATAGTATGATGATAGGACTGTATGT 37672
Db .43 ----- 43
QY 37673 CATTAGAAAGGTTTTTTTTTTCAGCCAAATAATATGATCTTTTGCCCATAGG 37732
Db 44 -----PheSerPheProGluLeuGlnValLeuAspLeuSer-----Arg 56
QY 37733 TGTGAATGAAACAATTTGAGACAGCAAGCATGAGTCTTACACACCTCTCAACTG 37792
Db 57 CysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeu 76
QY 37793 ATATGACAGAAACCTATCCAGAGTTTTCAGGAGAGTTTCTGTGACTAACAAGT 37852
Db 77 IleuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
QY 37853 TTAGCAATCTGGTGGCTGTGAGACAAATTTGGCTCTTGAAGAGCTTCCATTGGA 37912
Db 97 LeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSerLeuGluAsnPheProIleGly 116
QY 37913 CAGCTTATACCTTAAAGAACTCAATGGCTCAACAATTTATATACATCTCTGTAAGTTA 37972
Db 117 HisLeuLysThrIleLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeu 136
QY 37973 CCTGCATATTTTTCATCTGACGAACTTAGACATGATGATCTTTCTTATACCTATAT 38032
Db 137 ProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerHisLysIle 156
QY 38033 CAATCTATCTGTCACAGACTTACAGTTTCTAGCTGAAATTCACAGTCAATCTCTCT 38092
Db 157 GlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSer 176
QY 38093 TTAGACATGTTTGAACCCATGACTTCAATTCACACCAAGCTTTCAGGAAATTAG 38152
Db 177 LeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArg 196
QY 38153 CTCATGATGAGCTCTAGAGGTAAATTTTAATAGCTCAATATATAGAAACTTGGCTT 38212
Db 197 LeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeuAsnValIleMetLysThrCysIle 216
QY 38213 CAATACCTGGCTGTTTACAGCTCCATCGTTGATCTTGGAGAAATTTAAGTGAAGG 38272
Db 217 GlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGlyLysPheArgAsnGlnGlu 236
QY 38273 AATTCGAAATTTTGAACCTCTATATCATGAGAGACATATGTATGTACATGATAGAG 38332
Db 237 AsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeuGlyAsnLeuThrIleGlnGlu 256
QY 38333 TTCAGTTAATATACAAATGATTTTTCAGATGATATTTTGAAG--TTCATTTGCTTG 38389
  
```

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Db 257 PheArgLeuAlaTyrLeuAspTyrTyrLeuAspArgPheIleLeuAspLeuPheAsnCysLeu 276
QY 38390 GCGAATTTTCTGCAAGTCTCTGGCAGGTATATCTTAAATATCTAGAAAGATTTCT 38449
Db 277 ThrAsnValSerSerPheSerLeuValSerValThrIleLysSerValLysAspPheSer 296
QY 38450 AATCATTTCAATATGCAATCTTATATCATATGATGATGATGATGATGATGATGATGAT 38509
Db 297 TyrAsnPheGlyTyrGlnHisLeuGlnValLysCysLysPheGlyGlnPheProThr 316
QY 38510 CTGATCTACCTTTCTTAAAGTTTGAATTAATCTATGACAAAGGCTCTATGACTTT 38569
Db 317 LeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsnLysGlyValAsnAlaPhe 336
QY 38570 AAAAAAGTGGCCCTTACCAAGTCTGAGTATCTATGATCTTATGATGATGATGATGAT 38629
Db 337 SerGluValAspLeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPhe 356
QY 38630 AGTGGTTCGTTGTTTATTTGATTTGGAACAAACAGCTGAGACCTTATGACTGAGC 38689
Db 357 LysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSer 376
QY 38690 TTCAATGTCATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38749
Db 377 PheAsnGlyValIleThrMetSerSerAsnPheLeuGlnGlnGlnIleLeu 396
QY 38750 GATTTTCAACATCTACTTTAAAAAGGCTCACAGAAATTTCTGAGCTTTTATCCCTTGA 38809
Db 397 AspPheGlnHisSerAsnLeuLysGlnMetSerLysPheSerValPheLeuSerLeuArg 416
QY 38810 AAGTACTTATACCTTGAATCTCTTATATACCAACAAATTTGACTCGATGATATTT 38869
Db 417 AsnLeuLysTyrLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePhe 436
QY 38870 CTGGCTTTCACAGTCTCAACACATTTAAAAATGGCTGGCAATTTCTTCAAGACACACC 38929
Db 437 AsnGlyLeuSerSerLeuGlnValLeuLysMetValIleGlyAsnSerPheGlnGluAsnPhe 456
QY 38930 CTTTCAATGCTCTTTCGAAACACACAACTTGACATTTCTGATCTTTTCAATATGCA 38989
Db 457 LeuProAspLysPheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGln 476
QY 38990 TTGGAACAATATCTTGGGGGTATTTGACACCTTCATGACTTCAATATTAATATG 39049
Db 477 LeuGlnIleLeuSerProThrAlaPheAsnSerLeuSerLeuGlnValLeuAsnMet 496
QY 39050 AGTCACAACATCATTTGTTTGGATTTCAATCCATATTAACCAAGCTGTATTTCCCTGAGC 39109
Db 497 SerHisAsnAsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGln 516
QY 39110 ACTTGTATTCAGTTTCAATTCGATAGACATCT--AAAGAAATCTGCAACATTTT 39166
Db 517 ValLeuAspTyrSerLeuAsnHisIleMetThrSerLysGlnGlnIlePhe 536
QY 39167 CCAAGAGCTAGCTCTTCAATCTTATCTAACAATCTGTGTGCTGTATATGATGACAT 39226
Db 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHis 556
QY 39227 CAGAAATCTCTGAGTGGCTCAAGGACACAGACAGTCTTGGAGATGTTGAACAATG 39286
Db 557 GlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeuLeuValGluValArgMet 576
QY 39287 ACATGTCACACCTGATAGATGAATACTCTTATGTTGATTTTAATATTTTACC 39346
Db 577 GluLysAlaThrProSerArgLysGlnGlyMetProValLeuSerLeu--AsnIleThr 595
QY 39347 TGTATATGTAACAAGAAATCATCAGTGTGATGATGATGATGATGATGATGATGATGAT 39406
Db 596 CysGlnMetAsnLysThrIleIleGlyValSerValLeuSerValLeuValSerVal 615
QY 39407 GTAGCATTTTGTATATACCACTTCTATTTTACCTGATATCTTATGCTGCTGTAAG 39466
  
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Dh      616 ValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuAlaGlyCysIleLys 635
Qy      39467 TACAGCAGAGGAAAGATCTATGATGATCTTGTGATCTACTGAGTCAGAAAGAGAC 39526
Dh      636 TyrClValrGgIyGluAnIleTyrAspIaPheValIleTyrSerSerGlnAsp 655
Qy      39527 TGGGTGAAATGAGCTGTGAAGATTTTGAAGAGAGAGTGCCTCCCTTCACCTGTC 39586
Dh      656 TrpAlaIArgenGluLeuValLysAsnLeuGluGluValProPheGlnLeuCys 675
Qy      39587 CTTTACTACAGACATTTATTCCTGTGTAGCCATTTGCTGCCAATCATTCAGAGAGGC 39646
Dh      676 LeuHisTyrArgAspPheIleProGlyValAlaIleAlaAsnIleIleHisGluGly 695
Qy      39647 TTCCACAGAGCCGGAAGGTATTTGTGTAGTGTCTGACACCTTATTCAGAGCGTTGG 39706
Dh      696 PheHisLysSerAlaGlyValIleValValSerGlnHisPheIleGlnSerArgTrp 715
Qy      39707 TGTATCTTGTGAATATGAGATTGTCAAAACATGAGAGTTTTCAGACGCCCTCTGACATC 39766
Dh      716 CysIlePheGluTyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIle 735
Qy      39767 ATCTTCATGTCTTGAAGAGCTTGAAGAGTCCCTGCTGAGCAGCAGGTGAAATTGTAT 39826
Dh      736 IlePheIleValLeuGlnLysValGluLysThrLeuLeuArgArgGlnValGluLeuTyr 755
Qy      39827 CGCCTTCTTGCAGAAACACCTACTGGAATGGAGGACATCCTCTGGGGAGGACATC 39886
Dh      756 ArgLeuLeuSerAlaGlnThrTyrLeuGluTyrGluLysSerValLeuGlyArgHisIle 775
Qy      39887 TTCTGAGAGACCTTAAATAATGCGCTATTTGGATGAGAAAGCCTCGAATCTGAGCAACA 39946
Dh      776 PheIleTrpArgGluArgLysAlaIleLeuLeuAspGlyLysSerTrpAsnProGluGlyThr 795

RESULT 11
AD057797
ID      AD057797 standard; protein; 801 AA.
AC
AC      AD057797;
XX
DT      12-AUG-2004 (first entry)
XX
XX      Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
Dh      Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
XX      toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS      Saimiri sciureus.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 14
FT      /label= Leu, Phe
XX
XX      MO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PF      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
XX
XX      WPI; 2004-400726/37.
XX      DR      N-PSDB; AD057795, AD057796.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
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PS      Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX      The invention relates to a novel method for identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an old world monkey
XX      comprising comparing the TLR4 polynucleotide sequence of the Old World
XX      monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX      method of the invention has antibacterial, immunosuppressive, and
XX      antiasthmatic activity. The method is useful in identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an old world monkey where the
XX      change may be associated with reduced sensitivity to Gram-negative
XX      bacterial infection. The methods, agents and composition are useful in
XX      treating sepsis, severe sepsis or septic shock and asthma. The present
XX      sequence represents squirrel monkey TLR4.
XX
SQ      Sequence 801 AA:
XX
XX      Alignment Scores:
XX      Pred. No.:      3,79e-233      Length:      801
XX      Score:      2594.00      Matches:      509
XX      Percent Similarity:      78.84%      Conservative:      87
XX      Best Local Similarity:      67.33%      Mismatches:      154
XX      Query Match:      2.99%      Indels:      6
XX      DB:      8      Gaps:      4
XX
XX      US-09-396-985B-48 (1-50000) x AD057797 (1-801)
Qy      37685 TTTTTCAGCAAAATATCATATTTGATCTTTGCCCATGAGTGTGAATGAA 37744
Dh      44 PheAsnProGluLeuGlnValLeuAspLeuSer-----ArgCysAspIleGln 60
Qy      37745 ACAATTGAGACAGAGGATGAGCATGGCTTACACACCCTCTCAAACTTGATATGACAGGA 37804
Dh      61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
Qy      37805 AACCTTATCCAGAGTTTTCCTCCCAAGAGTTTCTCTGAGACTAACAGTTTGAAGATCTG 37864
Dh      81 AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
Qy      37865 GTGGCTGTGAGACAAATATGGCTCTCTAGAAAGCTCCCTTATGAGACGTTATTAAC 37924
Dh      101 ValAlaValGluThrHisLeuLeuSerLeuGlnAsnProIleGlyHisLeuLysThr 120
Qy      37925 TTAAGAACTCATGTGGCTCACAATTTATATCATTTCTGTAAAGTTACCTGATATTTT 37984
Dh      121 LeuLysAspLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPhe 140
Qy      37985 TCCAAATGTGCAAGACCTAGTACATGTGATCTTTCTTATACATATATTCAAATATTA 38044
Dh      141 SerAsnLeuThrAsnLeuGluHisLeuAspLeuSerSerAsnAsnIleGlnAsnIleTyr 160
Qy      38045 GTCAAGCAGCTTACAGTTTCTACGTAAGAAATCCCAAGTCAATCTCTCTTACAGATGCT 38104
Dh      161 CysLysAspLeuGlnValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
Qy      38105 TTGAACCCCAATGATCTTATTCAGAACCAAGCCTTTCAGGGAATTAAGTCCATGAATG 38164
Dh      181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeu 200
Qy      38165 ACTCTAAGAGGTAAATTTTATATAGCTCAAAATATATGAAAACCTTGCTCAAAACCTGGCT 38224
Dh      201 ThrLeuArgAsnAsnPheAspSerLeuAsnAlaMetCysThrCysIleGlnGlyLeuAla 220
Qy      38225 GGTTTACAGTCCATCGGTGATCTTGGGGAATTTTAAATGATGAAGGAATTCGAAAT 38284
Dh      221 GlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluHisArgAsnIleGlnAsp 240
Qy      38285 TTTGAACCTCTATCATCAGAGAGAGCATATGATGTGACCATTAATGAGTTCAAGTTTAA 38344
Dh      241 PheAspLysSerAlaLeuGluGluGlyLeuCysAsnLeuThrIleAsnGluPheArgLeuAla 260
Qy      38345 TATACAAATGATTTTTCAGATGATATTTGTTAAG---TTCCATTTGCTTGGGGAATGTTCT 38401
Dh      261 TyrLeuAspAspPheLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnValSer 280
```

QY 38402 GCAATGCTCTGGCAGGTGTATCTATAAATCTAGAAGATGTTCTTAAACATTTCGA 38461
 Db 281 SerPheSerLeuValAsnValHisIleLeuArgValGluAspPheSerTyrAsnPheArg 300
 QY 38462 TGGCAATCTCTTACATCATTAAGATGTCACCTTAAGACAGTTTCCAACTCTGGATCTACC 38521
 Db 301 TrpGlnIleLeuGluLeuValAsnCyValPheGlnGlnPheProPheLeuIleuLeuVal 320
 QY 38522 TTTCTTAAGTTTGAATCTTAACTTAAGCAAGGCTCTATCAGTTTAAAAAGTGGCC 38581
 Db 321 SerLeuValArgLeuThrPheThrAlaAsnLysGlyArgAsnHisPheSerGluValAsp 340
 QY 38582 CTACCAAGTCTCAGGTATCTAGATCTTAGTAAATGACATGACGTGATTAAGTGTCTGT 38641
 Db 341 LeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysCys 360
 QY 38642 TCTTATTTCTGATTTGGGAACAACAGCTGAGACATTAAGCCTTCAAGCTTCAATGTCGC 38701
 Db 361 SerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnAspVal 380
 QY 38702 ATCATTTATGATGGCAATTTGATGGCTGTAGAAGCTGACAGCCTTGATTTTCAGAC 38761
 Db 381 IleThrMetGlySerAsnPheLeuGlyLeuGluGlnIleuAspPheGlnHis 400
 QY 38762 TCTACTTTAAAAAGGTCACAGAAATCTCAGCGTTCTTATCCCTTGAAGACTCTTAC 38821
 Db 401 SerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAspAsnLeuIleLys 420
 QY 38822 CTGACATCTCTTACTTAAACCAACAAATGACTTGATGATATTTCTTGCTTGACC 38881
 Db 421 LeuAspIleSerHisIleThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuPhe 440
 QY 38882 AGTCTCAACACATTTAAAAAGTCTGCAATCTTTCAAAGCAACACCTTTCAAATGTC 38941
 Db 441 SerLeuValIleLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuGluAspIle 460
 QY 38942 TTTGCAACACACAAACATCTGACATCTCTGATCTTTTAAATGTCATTTGCAACAAAT 39001
 Db 461 PheThrAspLeuAsnAsnLeuIlePheLeuAspLeuSerGluCysGlnMetGlnGlnIleu 480
 QY 39002 TCTTGGGGGATTTTGAACACCTCTCATGACTTCAATTTAAATATGAGTCACACAAAT 39061
 Db 481 SerProThrAlaPheAspSerLeuProArgLeuArgIleLeuAsnMetSerHisAsnAsn 500
 QY 39062 CTATGTTTGGATCATCCCATTTAACAAGCTGTATTCCTCAGACATCTTGATTCG 39121
 Db 501 PhePheAlaLeuAspIleThrPheProLysIleValAsnLysSerLeuGlnValLeuAspTyr 520
 QY 39122 AGTTTCATGCGATGAGACATCTTAAAGCA--ATACGCAACATTTTCCAAAGCTCA 39178
 Db 521 SerLeuAsnHisIleGlyThrSerLysAsnGlnGlnLeuGlnHisPheProSerSerLeu 540
 QY 39179 GCCTTCTTCATCTTAAACATTTCTGCTGTATATGATGTAAGACATCAGAAATTCCTG 39238
 Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
 QY 39239 CAGTGGGTCAAGAAACAGAGCAAGTCTTGATGATTTGAACAAATGACATGTGCAACA 39298
 Db 561 GlnTrpIleLysAspGlnArgLeuValGluValGluGlnMetGluCysAlaThr 580
 QY 39299 CCTGTAGAGATGATACCTCTTAGTGTGATTTTAATATCTTACCTGTTAATATGAC 39358
 Db 581 ProLeuAsnArgLysGlyIleProValLeuSerLeu--AsnIleThrCysGlnMetSer 599
 QY 39359 AAGCAATCATCAGTGTGTCAAGTGTCAAGTGTGATGATGATGATGATGATGATGATGAT 39418
 Db 600 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 619
 QY 39419 ATATACACTTCTATTTTACCTGATCTTATTCCTGCTGTAATAAGTACAGACAGAGA 39478
 Db 620 ValTyrLysPheTyrPheHisIleuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 639

QY 39479 GAAGACATCTATGATGATTTTGATCTACTCGATGACGAATGAGACTGGGTGAGAAAT 39538
 Db 640 GluSerThrTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAsn 659
 QY 39539 GAGCTGGTAAGAAATTTAAGAAAGAGATGTCCTGCTTCACTCTGCTTCACTACAGA 39598
 Db 660 GluLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCyLeuHisTyrArg 679
 QY 39599 GACTTATTCCTGGTGTAGACCATGCTGCGCAACATCTCCAGAAAGCTTCCAGAGAGC 39658
 Db 680 AspPheIleProGlyValAlaAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 699
 QY 39659 CGAAGGTATTTGAGTGTAGTGTACACATTTATTAAGACCCCTGCTGATCTTTGAA 39718
 Db 700 ArgLysValIleValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlu 719
 QY 39719 TATGATGTTGCTCAACATGACGATTTCTGAGACGCGCTTGGCATCATCTTCAATGTC 39778
 Db 720 TyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
 QY 39779 CTGAGAAGGTTGAGTGAAGTCCCTGCTGAGACAGAGGTGGAATGTATCGCTTCAAGC 39838
 Db 740 LeuGlnLysValGlnLysSerLeuLeuArgGlnIleValGluLeuTyrArgLeuLeuSer 759
 QY 39839 AGAAACACCTTACCTGGAATGAGAGACATCTCTGGGAGAGCACATCTTGGAGAGA 39898
 Db 760 ArgAsnThrTyrLeuGlnTyrPgluAspSerValLeuLysArgHisIlePheThrArgArg 779
 QY 39899 CTTAAAAAGCTTATTTGATGAGAAAACCTCGAATCTTGAAGCAACA 39946
 Db 780 LeuArgValAlaLeuLeuAspGlyArgProThrAsnProGlnGlyThr 795
 RESULT 12
 AAEI6116
 ID AAEI6116 standard; protein; 837 AA.
 AC AAEI6116;
 XX 26-MAR-2002 (first entry)
 DT
 XX Human DNAX Toll like receptor (TLR) 4 #2, alternative version.
 DE
 XX Human; DNAX Toll like receptor; TLR; therapy; immunological disorder;
 KW Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 211
 FT /label= "Unknown
 FT /note= "Encoded by AAY"
 PN WO200190151-A2.
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016766.
 XX
 PR 25-MAY-2000; 2000US-0207558P.
 XX
 PA (SCHE) SCHERING CORP.
 PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 DR WPI; 2002-063085/11.
 DR N-PSDB; AAD26306.
 XX
 PT New DNAX Toll like receptor (TLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX
 PS Claim 3; Page 240-243; 297pp; English.

XX The invention relates to mammalian receptor proteins, e.g., primate, CC human DNAX Toll like receptor (DTR) protein and their corresponding CC nucleic acids. The DTR is useful for treating conditions exhibiting CC abnormal expression of the receptors of their ligands. Such abnormality CC is manifested by immunological disorders. In particular, the DTR is CC useful for treating various disease or disorders associated with abnormal CC expression or abnormal triggering of response to a ligand. The DTR is CC also useful as an immunogen for the production of antisera or antibodies CC specific, e.g., capable of distinguishing between other interleukin (IL)- CC receptor family members, for the DTR or its various fragments. The CC purified DTR can be used to screen monoclonal antibodies or antigen- CC binding fragments. The antibodies are useful for screening expression CC libraries for particular expression products. These are useful for CC detecting or diagnosing various immunological conditions related to CC expression of DTR or cells that express it. The present sequence is CC human DTR4 protein, alternative version. The DTR4 gene is located on CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to CC be similar to the sequence shown in page 41 (AAB16102). However these CC sequences differ at several locations

SQ Sequence 837 AA;

Alignment Scores:	
Pred. No.:	4.33e-233
Score:	2593.50
Percent Similarity:	73.56%
Best Local Similarity:	61.69%
Query Match:	2.98%
DB:	5
US-09-396-985B-48 (1-50000) x AAE16116 (1-837)	
	length: 837
	Matches: 525
	Conservative: 101
	Mismatches: 172
	Indels: 53
	Gaps: 9

US-09-396-985B-48 (1-50000) x AAE16116 (1-837)

Oy	37400	TGAAAAAATGCATAAAATTATCTAGACACTACATCATCACTGGTCTTTATGTACC	37459
Dd	25	TrpIupProCysValGlu---ValProAsnIleThrTyrlin-----	37
Oy	37460	GTTATGATCTTGATGTGATTTTTCTTAAGGAATTTGGTCGTGACATAGTGATGTTT	37519
Dd	38	CysMetGluLeuAsnPhenylrYlVsiIeProAspAsnLeupro-----	51
Oy	37520	ATCATCACTGTAGCAAGTGTGAAAATGACAATCTGCGAGTTTCCTCCGTGCACACC	37579
Dd	52	-----PheSerThrLyAsnLeuAspLeuSerPheAsnProLeuArgHis----	66
Oy	37580	ATCATCACCTGTTTGGCTGTGTACAGTTTCTCTTTACAAATAACATGATATCATATCT	37639
Dd	67	-----LeuGlySerTySerPhe-----	72
Oy	37640	GTTTGATCATAGATGGTAGGACCTGTATTGTCATTAGAAAAGGTTTTTTTCAGCAA	37699
Dd	73	-----PheSerPheProGlu77	
Oy	37700	AAATACATAATGTGGTATCTCTTTGCCCATAGTGGTGAAATTTGAAATTAAGAACAAG	37759
Dd	78	LeuGlnValLeuAspLeuSer-----ArgCysIuIleGlnHrIleGluAspGly94	
Oy	37760	GCATGGCATGGCTTACACACACCTCTCAACTGTGATCTGACAGAAACCTATCCAGGT	37819
Dd	95	AlaTyrlnSerLeuSerHisIleLeuSerThrLeuIleLeuThrgLysAnPrIleGlnSer114	
Oy	37820	TTTTCCCAGGAAGTTCTCTGSCATCAACAAGTTTAGAAATCTGGTGGCTGTGGAGACA	37879
Dd	115	LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIuNysLeuValAlaValGluThr134	
Oy	37880	AAATGGCGCTCTAGAAAAGCTTCCCATTTGACACAGCTTAACTTAACCTTAAAGAACCTCAAT	37939
Dd	135	AsnLeuAlaSerLeuGluAsnPherProIleGlyHisIleuLySerThrLeuLySgluLeuAsn154	
Oy	37940	GTGGCTCACAATTTTATCATCTCTGTAGTACCTGCATATATTTTCCAATGTGAGAAC	37999
Dd	155	ValAlaHisAsnLeuIleIleGlnSerPheLyIeuSerProGluTyrlPheSerPheLeuThrPan174	

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Db      535  ThrProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 554
Qy      39137 GAGCATCT---AAAGGAATCTGCACATCTTCCAAAGAGCTTACGCTTCTCAATCTT 39193
Db      555  MetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 574
Qy      39194 ACTACACATTCCTGCTTGTATATGTGACATCAGAAATCTCGAGTGGGTCAAGGA 39253
Db      575  ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrrPLeuAsp 594
Qy      39254 CAGAGCAGCTTCTTGGAATGTTGACAAATGCACATGTGCACACCTGTGAGATGCAT 39313
Db      595  GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaTrnProSerAspLysGln 614
Qy      39314 ACCCTTGAATGTTGATTTAATTAATCTTACCTGTTATATGTCACAGACATCATCAGT 39373
Db      615  GlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleLeuGly 633
Qy      39374 GTGTCAGTGTCACTGTGATTTGGTATCCACTGATGATTCGATATACACTTCTAT 39433
Db      634  ValSerValLeuSerValLeuValValSerValValAlaValLeuValTyrLysPheTyr 653
Qy      39434 TTTCACCTGATATCTTATTTGCTGGCTGTAAAGATACAGACAGAGAAAGCATCTATGAT 39493
Db      654  PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleTyrAsp 673
Qy      39494 GCATTGTGATCTACTCGAGTCAGATGACATGAGACCTGGGAGAAATGAGCTGTAAAGAT 39553
Db      674  AlaPheValIleTyrSerSerGlnAspGlnAspIrrValAlaGlnGlnLeuValLysAsn 693
Qy      39554 TTAGAAGAAGAGAGGCCCGCTTCACTGCTGCTCACTGCTCAAGAGACTTATTCCTGCT 39613
Db      694  LeuGlnGlnGlyValProProPheGlnLeuGlySerHisTyrArgAspPheIleProGly 713
Qy      39614 GTAGCCATTTGCTGCCCAATCATCATCCAGAGAGCTTCCACAAAGCCGGAAGCTTATGCTG 39673
Db      714  ValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal 733
Qy      39674 GTAGTGTCTAGACACTTATTCAGACCGCTGTGCTATCTTGAATATGAGATGCTCA 39733
Db      734  ValValSerGlnHisPheIleGlnSerTyrTrrPcysIlePheGlnTyrGlnIleAlaGln 753
Qy      39734 ACATGACAGTTCTTGAGACAGCCGCTCTGACATCATCTTATGCTTGAAGAGGTTGAG 39793
Db      754  ThrTrrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 773
Qy      39794 AAGTCCCTGCTGAGGACAGAGCTGGAATGTATCGCTTCTTACAGAAACCTTACCTG 39853
Db      774  LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
Qy      39854 GAATGGAGAGGACATCTCTGGGAGGACATCTTCTGAGAAAGCTTAAAGCCCTA 39913
Db      794  GlnTrrPgluAspSerValLeuGlyAlaGlnHisIlePheTrrPArgLysArgLysAlaLeu 813
Qy      39914 TTGATGGAAGAAAGCCTGATCCTGAGCAACA 39946
Db      814  LeuAspGlyLysSerTrrPAsnProGlnGlyThr 824

RESULT 13
AD057782
ID      AD057782 standard; protein: 808 AA.
XX
AC      AD057782;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX

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OS      Pan troglodytes.
XX
FN      WO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PE      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
XX
DR      MPI; 2004-400726/37.
XX
N-PSDB; AD057780, AD057781.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1, SEQ ID NO 3; 11pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX
SQ      Sequence 808 AA;
XX

Alignment Scores:
Pred. No.:      5,87e-233      Length:      808
Score:          2592.00      Matches:      524
Percent Similarity: 74.17%      Conservative: 99
Best Local Similarity: 62.38%      Mismatches: 165
Query Match:    2.98%      Indels:      52
DB:             8      Gaps:      8

US-09-396-985b-48 (1-50000) x AD057782 (1-808)
Qy      37433 ACATATCAACTGCTTATATGATACCCAGTTATGATTTGATTTTCTAATGAT 37492
Db      6  ThrTyrGln-----CysMetGlnLeuAsnPheTyrLysIleProAsp 19
Qy      37493 TTGTCGCTGACATAGTGATGATGATTATCATCTGATAGAGATGGAATATGACAAT 37552
Db      20  AsnLeuPro-----PheSerTrnLysAsnLeuAsp 29
Qy      37553 CTGCAAGATTCTCTCTCGCTGCTACACCATCATCAGCTGTTTGTCTGTACAGTTTCTC 37612
Db      30  LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 43
Qy      37613 TTTCACATTAACATGATATATCATATCTGTTGATCATAGTATGAGGACCTGTATGT 37672
Db      43  -----
Qy      37673 CATTGAAAGGGGTTTTTTTTTTCAGCAAAATATCAATTAATGATATCTTTTGCCATAGG 37732
Db      44  -----PheSerPheProGlnLeuGlnValLeuAspLeuSer-----Arg 56
Qy      37733 TGTGAATTTGAATTAATGGAAGACAGACATGGATGGCTTACACACCTCTCAAACTTG 37792
Db      57  CysGlnIleGlnTrnIrrGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeu 76
Qy      37793 ATACTGACAGAAACCTATCTCAGAGTTTCCCGAGAAATTTCTGTGACTTAACAAGT 37852

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Dh 77 IleuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
Qy 37853 TTGAGAGATGCTGGGCTGTGGAGACAAATTTGGCCCTCTAGAAAGCTCCCATTTGA 37912
Dh 97 LeuGlnIysLeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGly 116
Qy 37913 CAGCTTAACCTTAAGAAATCAATGTGGCTCACAAATTTTATACATCTTCCTTAAGTTA 37972
Dh 117 HisLeuIysThrLeuIysGluLeuAsnValAlaHisLeuLeuIleGlnSerPheIysLeu 136
Qy 37973 CTGCATATATTTTCCAAATGTAGCAACCTTATGATCATGTGATCTTTCTTATATATATT 38032
Dh 137 ProGluIysPheSerAsnLeuThrAsnLeuGluHisLeuPheLeuSerSerAsnIle 156
Qy 38033 CAAGACTTTACTGTCAACGACTTACATTTCTACGTAAATTCACAAAGTCATCTTCT 38092
Dh 157 GlnSerIleIysCysThrAsnLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSer 176
Qy 38093 TTAGACATGCTTTGAAACCAATGTGATCTTCAACACCAAGCCTTTCAGGAAATTAA 38152
Dh 177 LeuAsnLeuSerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArg 196
Qy 38153 CTCCATGACTGACTCTTAAAGGTAATTTTATATAGCTCAATATATATGAAACTTGCCTT 38212
Dh 197 LeuHisLeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetIysThrCysIle 216
Qy 38213 CAAGACCTGGCTGGTTTACACGCTCATCGGTGATCTTGGAGAAATTAAAGATGAAG 38272
Dh 217 GlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGly 236
Qy 38273 AATCTGAAATTTTGAACCTCTATCATGGAAGAGACTATGTGATGTGACATTTGATGAG 38332
Dh 237 AsnLeuGluIysPheAspIysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlu 256
Qy 38333 TTCAAGTTAACATTTACAAATGATTTTTCAGATGATTTGTTAAG--TTCCATTTGCTTG 38389
Dh 257 PheArgLeuAlaIysLeuAspIysCysThrLeuAspArgIleIleAsnLeuPheAsnCysLeu 276
Qy 38390 GCGAATTTTCTGCAATGCTCTGGCAGGTGATCTTAAATTCAGAAAGATGTTCT 38449
Dh 277 ThrAsnAlaSerSerPheSerLeuValSerValThrIleIysSerValIysAspPheSer 296
Qy 38450 AAACATTTCAATGCAATCTTATCATCATTTAGATTCATTAAGTCAATTTCCAACT 38509
Dh 297 TyrAsnPheGlyTyrGlnHisLeuGluLeuValAsnIysIysPheGlyGlnPheProThr 316
Qy 38510 CTGGATTTACCTTTCTTAAAGTTTGACTTAACTATGAACAAAGGATCTTATCAGTTT 38569
Dh 317 LeuIysLeuIysSerLeuIysArgLeuThrPheThrSerAsnIysGlyIysAsnAlaPhe 336
Qy 38570 AAAAAGTGGCCCAAGCTCAGCTATCTAGATCTTATGAATTCAGTCAAGCTT 38629
Dh 337 SerGluValAsnLeuProSerLeuGluPheLeuAsnLeuSerAlaArgAsnIysLeuSerPhe 356
Qy 38630 AGTGGTGTCTGTTCTTATCTGATTTGGAAACAAAGCCTGAGACCTTGAAGCTCAGC 38689
Dh 357 IysGlyIysCysSerGlnSerAsnPheGlyThrThrSerLeuIysIysIysLeuAsnLeuSer 376
Qy 38690 TTCAATGTGCTCATTTATGAGTCCAAATTTCAATGGATCTGAAGAGCTGACAGCTTG 38749
Dh 377 PheAsnIleValIleThrMetSerSerAsnPheLeuGluGlnGluGlnHisLeu 396
Qy 38750 GATTTTACAGCTTACTTAAAGGGTCAAGATTTCTCAGGTTCTTATCCCTTGA 38809
Dh 397 AspPheGlnHisSerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArg 416
Qy 38810 AAGCTTATTAACCTTGAATCTTATATACAAACAAATTTGATCTGATGATATTT 38869
Dh 417 AsnLeuLeuIysThrLeuAsnIleSerHisThrHisThrArgValAlaPheAsnGlyIlePhe 436
Qy 38870 CTGGCTTGAACGACTCTCAACACATTAATAATGGCTGGCAATTTCTTCAAGACACACC 38929
Dh 437 AsnGlyLeuSerSerLeuGluValLeuIysMetAlaGlyAsnSerPheGlnGluAsnPhe 456

Qy 38930 CTTTCAATGCTTTTGCAAAACACAAACATTTGACATTTCTGTGATCTTTTAATGTCAA 38989
Dh 457 LeuProAsnIlePheThrGluLeuArgAsnLeuThrPheLeuAsnLeuSerGlnCysGln 476
Qy 38990 TTGAAACAATATCTTGGGGGATTTTGAACCCCTCCATAGACTTCAATTAATTAATATG 39049
Dh 477 LeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMet 496
Qy 39050 AGTCACAAACATTTATTTTGTGATTTCCCATTTATPACCAAGCTGTATTCCTTCAGC 39109
Dh 497 SerHisAsnAsnPhePheSerLeuAspThrPheProTyrIysCysIysLeuAsnSerLeuGln 516
Qy 39110 ACTCTTATGCTGACTTCAATGCCATAGACACTCT--AAAGAAATCTGCAACATTTT 39166
Dh 517 ValLeuAspIysSerLeuAsnHisIleMetThrSerIysGlnGluLeuGlnHisPhe 536
Qy 39167 CCAAAGTCTAGCCTTTCTTCAATCTTATCTTACAAATTTCTGTGCTTGTATATGTGAACAT 39226
Dh 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsnPheAlaCysThrCysGlnHis 556
Qy 39227 CAGAAATCTCTGACGTGGCTCAAGAAACAGACAGCTTTGTGGTGAATGTGAACAAATG 39286
Dh 557 GlnSerPheLeuGlnIleTyrIleIysAspGlnArgGlnLeuLeuValGluValGluArgMet 576
Qy 39287 ACATGTGCAACACCTGTAGAGATGAATACCTCTTATGTTGGATTTTATTAATTTACCC 39346
Dh 577 GluCysAlaIleThrProSerAspIysGlnGlyMetProValLeuSerLeu--AsnIleThr 595
Qy 39347 TGTATATATGTACAAACATCATCACTAGTGTGTCAAGTGTCAAGTGTGATTTGCCACT 39406
Dh 596 CysGlnMetAsnIysThrIleIleGlyValSerValLeuSerValLeuValIleVal 615
Qy 39407 GTAGCATTTTGTATATPACCTCTTATTTTCACTGTATACTTATTTGTGGCTGTAAAG 39466
Dh 616 ValAlaValLeuValIysIysPheIysPheHisLeuMetLeuLeuAlaGlyCysIleIys 635
Qy 39467 TACAGCAGAGAGAAACATCTATGTAGCATTTGTGTACTGTGATCTGAGTCAAGATGAGAC 39526
Dh 636 TyrGlyArgGlyIysLeuAsnIleIysThrAsnAlaPheValIleIysSerSerGlnAsnArgIysPhe 655
Qy 39527 TGGGTGAATGAGCTGTGAAGAAATTTGAAGAAAGAGTGGCCGCTTTCACCTTGC 39586
Dh 656 TrpValArgAsnGluLeuValIysAsnLeuGlnGluIysValIleProPheGlnLeuCys 675
Qy 39587 CTTTCACTACAGACATTTATTTCTGTGTAGCCATTTGCTCCAAACATCATCCAGAAAGC 39646
Dh 676 LeuHisIysIysArgAsnPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGly 695
Qy 39647 TTCCAAAGACCGGAAAGGTTATTTGTGTAGTGTAGACATTTTTCAGAGCCGTTTG 39706
Dh 696 PheHisIysSerIysGlyValIleValValValSerGlnHisPheIleGlnSerHisArgTrp 715
Qy 39707 TGTATCTTGAATATGATTTGCTCAAAACATGSCAGTTTTCAGACGSCCTGTGCATC 39766
Dh 716 CysIlePheGluIysGluIleAlaGlnIleThrTrpGlnPheLeuSerSerAlaGlyIle 735
Qy 39767 ATCTTCAATTTGCTTGAAGAGTTTGAGAACTCCCTGTGAGGACAGAGGTGGAATTTAT 39826
Dh 736 IlePheIleValLeuGlnIysValIysIysThrLeuLeuIysArgIleValIleGluLeuIys 755
Qy 39827 CGCCTTGTAGCAAAACACTACCTGGAATGGAGAGCAATCTCTGGGAGAGGACATC 39886
Dh 756 ArgLeuLeuSerArgAsnIleIysIysLeuGluIleTrpGlnIysSerValLeuGlyArgHisIle 775
Qy 39887 TTCTGAGAAAGACTTAATAATGGCCTATTGGATGAGAAACCTCGAATCTTGAGCAACA 39946
Dh 776 PheTrpArgIysLeuIysGlyValAlaLeuLeuAspGlyIysSerTrpAsnProGluGlyThr 795
RESULT 14
AAW86352
ID AAW86352 standard; protein; 799 AA.
XX

AC AAW86352;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human DNAX toll-1-like receptor DTLR4.
XX
KW DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin-1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN MO9850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
DR WPI; 1999-059670/05.
DR N-PSDB; AAV80666.
PT Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
FT metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Example; Page 115-117; 171pp; English.

The present invention specifically describes human DNAX toll-1-like
receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
in the present invention. Also described are: (1) a fusion protein
comprising a DTLR protein or peptide; (2) a binding compound, preferably
an antibody or antibody fragment which specifically binds to a DTLR
protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
; (4) an expression vector comprising the nucleic acid of (3); and (5) a
host cell comprising the vector of (4). The host cell of (5) can be used
to produce the DTLR proteins. The DTLR proteins can be used to alter
phosphate metabolism, to modulate inflammatory function, innate immunity
responses or morphological effects. The DTLR proteins can be used in the
treatment of conditions exhibiting abnormal expression of the receptors
of their ligands. These abnormalities are typically manifested by
immunological disorders

Sequence 799 AA:
XX
XX

Alignment Scores:			
Pred. No.:	7.24e-233	Length:	799
Score:	2591.00	Matches:	508
Percent Similarity:	79.76%	Conservative:	95
Best Local Similarity:	67.20%	Mismatches:	147
Query Match:	2.98%	Indels:	6
	2	Gaps:	4

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US-09-396-985B-48 (1-50000) x AAW86352 (1-799)
OY      TTTTTCAGCAAAATCATTAATTGTGATCTTTTGCCCATGAGTGTGAATTGAA 37744
Db      |||   |||   ::   :|||   :|||   |||   |||   |||   |||   |||
        PheserherprogluleuglnValIleuAapIeuser-----ArgCysguilegln 51
OY      ACAATTGAAGAACAAGCATGGCATGGCTTAACACCACCTGTGAATTGATCTGACAGGA 37804
Db      |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
        ThrltlelunspglalyalatyrgInserIeuserHIsIeuserThrltleuIleuThrGly 71
OY      AACCTTTCAGAGGTTTTCCCACAGAAAGTTCTCGACTACATCAAGTTTAGAGATCTG 37866
Db      |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
        AsnDroIlegInserIeuAlalauglglyAlaPhaserIdyleuserDerIeuglnIyIseu 91

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Qy	37865	GTGGCTGTGGAGCAAAATTTGGCTCTCTAGAAAGTCTCCATTGGAACAGCTTTAAACC	37922
Db	92	ValAlaValAluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuIleThr	111
Qy	37925	TTAAGAAACTCAATGTGGCTCAAAATTTATATACATTCCTGTAGTTACCTGCATATTTT	37984
Db	112	LeuIleGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIleLeuProGluIlePhe	131
Qy	37985	TTCATATTCAGCAACCTAGTACATGTGGATCTTTCTATATATTTCAAACTATTACT	38044
Db	132	SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnIleIleGlnSerIleIleYr	151
Qy	38045	GTCAAACGATCTAAGTTTCTACGTGGAAATTCACAAAGTCAATCTCTCTTACAGATGCT	38104
Db	152	CysThrAspLeuIleArgValLeuHisGlnMetProLeuLeuAsnSerLeuAspLeuSer	171
Qy	38105	TTGAACCCATTTGACTTTCATTCAGACCAAGCCTTTCAGGGAATTAAGCTCCATGAAC	38164
Db	172	LeuAsnProMetAsnMetIleGlnProGluIlePheIleGluIleArgLeuHisIleIle	191
Qy	38165	ACCTCTAAGAGTATTTTATATAGCTCAATATATATGAATCTTGCTTCAAAACCTGGCT	38224
Db	192	ThrLeuAspAsnAsnMetAspSerLeuAsnValMetIleCysIleGlnIleGluLeuAla	211
Qy	38225	GGTTTACAGCTCCATCGATGGTTGATCTTGGAGAAATTTAAAGATGAAGAGATGTGAAT	38284
Db	212	GlyLeuGluValHisArgLeuValLeuGlnGluIlePheAsnGlnGlyIleAsnLeuGluIle	231
Qy	38285	TTTGAACCCCTATATCATGGAAGACATATGTGATGTGACCATTTGATGAGTTCCAGTTAA	38344
Db	232	PheAspIleSerAlaLeuGlnGluIleCysAsnLeuThrIleGlnGluIlePheArgLeuAla	251
Qy	38345	TATACAAATGATTTTCAATATATGTTAAG---TTCCATTTGCTTGGCCAAATTTTCT	38401
Db	252	TyLeuAspIleTyIleLeuAspIleIleAlaPheAsnGlyLeuThrAsnValSer	271
Qy	38402	GCAATCTCTCGGACAGTATATCTATATTAATATCTAAGAAAGTTCCATAACATTTTCAA	38461
Db	272	SerPheSerLeuValSerAlaThrIleGluArgValIleAspPheSerIleYrAsnIleGly	291
Qy	38462	TGGCAATCCTTATCAATATTAAGATGTCAATTAAGACAGTTTCCAACTCTGATCTAAC	38521
Db	292	TyrGlnHisIleLeuGlnIleValLeuAsnGlyIlePheGlnIlePheProThrLeuIleIle	311
Qy	38522	TTTCTTAAAGTTTGACTTAATCTATGAACAAAGGCTCATATAGTTTAAAAAGTGGCC	38581
Db	312	SerLeuIleArgLeuThrPheThrSerAsnIleGlyIleAsnAlaPheSerGluValAsp	331
Qy	38582	CTACCAAGTCAAGCATCTAATCTTAAGTATGAATTAAGCATGAGCTTATAGTGGTGGT	38641
Db	332	LeuProSerLeuGluIlePheLeuAspLeuSerAlaGlnGlyLeuSerPheIleGlyCys	351
Qy	38642	TCTTATTTGATTTGGGAACAAACAGCTGAGACATTAGACTCAGCTTCAATGGTACC	38701
Db	352	SerGlnSerAspPheGluIleThrThrSerLeuIleTyIleLeuAspLeuSerPheAsnIleYal	371
Qy	38702	ATCATATTAAGTGGCAATTTCAATGGGCTTATGAAGCTGAGACCTGTGATTTTATGAC	38761
Db	372	IleThrMetSerSerAsnMetLeuGlnGluGlnIleLeuGlnHisIleLeuAspPheGlnHis	391
Qy	38762	TCTACTTTAAAAAGGTCACAAATTTCCAGGCTCTTATGCTCCCTTGAAGAACTATTTAC	38821
Db	392	SerAsnLeuIleGlnMetSerGluPheSerValPheLeuSerLeuAspAsnLeuIleYr	411
Qy	38822	CTTGACATCTTTATATATCAACCAAAATTAATCTGATGGTATATTTCTGGCTTGACC	38881
Db	412	LeuAspIleSerHisIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer	431
Qy	38882	AGTGTCAACACATTTAAATTTGGCTGGCAATCTTTGAAGACAAACCTTTCAAAATGTC	38941
Db	432	SerLeuGlnValLeuIleMetAlaGlyIleAsnSerPheGlnGluAsnPheLeuProAspIle	451

QY 38942 TTGGAAACACAACTGACATCTCGATGCTTCTTAATGTCATTTGGAACAATA 39001
Db 452 PheThrGluLeuArgAsnLeuThrPheLeuAspSerGlnCysGlnLeuGlnLeu 471
QY 39002 TCTTGGGGGGATTTGACACCCCTCCATAGACTTCAATTAATTAATAGATCAACAAT 39061
Db 472 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 491
QY 39062 CTATGTTGTTGGATTCATCCATTAATACAGCTGATTCCTCGACACTCTTGATTC 39121
Db 492 PhePheSerLeuAspThrPheProTyrLeuPheCysLeuAsnSerLeuGlnValLeuAspTyr 511
QY 39122 AGTTTCAATCGCATAGACATCT--AAAGAAATACGCAACATTTTCCAAAGACTCA 39178
Db 512 SerLeuAsnHisIleMetThrSerLeuSerGlnGlnLeuGlnHisPheProSerSerLeu 531
QY 39179 GCCTTTCTTCACTTACTTAACAATTTGTTGCTGTGATATGTAATGCAATCAAAATTCCTG 39238
Db 532 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 551
QY 39239 CAGTGGGTCAAGAACAGAACGACTTCTGGTGAAATGTTGAACAATGACATGTGCACA 39298
Db 552 GlnTrpIleLeuArgGlnArgGlnLeuValGlnValGlnArgMetGlnCysAlaThr 571
QY 39299 CCTGTAGAGATGATACCTCTTATGTTGATTTTAATATCTACTGTTATATGTCAC 39358
Db 572 ProSerAspLysGlnGlnMetProValLeuSerLeu--AsnIleThrCysGlnMetAsn 590
QY 39359 AAGACATCATCAGTGTGTCAGTGTGATGTGATGTGATGATGACATTTCTG 39418
Db 591 LysThrIleIleGlnValSerValLeuSerValLeuValValSerValValAlaValLeu 610
QY 39419 ATATACCATCTTATTTTACCTGATACTTATGCTGGCTGTAAAGTACAGCAGAGA 39478
Db 611 ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
QY 39479 GAAGACATCATATGATGATTTGATCTACTCGAGTCAAGATGAGAGCTGGTGAGAAAT 39538
Db 631 GlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValAlaAsn 650
QY 39539 GAGCTGTAAAGATTTAGAAAGAGAGTCCCGCTTTCACCTCTGCTTCACTACAGA 39598
Db 651 GluLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
QY 39599 GACTTATCTCTGCTGTAACCATGCTGCGCAACATCATCCAGAGAGCTTCAACAAGC 39658
Db 671 AspPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 690
QY 39659 CGAAGGTTATGTGATGATCTAGACACTTATTCAGAGCCGTTGGTGTATCTTGAA 39718
Db 691 ArgLysValIleValIleValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 710
QY 39719 TATGAGATTGCTCAAACTGAGCAGTTTCTGAGACGCGCTCTGCGATCATCTTCAATGTC 39778
Db 711 TyrGlnIleAlaGlnIleTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
QY 39779 CTTAGAAGAGTTGAGAGACTCCCTGCTGAGCGAGCAGGTGGAATGTATCGCTTCTTAC 39838
Db 731 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
QY 39839 AGAAACACCTTACCTGGAATGAGAGAGCAATCTCTCGGGGAGAGCACTTCTGAGAGA 39898
Db 751 ArgAsnThrTyrLeuGlnTyrGlnLysPheSerValLeuGlnYArgHisIlePheTrpArgArg 770
QY 39899 CTTAAAAATGCCCTATTGATGATGAAAAAGCTCGAATCCCTGAGCAAAAC 39946
Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThr 786

RESULT 15
AAE16093
ID AAE16093 standard; protein; 799 AA.
XX
AC AAE16093;

XX 26-MAR-2002 (first entry)
DT Human DNAX Toll like receptor (DTLR) 4 #1.
XX
DE Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KM Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
XX Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kaetzelin RA, Ho SWK, Liu Y;
XX
XX WPI; 2002-083085/11.
DR N-PDB; AAD26283.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 1; Page 35; 297pp; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ Sequence 799 AA;
SQ
Alignment Scores:
Pred. No.: 7.24e-233 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2.98% Indels: 6
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QY 37745 ACAATTGAAGACAGGATGCGATGCTTACACCACTCTCAACTGATAGTACAGAGA 37804
Db 52 ThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGly 71
QY 37805 AACCTATCGAAGTTTTCCTCCAGAGAAATTTCTGTGACTTAACAAGTTTAGAATCTG 37864
Db 72 AspProIleGlnSerLeuAlaLeuGlnYAlaPheSerGlyLeuSerSerLeuGlnLysLeu 91

QY 37865 GTGGCTGTGAGACAAATGGCCCTCTAGAAAGCTTCCCTATTGACAACTTAAACC 37924
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 QY 37925 TTAAGAAGCTCAATGTGGCTCACAATTTTATACATTCCTGTAAAGTTACCTGCAATTTT 37984
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 QY 37985 TCCAACTGACAACTGATGATGATGATTTCTTTATACCTTATATCAACTTAATAC 38044
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 QY 38165 ACTGTAAGAGGTATTTTATAGCTCAATATATGAAGAACTTGCTCAAACTGGCT 38224
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 DB TyrLeuAsnProIleGlyLeuAsnProIleLeuAsnProIleAsnProIleAsnProIle 271
 QY 38402 GCAATGCTCTGAGAGGTGTCTATTAATAATCTAGAAAGTGTCTTAATCAATTTGAAA 38461
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 QY 38462 TGGCAATCTTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38521
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 QY 38702 ATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38761
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 QY 38762 TCTTCTTAAAGAGTCAAGATCTCAGCTTCTTATCTTATCTTAAAGAGTCTTATCTTAC 38821
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 QY 38822 CTGATCATCTTATCAATCAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 38881
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DB 452 PheThrGluLeuArgAsnLeuThrPheLeuAsnProIleGlnGlnGlnGlnGlnGlnGln 471
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 QY 39239 CAGTGGGTCAAGGACAAAGCAAGTCTTGTGATATGATGATGATGATGATGATGATGATGAT 39298
 DB GlnThrPheLysAsnGlnMetGlnLeuValGluValGluArgMetGluCysAlaThr 571
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 QY 39359 AAGACATCATCATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39418
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 QY 39419 ATATACCACTTATTTTCACTGATCTTATGATGATGATGATGATGATGATGATGATGATGAT 39478
 DB ValTyrAsnProIleThrPheHisLeuMetLeuValAlaCysIleLysTyrGluArgGly 630
 QY 39479 GAAAGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39538
 DB GluAsnIleThrAsnProIleAlaIleValAlaAsnIleIleThrSerSerGlnAsnProIleValArgAsn 650
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 QY 39599 GACTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39658
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 QY 39659 CGGAAGGTATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39718
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 QY 39719 TATGATGATCTCAACATGAGCAATTTCTGAGACCGCTTGGCATCATCTTCAATGTC 39778
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 QY 39779 CTGGAAGGTGAGAAAGTCCCTGAGGACAGCTGGAATTTGATGATGATGATGATGATGATGAT 39838
 DB LeuGlnLysValGluLysThrLeuLeuArgGlnGlnAlaGluLeuTyrArgLeuLysSer 750
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Search completed: March 30, 2005, 02:13:46
 Job time : 4273.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n3p model

Run on: March 29, 2005, 14:31:58 ; Search time 447 Seconds
(without alignments)
16700.014 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 2054180

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=b1osome2 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database :

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6: /cg2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	502.5	0.6	661	1	US-08-514-014-4
3	502.5	0.6	661	2	US-08-513-823-4
4	464	0.5	784	4	US-09-982-308B-23
5	402.5	0.5	775	4	US-09-949-016-8799
6	365.5	0.4	1029	4	US-09-513-999C-7214
7	269.5	0.3	1059	4	US-09-907-794A-290
8	269.5	0.3	1059	4	US-09-905-125A-290
9	269.5	0.3	1059	4	US-09-902-775A-290
10	269.5	0.3	1059	4	US-09-906-700-290
11	269.5	0.3	1059	4	US-09-903-603A-290
12	269.5	0.3	1059	4	US-09-904-920A-290

13	269.5	0.3	1059	4	US-09-909-064-290	Sequence 290, App
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24	269.5	0.3	1119	4	US-09-906-618-294	Sequence 294, App
25	266.5	0.3	1053	4	US-09-513-505-6	Sequence 6, Appli
26	266.5	0.3	1053	4	US-09-513-505-8	Sequence 8, Appli
27	264.5	0.3	605	3	US-09-063-950-5	Sequence 5, Appli
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38	239	0.3	112	4	US-09-543-681A-8319	Sequence 8319, Ap
39	238.5	0.3	605	1	US-08-190-802A-49	Sequence 49, Appli
40	238.5	0.3	605	3	US-08-477-346-49	Sequence 49, Appli
41	238.5	0.3	605	3	US-08-473-089-49	Sequence 49, Appli
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43	238.5	0.3	605	4	US-09-538-092-1087	Sequence 1087, Ap
44	238.5	0.3	603	4	US-09-949-016-10995	Sequence 10995, A
45	237.5	0.3	603	1	US-08-190-802A-50	Sequence 50, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
Sequence 9438, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTUR, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9438
LENGTH: 844
TYPE: PRT
ORGANISM: Human
US-09-949-016-9438
Alignment Scores:
Pred. No.: 3.04e-237
Score: 2592.00
Percent Similarity: 74.17%
Best Local Similarity: 62.38%
Query Match: 2.98%
DB: 4
Gaps: 8
US-09-396-985B-48 (1-50000) x US-09-949-016-9438 (1-844)
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Qy      37553 CTGCAGAGTTCCCTCTGCTGACACCATCATCACTGTTTGGCTGTGACAGTTTCTC 37612
Db      66  LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 79
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Db      513  LeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMet 532
Qy      39050 AGTCACAACTATATGTTTGTGATTCATCCCAATTATACCAAGCTGTATTCCTTCAGC 39109
Db      533  SerHisAsnAsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGln 552
Qy      39110 ACTCTGATTTGCAAGTTTCATGCGATGACAGACTCT---AAAGAAATACGCAACATTTT 39166
Db      553  ValLeuAspTyrSerLeuAsnHisIleMetThrSerLysValGlnIleuGlnHisPhe 572
Qy      39167 CSAAGAGTCAAGCTCTTCAATCTTATCAACAAATTTCTGCTCTGATATGTAACAT 39226
Db      573  ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHis 592
Qy      39227 CAGAAATCTCGAGTGGTCAAGAAACAGACAGAGTCTTGGTGAATGTTGAACAAATG 39286
Db      593  GlnSerPheLeuGlnIleThrIleLysAspGlnArgGlnLeuValGluValGluArgMet 612
Qy      39287 ACATPGCAACACCTGTAAGAGATTAACCTCTTGAGTGTGATTTTATTAATTTGACC 39346
Db      613  GluCysValAlaThrProSerAspLysGlnIleuMetProValLeuSerLeu---AsnIleThr 631
Qy      39347 TGTATATGTACAAACAATCATCAGTGTGCTGAGTGTGATGATGATGATGATGATGATGATGAT 39406
Db      632  CysGlnMetCysIleThrIleIleGlyValSerValLeuSerValLeuValSerVal 651
Qy      39407 GTAAGATTTGTGATATACACTTCTATTTTCACTGATACCTTATTTGCTGCTGTTAAAG 39466
Db      652  ValAlaValLeuValTyrLysPheTyrPheHisIleuMetLeuIleuAlaGlyCysIleLys 671
Qy      39467 TACAGCAAGAAAGAAACATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39526
Db      672  TyrGlyValGlyGlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlyAsp 691
Qy      39527 TGGGTGAAATGAGCTGTAAGAAATTTAGAAAGAGAGTGGCCGCTTTCACCTTGC 39586
Db      692  TrpValArgAsnGluLeuValLysAsnLeuGlnGluValAlaProPhePheGlnLeuCys 711
Qy      39587 CTTCACTACAGACATTTATCTCTGCTGTAAGCAATTTGCTGCAACATGATTCAGAAAGGC 39646
Db      712  LeuHisTyrArgAspPheIleProGlyValAlaIleAlaIleAsnIleIleHisGlnGly 731

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QY      39647  TTCACAAAGACCGGAAGTTATGTGTGCTAGCTTACGACACTTATTTGAGACCGGTGG      39706
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QY      39707  TGTATCTTTGAATATGAGATTGCTCAAAACATGCGACGTTTCTGAGACCGCGCTCTGCGATC      39766
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Db      752   CysIlePheGluIuYrGluIleIaGlnThrTrpGlnPheLeuSerSerArgIaGlyIle      771
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QY      39767  ATCTTCATGTGCTCTTGAAAGGTTGAGAAAGTCCCTGCTGAGCGACAGGTGGAAATTGNT      39826
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Db      772   IlePheIleValLeuGlnIysValIgluYsThrIleuLeuArgIlnIvalIgluLeuYr      791
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QY      39827  CGCCTCTCTTGAGCAGAAACACCTACCTCGATGAGGAGAGACATCTCTGGGGAGGCACATC      39886
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Db      792   ArgLeuLeuSerArgIaGlnThrIYrIleGlnItrpGlnIuSpSerValLeuGlnArgHisIle      811
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QY      39887  TTCTGGAAGACCTTAAATAATGCCCTATTGGAATGAGAAAGCCTCGAATCTTGAGCAGAAC      39946
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Db      812   PheItrpArgArgLeuArgIysAlaIleuLeuAspGlyIlySerSerTrpAsnProGluGluYThr      831
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RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKenough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514, 014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

Alignment Scores:
Pred. No.:      6e-38      Length:      661
Score:          502.50     Matches:      164
Percent Similarity: 46.31%  Conservative: 112
Best Local Similarity: 27.52% Mismatches:    275
Query Match:    0.58%     Indels:      45
Db:             1         Gaps:        18

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QY	37790	TTGATACGTG	CAAGAAACCC	TTACAGAT	TTTTTCC	CCAGAAAGTTTCT	CGACATTA	37849	
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Db	106	LeuValLeu	ThrGlySnp	ProLeuIle	PheMetIa	GluThrSer	LeuSnpIlePro	125	
QY	37850	AGTTAGAGAT	CTGTGTCGTG	AGACAA	ATTGGCCT	CTTGAAAGCTT	CCCTAT	37909	
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Db	126	SerLeu	HisIleSer	PheLeuIle	GlnThrGlyIle	SerAsnLeuGlnPheIle	ProVal	145	
QY	37910	GGACAGCTTA	CACTTAAGAA	AGCTCAAT	GTGGCTCA	CAATTTATAT	CACTTCGTAG	37965	
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QY	37970	TTACCTGCAT	ATATTTTCC	AACTGAC	AGCACTTA	GTAGATGAGAT	CTTTCTTAT	38029	
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QY	38030	ATTCAAC	TATTACTG	TCAACGA	CTTACAGTT	CTTACGTGA	AAATCC	38089	
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Db	185	IleHis	IleTyrlle	SerArgIle	SnpMetArg	SerLeuGln	-----	AlaIleAsnLeu	202
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Db	223	ValPhe	GlnSerLeu	AsnPhe	GlyGlnThr	ProAsnLeu	SerValIlePhe	AsnGly--	241
QY	38210	CTTCAAA	ACCTGGCTG	TTTACAC	CGTCATCG	GTGATCTTG	GGAGAA	38269	
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Db	242	LeuGln	AsnSerThr	-----	ThrGln	SerLeuThr	PheGlnIle	258	
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Db	259	AspAsp	GluAspIle	---Ser	SerIle	MetLeu	GlyLeu	38386	
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Db	278	SerLeu	AsnLeu--	GlnGln	IleAsp	PheSerAspIle	SerSerThr	38446	
QY	38387	TTGGCAAT	GGTTTCTG	CAATGTC	CTGCGAC	GTATCAT	TAATCA	38446	
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Db	297	Phe	ThrGln	Ile	GlnIle	AsnLeu	SerLeuThr	38446	
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QY	38447	CCTMAA	CATTTCA	ATGGCA	ATCTTAT	CAATCATTA	GA-----	38485	
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Db	314	Pro	SerGly	MetLeu	-----	GlyLeu	AsnLeu	38485	
QY	38486	-----	---TGT	CACTTAA	GA-----	CA	38486		
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Db	332	His	Phe	Asp	Pgl	MetLeu	CysGlnIle	38524	
QY	38525	CTTA	AAAGTTTGA	CTTAACT	TATGA	CAAAAGGCT	CTATCAG	38584	
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Db	352	Ile	Arg	Gly	AsnVal	IleVal	LeuSnpIle	38584	
QY	38585	CCAAG	CTCAG	CTATCT	AGATCT	TATAGT	AGAAATG	38644	
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Db	370	Gly	AsnLeu	GlnThr	LeuAsp	PheSer	IleAsnAspIle	38644	
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QY	38645	TATTC	GATTTTGG	AAACAA	ACGCTG	AGACCTTA			

QY 38762 TCTACTTTAAAGGGTCACAGAAATTCAGAGCTTCTTATCCCTTGAAAGACTTCTTAC 38821
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QY 38822 CTTCAGATCTCTTATTAATAACCAAAATTAAGTCTGAGTATTAATTTCTTGAGACC 38881
DB 450 LeuAsnLeuThrTyrCysPheLeuAspThrSerAsnGlnHisLeuAlaGlyLeuPro 469
QY 38882 AGCTTCACACATTAATAAATGGCTGCAATTTCTTCAAGAACAAACCTT-----TCA 38935
DB 470 ValLeuArgHisIleuAsnLeuLysGlyAsnHisPheGlnAspGlyThrIleThrLysThr 489
QY 38936 AATGCTCTTGCAACAACACAACTTGACATTCCTGAGATTTCTTAATGTCAATTGGA 38995
DB 490 AsnLeuLeuGlnThrValGlySerLeuGlnValLeuIleLeuSerSerCysGlyLeuLeu 509
QY 38996 CAATATCTTGAGGGGATTTTGAACACCTTCATGACTCTCAATTAATTAATGAGTAC 39055
DB 510 SerIleAspGlnGlnAlaPheHisSerLeuGlyLysMetSerHisValAspLeuSerHis 529
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QY 39107 AGCACTCTGATTCAGATTTCAATCGCATAGACATCTAAAGAAATGACTGCAACATTTT 39166
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QY 39167 CCAAGAGCTTACGCTTCTTCAATCTTACTTAACAAATTCCTGCTGTATATGTAACAT 39226
DB 566 LeuSerGlnGlnSerThrIleAsnLeuSerHisAsnProLeuAspCysThrCysSerAsn 585
QY 39227 CAGAAATCTCGACGCTGTCACAGAACAGAAAGATTTGGTGAATGTTGAACAAATG 39286
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DB 626 GlyIleThrAlaIleGlyIlePhePheLeuIleValIlePheLeuLeuAlaIleLeu 645
QY 39395 GTGGTATCCACTGATTCGATATACCACTTCAATTTTCAACCG 39442
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RESULT 3
US-08-833-823-4
Sequence 4, Application US/08833823
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-Apr-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELEPHONE: (617) 498-8224
TELEFAX: (617) 498-8224
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4
Alignment Scores:
Pred. No.: 66-38 Length: 661
Score: 502.50 Matches: 164
Percent Similarity: 46.31% Conservative: 112
Best Local Similarity: 27.52% Mismatches: 275
Query Match: 0.58% Indels: 45
DB: 2 Gaps: 18
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QY 37790 TTGATCTGACAGAAACCTTATCCAGAGTTTCCCAAGAGTTTCTGCAATAACA 37849
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QY 37850 AGTTTGAAGATTTGGTGGCTGAGAGCAAAATGGCCCTCTTAAGACTCCCAT 37909
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QY 38090 TCTTGAACATGCTTTGAACCAATTAAGTCAATTCACAGCAAGCTTTCAAGGAT 38149
DB 203 SerLeuAsnPheAsnGlnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThr 222
QY 38150 AAGCTCCATGAACCTGATTAAGAGGTATTTTAATAGCTCAATATATGAAGAACTTGC 38209
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 Db 352 IleArgGlnValLeuLysLeuHisLeuGlyValGlyCysLeuGlnLys-----Leu 369
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 Qy 38882 AGTCTCAACACATTAATAATGGCTGGCAATCTTTCAAGACAAACACCTT-----TCA 38935
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 Qy 38936 AATGCTTTGGCAACACAAACAACTTGAATCTCTGATCTTTTGAATGTCAATTGAGAA 38995
 Db 490 AsnLeuGlnThrValGlySerLeuGlnValLeuLeuSerSerCysGlyLeuLeu 509
 Qy 38996 CAATATCTGGGGGGATTTGACACCTCCATGACTTCAATATTAATATAGATGAC 39055
 Db 510 SerLeuAspGlnAlaPheHisSerLeuGlyLysMetSerHisValAspLeuSerHis 529
 Qy 39056 AACATCTAATG-----TTTTGATTTCA---TCCCATTTAACAAGCTGATTTCCCTC 39106
 Db 530 AsnSerLeuThrCysAspSerIleAspSerLeuSerHisLeuLysGlyIleTyr----- 547
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 Db 548 -----LeuAnLeuAlaIleAsnSerIleAsnIleIleSerProAlaGlyLeuProIle 565
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 Qy 39227 CAGAAATCTCTGAGTGGGTCAAGAAACAGAGCTTCTTGAGAAATGTTGAACAATG 39286
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 Qy 39287 ACATGTGCAACACCTGTAGAGATGAAT-----ACCTTCCTTATGATGCTGATTT 39334
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 RESULT 4
 US-09-982-308B-23
 ; Sequence 23, Application US/09982308B
 ; Patent No. 6531290
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalle, Barbara
 ; APPLICANT: Pan, Xuedong
 ; APPLICANT: Lundell, Daniel
 ; APPLICANT: Lunn, Charles A.
 ; APPLICANT: Tan, Jimmy C.
 ; APPLICANT: Zavodny, Paul J.
 ; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
 ; FILE REFERENCE: JB0601QC
 ; CURRENT APPLICATION NUMBER: US/09/982,308B
 ; CURRENT FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 09/156,163
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 08/889,909
 ; PRIOR FILING DATE: 1997-07-10
 ; PRIOR APPLICATION NUMBER: 60/021,710
 ; PRIOR FILING DATE: 1996-07-12
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 784
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-982-308B-23
 Alignment Scores:
 Pred. No.: 3,13e-34 Length: 784
 Score: 464.00 Matches: 207
 Percent Similarity: 41.96% Conservative: 122
 Best Local Similarity: 26.40% Mismatches: 305
 Query Match: 0.53% Indels: 150
 DB: 4 Gaps: 32
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 Qy 37838 TCTGGACTAACAAGTTTGAAGAAATCTGGTGTGAGACAAATAATGGCCCTCTGAA 37897
 Db 97 SerSerLeuGlySerLeuGlnHisLeuAspLeuSerTyrAsnTyrLysSerAsnLeuSer 116
 Qy 37898 AGCTTCCTATTTGGACAGCTTATTAACCTTAAGAACTCAATGTGGCTCAATTTTATA 37957
 Db 117 SerSerTrpPheLysProLeuSerSerLeuThrPheLeuAnLeuLeuGlyAsnProTyr 136
 Qy 37958 CATTCCTGTAAGTTACTCTGCATATTTTCCAAITGACGAACCTTAGTACATGTGATCTT 38017
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 Qy 38066 CGTGAATAATCCACAAGTCAATCTCTTTAGACATGCTTTTGAACCAATTTGACTTCAAT 38125
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 Db 190 GlnProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleuHisMetLysGln 209
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Db      210 Histleuleuleuengulilephevalaspvalthrserservalgu---Cysleuglu 228
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Qy      38264 GAT-----GAAAGAACTGGAAATTTTGAACCTCTATCATGGA 38305
Db      249 SerleuileuylsyrpethrphetrargasnvalylsrhargglusSerleuphegln 268
Qy      38306 -----GCACTATGATGTGACCATATGATGATTCAGG 38338
Db      269 ValMetLysleuLeuasnGlnlleSerGlyleuLeuGluLeuGluPheAspArgCysThr 288
Qy      38339 TTAAACATATACAAATGATTTT-----TCAGATGATATTTGTAAGTTCCATTCCTGGCG 38392
Db      289 LeuasnGlyValGlyAsnpheargAlaserAspAsn----- 300
Qy      38393 AATGTTCTGCAATGCTCTGGCAGGATCTATAAATATCTAGAAGATGTTCCATAA 38452
Db      301 -----AspArgValIleAsp 305
Qy      38453 CATTTCAATGGCAATCTTATCATCATATGATGATCACTTAAGCAAGTTCCAACTCTG 38512
Db      306 ProglyylsValGluThrleuThrIlearghrgleuhsileProargPheTyLeuphe 325
Qy      38513 ---GATTCACCTTTCTTAAAAAGTTTGACTTAACTATGAACAAAGGCTCATACGTTT 38569
Db      326 TyzAspLeuSerThrleuTySerleuThrgluArgValylsArgIlethValGluAsn 345
Qy      38570 AAAAAAGTG-----GCCCTACCAAGCTTCAGCTATCTA 38602
Db      346 SerlylsvAlPheleuValProCysleuLeuSerGlnhlsleuylsSerleuGluTyLeu 365
Qy      38603 GATCTTGTAGTAAATGCA-----CTGAGCTTTAGTGGTGC---TGTTCT 38644
Db      366 AspLeuSerGluAsnleuMetValGluGluTyLeuylsAsnSerAlaCysGluAspAla 385
Qy      38645 TATTCTGATTTGGGACAAACAGCCTGAGA-----CACTTA---GACCTCAGCTTCAAT 38695
Db      386 TyrProSerleuGlnThrleuIleuArgGlnAsnhsileuAlaserleuGluTyLeuThr 405
Qy      38696 GGTCGCATCATATGAGGCCAATTTGATGGCTAGAGAGCGTCAGACATCGGATTTT 38755
Db      406 GlyIuThrleuLeuThr-----LeuylsAsnleuThrAsnIleAspIle 420
Qy      38756 CAGCACTCTACTTTAAAAAGGTCACAGAAATTCAGCGTTCTTATCCCTTGAAGCTA 38815
Db      421 SerlylsvAsnSerPhehlsrMetProgluThrCysGlnThr-----ProgluTyLeuMet 438
Qy      38816 CTTTACCTTGACATCTCTTATACCTAACACCAAAATGACCTTGATATTTCTTGGC 38875
Db      439 LysTyrlsleuAsnleuSerSerThr----- 446
Qy      38876 TTGACACAGTCTCAACACATTAATAATGGCTGGCAATCTTCAAGAACAACCCCTTCA 38935
Db      447 -----ArgIleHisSerValThr 452
Qy      38936 AATGCTTTTGCAAAACACAACAACTTGACATTCCTGATCTTTTGAATGTCATTTGAA 38995
Db      453 GlyCysIleProlylThr-----LeuGluIleleuAspValSerAsnAsnleuAsn 470
Qy      38996 CAAATATCTTGGGGGAGTATTTGACACCTCCATGAGCTTCAATATTAATATAGATGAC 39055
Db      471 LeuPheSerleu-----AsnleuProGlnleuylsGluLeuTyIleSerArg 486
Qy      39056 AACATCATATGTTTGGATTCATCCATATAACACGCTGATTCCTCCAGACACTT 39115
Db      487 AsnlylsvMetThrleuProAspAla-----SerleuLeuPrometleuValleu 504
Qy      39116 GATTGCAAGTTTCAATCGCATAGAGCA---TCTAAGAGAAATACTGCAACATTTTCCAAG 39172

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Db      505 LysIleSerArgAsnAlaIleThrThrPheSerlyeGluGluLeuAspSerPhe---His 523
Qy      39173 AGCTACGCTCTTCTTCAATCTTACTAATTCCTGTTGCTTGTATATGTAACATGAGAA 39232
Db      524 ThrleuylsThrleuGluAlaGlyAlaGlyAsnAsnPhelIleCysSerCysGlu----- 540
Qy      39233 TTCCTCAGTGGCTGACAGAAACAGAAAGCAATTTCTTGGTGAATGTT----- 39277
Db      541 PheLeuSerPheThrGlnGlnGluin---GlnAlaLeuAlaLysValleuIleAspTrpPro 559
Qy      39278 GAACAAAATGACATGTGCACACCTGTGAGATGAATACCTCTTACTGTTGAT----- 39331
Db      560 AlaAsnTyrlsleuCysAspSerProSerhlsValArgGlyGlnGlnValAlaGlnAspValArg 579
Qy      39332 TTTAATATATCTACCTGTTATATGTAATGTAACAGACATCATCAGTGTGCAGTGTG 39391
Db      580 LeuSerValSerIuylsYshlsArgIleAlaLeuValSerIeTyMetCysCysAlaLeuPhe 599
Qy      39392 ATTGTGGTATCCACTGTAGCAATTTCTGATATACCACTTC-----TATTTTCAC 39439
Db      600 LeuLeuIleleuLeuThrGlyValleuCysHlsArgPhehlsGlyLeuTrpTyMetLys 619
Qy      39440 CTGATA-----CTTATGCTGCTGTAAAAAGTACACGACAGAGAAAGC----- 39484
Db      620 MetMetTrpAlaThrleuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIle 639
Qy      39485 ATCTATGATGCAATTTGTGATCTCTGAGTCACAGAAATGAGACCTGGGTGAGAAATGAGCTG 39544
Db      640 CysTyAspAlaPheValSerTySerGluArgAspAlaTyTrpValGluAsnleuMet 659
Qy      39545 GTAAGATTTAGAAAGAGAGAGGCGCCGCTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 39604
Db      660 ValGlnGluLeuGluAsnPheAsnProProhlyleuCysleuhsileuylsArgAspPhe 679
Qy      39605 ATTCTGTGTGTAGCCATGCTGCTGCCAAATCATATCAGAGAGCTTCCAAAGAGCCGAGAG 39664
Db      680 IleProGlylserIleIleAspAsnIleIle---AspSerIleGluLysSerhlsLys 698
Qy      39665 GTTATGTGTGTAGTGTGTAGACCTTATATTCAGAGCGTGTGATCTTGTAAATATGAG 39724
Db      699 ThrValPheValleuSerGluAsnPheValylsSerIuTrpCyslylTyGluLeuAsp 718
Qy      39725 ATTGCTCAAAATGAGGAGGAGTTTCTGAGACGCGCTGTGACATCTTCAATGTCCTTGTAG 39784
Db      719 PheSerhlsPheArgleuPheAspGluAsnAsnAspAlaAlaIleleuIleleuGlu 728
Qy      39785 AAGGTGAGAGGCTCTGCTGAGGACAGCAG---GTGAAATGTATGCGCTTCTTACAGCA 39841
Db      739 ProIleGluylsAlaIleProGlnArgPheCysleuLeuArgylsIleMetAsnThr 758
Qy      39842 AACACCTGCTGGAAGGAGGAGCAATCCCTGGGAGGACATCTTCTGAGAGAGCTT 39901
Db      759 LysThrTyrlsleuGluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnleu 778
Qy      39902 AAAAATGCCTTA 39913
Db      779 ArgAlaAlaIle 782

RESULT 5
US-09-949-016-8799
Sequence 8799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores:
Pred. No.: 2,296-28      Length: 775
Score: 402.50           Matches: 196
Percent Similarity: 40.08% Conservative: 107
Best Local Similarity: 25.93% Mismatches: 276
Query Match: 0.46%      Indels: 177
DB: 4                  Gaps: 31

US-09-396-985B-48 (1-50000) x US-09-949-016-8799 (1-775)
QY 37778 CACCTCTCAACTTGATCTGACAGAGAAACCTTATCCAGAGTTTCCCGAGAGTTTC 37837
DB 112 AsnLeuGlnAlaLeuValLeuThrSerAsnGlyIleAsnThrIleGluGlnAspSerPhe 131
QY 37838 TCTGACTAACAAGTTTAGAGATCTGGTGGCTGAGAGACAAATTGGCTCTTAGAA 37897
DB 132 SerSerLeuGlySerLeuGlnHisLeuAspLeuSerTyraSerTyLeuSerAsnLeuSer 151
QY 37898 AGCTTCCTTATGACACCTTATTAACCTTAAGAAACTCAATGAGCTTCACAATTTTATA 37957
DB 152 SerSerTyPheLeuProLeuSerSerLeuThrPheLeuAsnLeuGlyAsnProTy 171
QY 37958 CATTCCTTAAGTTACCTGCATATTTTCCATCTGACAGAACTTGACATGAGATCTT 38017
DB 172 LysThrLeuGlyGluThrSerLeuPheSerHisLeuThrLysLeuGlnIleLeuArgVal 191
QY 38018 TCTTATTAACATATTCAAACTATTAAGCTTATGTCACAGACTTACAGTTTCTA 38065
DB 192 GlyAsnMetAspThrPheThrLysIleGlnArgLysAspPheAlaGlyLeuThrPheLeu 211
QY 38066 CGTGAAAATCCACAAGTCATCTCTTTTAAACATGCTTTGAAACCAATTGACTTCAT 38125
DB 212 GluGlu -----LeuGlnIleAspAlaSerAspLeuGlnSerTy 224
QY 38126 CAAGCAAGCCTTTCAGAGAAAT-----AAGCTC 38155
DB 225 GluProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHisMetLysGln 244
QY 38156 CATGAACCTGACTTAAGAGTAAATTTTATAGCTCAATATATGAAGAACTTGACCTTCA 38215
DB 245 HisIleLeuLeuLeuGlnIlePheValAspValThrSerSerValGlu---CysLeuGln 263
QY 38216 -----AACCTGCTGGTTTACACGTCATCGATTGACCTTGAGGAGAAATTTTAA 38263
DB 264 LeuArgAspThrAspLeuAspThrPheHisPheSerGlnLeuSerThrGlyGlnThrAsn 283
QY 38264 GAT-----GAAGGAATCTGGAAATTTTGAACCTCTATATCAAGAA 38305
DB 284 SerLeuIleLysLysPheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGln 303
QY 38306 -----GACATGATGTAGTGACCATGATGATGATGATGAG 38338
DB 304 ValMetLysLeuLeuAsnGlnIleSerGlyLeuLeuGlnLeuGluPheAspSerPheThr 323
QY 38339 TTAACATATACAAATGATTT-----TCAGATGATTTTGAAGTTCCATTTGCTTGCG 38392
DB 324 LeuAsnGlyValGlyAsnPheArgAlaSerAspAsn----- 335
QY 38393 AATGTTTCTGCATGTCTCTGACAGGTGATCTATATAAATATCTAGAAGATGTTCTTAA 38452
DB 336 -----AspArgValIleAsp 340
QY 38453 CATTTCAATGAGCAATCTTATCAATCATTTAGATGTCAACTTAAGCAAGTTTCAACTCTG 38512

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DB 341 ProGlyLysValGluThrLeuThrIleArgArgLeuHisIleProArgPheTyLeuPhe 360
QY 38513 ---GATCTACCTTTCTTAAAGTTTGACTTAACTATGAACAAAGGCTTATACGTTT 38569
DB 361 TyrAspLeuSerThrLeuTySerLeuThrGluArgLysArgIleThrValGlnAsn 380
QY 38570 AAAAAAGTG-----GCCCTACCAAGCTCAGCATCTA 38602
DB 381 SerLysValPheLeuValProCysLeuLeuSerGlnHisLeuLysSerLeuGlnTyLeu 400
QY 38603 GATCTTAGTAGAAGATGCA-----CTGAGCTTTAGTGTTGC---TGTTCT 38644
DB 401 AspLeuSerGlnAsnLeuMetValGluGluTyLeuLysAsnSerAlaCysGlnAspAla 420
QY 38645 TATTCTGATTTGGACAACAAGCCTGAGA-----CACTTA---GACCTCAGCTTCAT 38695
DB 421 TrpProSerLeuGlnThrLeuIleLeuArgGlnAsnHisLeuAlaSerLeuGlnLysThr 440
QY 38696 GATGCATCATTTATGAGGCCAATTTCAATGGCTTAGAAGAGCTGACGACCTGGATTTT 38755
DB 441 GlyLysThrLeuLeuThr-----LeuLysAsnLeuThrAsnIleAspIle 455
QY 38756 CAGCACTCTACTTAAAGGGTCACAGAAATTCAGGCTTCTTATCCCTTGAAGAACTA 38815
DB 456 SerLysAsnSerPheHisSerMetProGluThrCysGlnTrp-----ProGlnLysMet 473
QY 38816 CTTTACCTTGACATCTCTTATACTTAACACCAAAATGACCTTGATATTTCTTGCC 38875
DB 474 LysTyLeuAsnLeuLeuSerThr----- 481
QY 38876 TTGACACGTCACACATTTAAATGCGTGGCAATCTTTCAAGACAAACACCTTTCA 38935
DB 482 -----ArgIleHisSerValThr 487
QY 38936 AATGCTTTTGCAACACACAACTTGACATCTCTGATCTTTTAAATGTCAATGTGAA 38995
DB 488 GlyCysIleProLysThr-----LeuGlnIleLeuAspValSerAsnAsnAsnLeuAsn 505
QY 38996 CAATATCTTGGGGGATTTTGAACACCTGCATGACTTCATTAATTAATGAGTCAC 39055
DB 506 LeuPheSerLeu-----AsnLeuProGlnLeuLysGluLeuTyIleSerArg 521
QY 39056 AACATCTATGTTTGTGATTCATCCCATTAATACACGCGTATTCCTCAGACATCTT 39115
DB 522 AsnLysLeuMetThrLeuProAspAla-----SerLeuLeuProMetLeuLeuValLeu 539
QY 39116 GATTGACGTTTCAATCCCATAGAGACA---TCTAAGGAATACCTGCAACATTTTCAAG 39172
DB 540 LysIleSerArgAsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe---His 558
QY 39173 AGCTACGCTTCTTCAATCTTACTTAACAATTTGCTGCTGTATATGTAACATCAGAA 39232
DB 559 ThrLeuLysThrLeuGlnAlaGlyLysAsnHisPheIleCysSerCysGlu----- 575
QY 39233 TTCTGACAGTGGGTCAAGAAACAGAAAGCATGTTCTTGATGATTT----- 39277
DB 576 PheLeuSerPheThrGlnGlnGlu---GlnAlaLeuAlaLysValLeuIleAspTrpPro 594
QY 39278 GAACAAATGACATGTGACACACCTGTAGAGATGAATACCTCTTATGTTGATTTTAAAT 39337
DB 595 AlaAsnTyLeuLysCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArg 614
QY 39338 AATTTCACTGTTATATGATACAGACAAATCATCATGCTGTCAGTGCATGATTTGTG 39397
DB 615 LeuSerValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeu--- 633
QY 39398 GTATCACTGTAGATTTTGATATATCACTTCAATTTTCAACCTGATATTAATTTGCTGCC 39457
DB 634 -----PheLeuLeuIleLeuLeuThrGly 641
QY 39458 ---TGTAAGATGAC----- 39469

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Db      642 ValLeuCyHhIbArGrPheHhISGLyLeuTrpTyMeLyMeMeMetTrpAlaTrpLeuGln 661
QY      39470 -----ACGAGAGGAGAAAGCATCTATGATGCATTTGTG 39502
Db      662 AlaLybArGlybSProArgLybAlaPAProSerArg--AsnIleCybTyZbAspAlaPheVal 680
QY      39503 ATCACTACCGAGTCAAGATAGCAAGCTGGGTGGAGAAATGAGCTGGTGAAGATTATAGAGAA 39562
Db      681 SerTySerGluTrGArbAlaTyTrpValGluAsnLeuMetAlaGlnGluLeuGluAsn 700
QY      39563 GGAAGTCCCGCGCTTTCACTCTCCCTTCACTACAGAGCTTTATTTCTGGTGTAGCCATT 39622
Db      701 PheAsnProProPheLybLeuCybLeuHhIbLybArGAspPheLeuProGluTybTrpIle 720
QY      39623 GCTGCCAATCATCATCCAGAGAGCTTCCACAGAGCCGGAAGGTATTTGGTAGTGCT 39682
Db      721 IleAspAsnIleIle--AspSerIleGluLybSerHhIbLybThrValPheValLeuSer 739
QY      39683 AGACACTTATTTACAGAGCCCTTGCTGTGTATCTTTGATATAGAGATTGCTCAAAACATGGCAG 39742
Db      740 GluAsnHhValLybSerGluTrpCybLybTyGluLeuAspPheSerHhIbPheArgLeu 759
QY      39743 TTTCTGACAGCCGCTCTGGCATCATCTTCATCTTCTTGTGAGAGAGTT 39790
Db      760 PheAspGluAsnAsnAspAlaIleIleLeuIleLeuLeuGluProIle 775

RESULT 6
US-09-513-999C-7214
/ Sequence 7214, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J. B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J. Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59.US2.REG
/ CURRENT APPLICATION NUMBER: US/09/513.999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/132,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 7214
/ LENGTH: 129
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 108
/ OTHER INFORMATION: Xaa=Ala or Asp or Gly
US-09-513-999C-7214

Alignment Scores:
Pred. No.:          2.39e-24          Length:          129
Score:              365.50           Matches:          73
Percent Similarity: 70.54%           Conservative:    18
Best Local Similarity: 56.59%         Mismatches:      37
Query Match:        0.42%            Indels:          2
DB:                  4                Gaps:            1

US-09-396-985B-48 (1-50000) x US-09-513-999C-7214 (1-129)
QY      36357 CTTAAGAAGAAATTCTCAACTGAGAGAACTAGATGACTGAAAGTACCTAAAAAAATGT 36298
Db      1 MetAspArgHhIbPheSerLybGluAspIleTyTrpAlaIbLybHhIbMetCybLybCyS 20
QY      36297 TTAACATCTTATGATCAGAGGAATGCAATCAAAACAACTCGATATATTCACATTCA 36238
Db      21 SerSerSerLeuAlaIleArgGluMetClnIleLybHhTrhMetArgTrHbLeuThr 40
QY      36237 CCAATGCAATGACTTAAGATCAAAAATCTCAAGTACAGCAGATGCTCGCAAG- TGTAGA 36179

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Db      41  ProValArgMetAlaIleIleLysLysSerGlyAlaAsnArgCysTrpArgGlyCysGly 60
QY      36178  GAMAGAGAAACACTCTTCCATTGCTGGCAGAACTGTAAATGTATATACCACTTGGAAA 36119
Db      61  GluIleArgThrIleuLeuHisCysTrpTrpAspCysLysIleValGlnProLeuTrpLys 80
QY      36118  TCGATTGGGCGTTCCTCAGAAAATTGACATGCTACTCTAGAGATCCAGCAATACCA 36058
Db      81  SerValTrpGlnPheuAspGlyLeuGluIleProPheAspProAlaIlePro 100
QY      36058  CTCCAAGCAAAATATCCAGATGAT--GCCTTCACTTGTATATAGACACATGCTTACT 36002
Db      101  LeuLeuGlyIleTrpProLys***TyrLysSerCysCysTrpLysAspThrCysThrHis 120
QY      36001  ATGTTCAATACCACTTTATTATTATTAATA 35975
Db      121  MetPheIleAlaIleuPheThrIle 129

RESULT 7
US-09-907-794A-290
/ Sequence 290, Application US/09907794A
/ Patent No. 6635468
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Macher, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/907,794A
/ CURRENT FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/22089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/

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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-290

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Alignment Scores:
Pred. No.: 1.35e-15      Length: 1059
Score: 269.50           Matches: 101
Percent Similarity: 42.78%      Conservative: 56
Best Local Similarity: 27.52%    Mismatches: 135
Query Match: 0.31%           Indels: 75
                               Gaps: 15

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US-09-396-985B-48 (1-50000) x US-09-907-794A-290 (1-1059)

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QY 38390 GCGAATGTTTGCATGCTCTGGCAGGTGATCTATAAATCTAGAGATGTTCT 38449
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 AlaaniethrleuSerleuAlaGlyAsnArgile-----ValGluileuPro 78
QY 38450 AAACATTTCAA---TGCATTCCTTATCAATCATTAGATGCTCAACTTAACAG----- 38500
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 79 GluHisleuLysGluPheGlnSerleuGlnThrleuAspLeuSerAsnAsnleuSer 98
QY 38501 -----TTTCCAACTCTGATCTACCCCTTTCT----- 38527
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuLysIleuLysLeuAsnSerAsnArg 118
QY 38528 ----- 38545
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 119 ValThrSerMetGluProGlyIleuPheAspAsnleuAlaAsnThrleuLeuValleuLys 138
QY 38546 ATGAACAAAGGCTCTATCAGTTT-----AAAAAGTGGCCCTTACCAAGTCTCAGC 38596
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProLysMetPheLysLeuProGlnleuGln 158
QY 38597 TATCTAGATCTTAGAGAAATGCACTGAGCTTACTGCTGCTTTTATTCTGATTTG 38656
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 159 HisleuGlnleuAsnArgAsnLysIleLysAsnValAspGlyLeuThrPheGlnGlyLeu 178
QY 38657 GGAACAAACAGCTGAGACACTTAGACCTTCACTGAGTGGCCATC--ATTATGAGT 38713
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 179 Gly-----AlaLeuLysSerleuLysMetGlnArgAsnGlyValThrLysleuMetAsp 196
QY 38714 GCCAATTCATGGCTTAGAAGAGCTGAGACACTGATTTTTCAGCACTACTTTAAA 38773
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 197 GlyAlaPheIleuLysLeuSerAsnMetGluIleleuGlnleuAspHisAsnleuThr 216
QY 38774 AGGTCACAGAAATC----- 38788
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 217 GluIleThrLysGlyIleuLysLeuLysleuMetleuGlnleuLeuHisleuSerGln 236
QY 38789 -----TCAGCTTCTTATCCCTTGAAGACTACTTACCTT 38824
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 237 AsnAlaIleAsnArgIleSerProAspAlaIlePheGlnPheCysGlnLysleuSerGlnleu 256
QY 38825 GACATCTCTTACTATAC--ACCAAAATGACTTCAGTGGATATATTTCTTGGCTTGACC 38881
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Db 257 AspleuThrPheAsnHisleuSerArgleuAsp--AspSerPheleuGlyleuSer 275
QY 38882 AGTCTCAACACATTAATAAATGGCTGCAATTTCTTCAAGACCAACCCCTTCAATGTC 38941
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 276 LeuLeuAsnThrleuHisIle--GlyAsnAsnArgValSerIleThrleuAlaAspCysAla 294
QY 38942 TTTCGAAACACACAACTTACATTCCTGGATCTTTCTTAATGTCATTTGAAACAAATA 39001
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 295 PheArgGlyleuSerSerleuLysThrleuAspLeuLysAsn-----AsnGluIle 311
QY 39002 TCTTGG-----GGGGTATTGACACCCCTCCATAGACTTCATTTATTA 39043
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 312 SerIleThrIleGluAspMetAsnGlyAlaPheSerGlyleuAspLysleuArgleu 331
QY 39044 AATATGATGCACAACTATGTTTGGATTCATCCCTTATTAACCAAGCTTATTC 39103
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 332 IleleuGlnGlyAsnArgIleArgSerIleThrLysLysAlaPheThrGlyleuAspAla 351
QY 39104 CTCAGCACTTGTGATTCAGCTTTTCATGCGATAGACATCTAAAGAAATCTGCAACAT 39163
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 352 LeuGlnHisleuAspLeuSerAspAsnAlaIleMetSerleuGlnGlyAsnAlaPheSer 371
QY 39164 TTTCGAAAGACTCTAGCTTTCTTCAATCTTACTAACAATTTGCTGCTTGTATGTGAA 39223
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 372 GlnMetLysLysleuGlnGlnleuHisleuAsnThrSerSerleuLysCysAspCysGln 391
QY 39224 CATGCAAAATTCCTGAGTGGGCTCAAGAAACAGAA--CAGTCTTGCTGTAATGTTGAA 39280
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 392 LeuLysIleuProGlnIleThrValAlaGlnAsnAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAAATGACATGTGCAACACCT 39301
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 411 -----SerCysAlaHisIlePro 415

RESULT 8
US-09-905-125A-290
Sequence 290, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07

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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 290
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-290

Alignment Scores:
Pred. No.:      1,35e-15      Length:      1059
Score:          269.50      Matches:      101
Percent Similarity: 42.78%      Conservative: 56
Best Local Similarity: 27.52%      Mismatches: 135
Query Match:      0.31%      Indels:      75
DB:               4          Gaps:      15

US-09-396-985B-48 (1-50000) x US-09-905-125A-290 (1-1059)

QY      38390 GCGAATGTTTCTGCAATGCTCTGCGAGGTGATCTATAAAATCTAGAAGATGTTCTT 38449
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 AlaenulthrleuSerleuAlaGlyAsnArgIle-----ValGluIleleuPro 78

QY      38450 AAAAATTTCAAA---TGGAATCCTTATCAATCACTTATGATGTCAACTTAAGCAG----- 38500
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      79 GluIhIseuYsGluPheGlnSerleuGluIhIreuAspIeuSerSerAsnIleSer 98

QY      38501 -----TTTCCAACTCTGGATCACTACCTTTCTT----- 38527
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      99 GluIeuGlnIhIraIaPheProAlaIeuGlnIeuYsIryIeuYrIleuAsnSerAsnArg 118

QY      38528 -----TTTCCAACTCTGGATCACTACCTTTCTT----- 38545
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      119 ValIhIserMetGluProGlyIryPheAspAsnIeuAlaEnIhIreuIleValIeuIys 138

QY      38546 ATGAACAAAGGGCTATCACTTT-----AAAAAGTGGCCCTACCAAGTCTCAGC 38596
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      139 IeuAsnIryAsnArgIleSerAlaIleProIryIhIserPheYsIleProGlnIeuGln 158

QY      38597 TATCTAGATCTTAGAGAAATGACCTGAGCTTATGTGGTTCCTTCTTATTTGATTTG 38656
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      159 HisIeuGluIeuAsnIryAsnIlyIleYsAsnValIseGlyIleuIhIreuGlnGlyIeu 178

QY      38657 GGAACAAACAGCTGAGCACTTGAAGCTTCAGTTCAATGTGGCATC---ATTATGAGT 38713
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Db      179 Gly-----AlaIeuIysSerIeuYsMetGlnIArgAsnGlyValIhIryIleuMetAsp 196

QY      38714 GCCAATTTCTAGTGTCTAGAGAGCTGACAGCAGCTGATTTTACAGCTTCTTAA 38773
        |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      197 GlyAlaPheIryGlyIeuSerAsnMetGluIleIeuGlnIeuAspIhIseAsnIleuThr 216

QY      38774 AGGCTCAGCAAGATTC----- 38788
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      217 GluIleIhIryIseGlyIryIleuYrGlyIleuIeuMetIeuGlnIleuIhIseIeuSerGln 236

QY      38789 -----TCAGCGTCTTATTCCTTGAAGAGCTTACTTTACTTT 38824
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      237 AsnAlaIleAsnArgIleSerProAspAlaIryGluPheCysGlnIysIeuSerGluIeu 256

QY      38825 GACATCTCTTATTAATAAC---ACCAAAATGACTTGGATGTATTTCTTGGCTTGACC 38881
        |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      257 AspIeuIhIryPheAsnIhIseIeuSerArgIeuAsp---AspSerSerPheIeuGlyIeuSer 275

QY      38882 AGTCTCAACACATTAATAATGGCTGGCAATTTCTTCAAGACAAACCCCTTCAAAATGTC 38941
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      276 IeuIeuAsnIhIryIeuIhIseIle---GlyAsnAsnArgValSerIryIleAlaIsePysAla 294

QY      38942 TTTCGAAACAAACAACTTGACATTCCTGATCTTTCTAAATGTCAATTTGAACAATA 39001
        |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      295 PheArgGlyIeuSerSerIeuIysIhIryIeuAspIeuIyAsn-----AasnGluIle 311

QY      39002 TCTTTGG-----GGGGTATTTGACACCTCCATAGACTTCAATTA 39043
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      312 SerIryPheIhIleGluAspMetAsnGlyAlaPheSerGlyIeuAspIysIeuArgIeu 331

QY      39044 AATATGAGTCACACAAATCTATTTGTTTGATTCATCCATTAACCAAGCTGATTC 39103
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      332 IleIeuGlnIyAsnIhIryIeArgSerIleIhIryIeYsAlaIaIhIerIryIleuAspAla 351

QY      39104 CTCAGCACTTGTATTTGACATTTCAATTCGATAGACATCTAAGAGATATGCAACAT 39163
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      352 IeuGluIhIseuAspIeuSerAspAsnAlaIleMetSerIeuGlnIyAsnAlaIaPheSer 371

QY      39164 TTTCGAAAGGCTAGGCTTCTTCAATCTTATTAACATCTCTGCTGTATATGAA 39223
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      372 GluMetIyIeYsIeuGlnIyAsnIhIseAsnIhIserSerIeuIeuCysAspCysGln 391

QY      39224 CATCAGAAATTCCTGAGGTGGTCAAGAACAGAG---CAGTTCTTGGTGAATGTTGAA 39280
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      392 IeuIySerIryIeuProGlnIryValAlaGluAsnAsnIhIserIhIryIeValAsnAla 410

QY      39281 CAAATGACATGTGCAACACCT 39301
        ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      411 -----SerCysAlaIhIspPro 415

RESULT 9
US-09-902-775A-290
; Sequence 290, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Aekhenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Mather, Jennie P.

```

```

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15

US-09-396-985b-48 (1-50000) x US-09-902-775A-290 (1-1059)
QY 38390 GCCAATTTCTGCAATGCTCTTGGCAGGTATCTATAAATATCTAGAAAGATTCTTCT 38449
DB 61 AAlasnllethrlleuSerleuAlaGlyAsnArglle-----ValGluilleuPro 78
QY 38450 AAACATTTCAAA--TGSCAATCCTTATTCATTCATTGATGTCACACTTAAGCAG----- 38500
DB 79 GluhlsleuylsglupneglnSerleuGluThrleuAspleuSerSerAsnAsnilleSer 98
QY 38501 -----TTTCCAACTCTGGATCTACCTTTCTT----- 38527

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DB 99 GluleuGlnThrAlaPheProAlaLeuGlnleuLysTyrlleuTyrlleuAsnSerAsnArg 118
QY 38528 -----AAAGTTGACTTTAACT 38545
DB 119 ValThrSerMetCysGluProGlyTyrlPheAspAsnleuAlaAsnThrleuValleuLys 138
QY 38546 ATGACAAAGAGGCTATACAGTTT-----AAAAAGTGCCCTTACCAAGTCTCAGC 38596
DB 139 leuAsnArgAsnArglleSerAlaIleProProLysMetPheLysleuProGlnleuGln 158
QY 38597 TATCTAATCTTACTAGAAATGCACTGAGCTTTAGTGCTGCTGTTCTTATTCGATTG 38656
DB 159 HlsleuGlnleuAsnArgAsnLyslleLysAsnValAspGlyleuThrPheGlnGlyleu 178
QY 38657 GGACAAACAGCCGTGAGAACCTTAGACCTTACAGCTTAAAGTGCGCATT-----ATTATGAGT 38713
DB 179 Gly-----AlaLeuLysSerleuLysMetClnArgAsnGlyValThrLysleuMetAsp 196
QY 38714 GCCAATTTTCATGGCTCTAGAAAGAGCTGCAGACCTGGATTCTTTCAGCACTTACTTAAA 38773
DB 197 GlyAlaPheThrPglLysleuSerAsnMetClnleuGlnleuAspHisAsnAsnleuThr 216
QY 38774 AGGGTCACAGAAATC----- 38788
DB 217 GluileThrLysGlyTrpLeuTyrlleuLysMetleuGlnGluLeuHisleuSerGln 236
QY 38789 -----TCAGCGTTCTTATCCCTTGAAGAGTACTTTAACTT 38824
DB 237 AsnAlaIleAsnArglleSerProAspAlaTrpGluPheCysGlnLysleuSerGluLeu 256
QY 38825 GACATCTCTTAACTAAC---ACCAAAATTCAGCTTCGATGATATTTCTTGAGTTCAGC 38881
DB 257 AspLeuThrPheAsnHisleuSerArgleuAsp---AspSerSerPheleuGlyleuSer 275
QY 38882 AGTCTCAACATTAATAAATGGCTGGCAATTTCTTCAAAGCAACACCTTTCAAATGTC 38941
DB 276 leuLeuAsnThrleuHisile---GlyAsnAsnArgValSerTyrlleuAlaAspCysAla 294
QY 38942 TTTGCAACACACAACTGACATTCCTGATCTTCTTAATGTCATTAATGCAATGCAACATA 39001
DB 295 PheArgGlyleuSerSerleuLysThrleuAspLeuLysAsn-----AsnGluIle 311
QY 39002 TCTTTG-----GGGGTATTTGACACCTCTCATTGACTTCAATTATTA 39043
DB 312 SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyleuAspLysleuArgleu 331
QY 39044 AATATGAGTCACAACTATGTTGTTTGGATTCCATCCATTAAACAGCTGTATTC 39103
DB 332 lleuGlnGlnLysAsnArglleArgSerlleThrLysLysAlaPheThrGlyleuAspAla 351
QY 39104 CTGACGACTTGTGATTCAGATTTCATGCGATAGACATCTAAAGAAATPCTGCAACAT 39163
DB 352 leuGluHisleuAspLeuSerAspAsnAlaIleMetSerleuGlnGlyAsnAlaPheSer 371
QY 39164 TTTCCAAAGAGTCTTAGGCTTCTTCAATCTTACTTAAATCTGTTGATGATGGA 39223
DB 372 GlMetLysLysleuGlnGlnleuHisleuAsnThrSerSerleuLysCysAspCysGln 391
QY 39224 CATCAGAAATCTCTGACAGTGCGTCAAGAAACAGAA---CAGTTCTTGGAATGTTGAA 39280
DB 392 leuLysTrpLeuProGlnTrpValAlaGluAsnAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTCACACACT 39301
DB 411 -----SerCysAlaHisPro 415

RESULT 10
US-09-906-700-290
; Sequence 290 Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

```



```

APPLICANT: Botstrein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batou, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-700-290

Alignment Scores:
Pred. No.: 1,35e-15      Length: 1059
Score: 269.50           Matches: 101
Percent Similarity: 42.78%      Conservative: 56

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[illegible]

Qy 39224 CATCAAAATTCCTGACGTGTCAGAAACAGAG---CACTTCTGTGTAATGTGAA 39280
Db 392 LeuysrTPlreuprGlntrPrValAlaGluAsnAenPheGlnSerPheValAsnAla--- 410
Qy 39281 CAATGACATGTGCAACACT 39301
Db 411 -----SerCyAlaHisPro 415

RESULT 11
US-09-903-603A-290
Sequence 290, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: GNE.1618P2C12
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/903,603A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 290
;; LENGTH: 1059
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-903-603A-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
Gaps: 15

US-09-396-985b-48 (1-50000) x US-09-903-603A-290 (1-1059)

Qy 38390 GCGAATGTTTCTGCAATGCTCTGCGACGTGTATCTATAAATATCTAGAAGATGTTCT 38449
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Qy 38501 -----TTTCAACTCTGAGATCCCTTCTT----- 38527
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Qy 38528 ----- 38545
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Qy 38546 ATGAACAAAGGCTTATTCAGTTT-----AAAAAGTGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProLysMetPheLysLeuProGlnLeuGln 158

Qy 38597 TATCTAGATCTTGTAGAAATGACAGCTGAGCTTGTGCTGCTTCTATTCTGATTTG 38656
Db 159 HisLeuGluLeuAsnArgAsnLysIleLysAsnValAspGlyLeuThrPheGlnGlyLeu 178

Qy 38657 GGAACAAACAGCTGAGACCTTAGACCTGACCTTCAATGAGTGCATC---ATTATGAGT 38713
Db 179 Gly-----AlaLeuLysSerLeuLysMetGlnArgAsnGlyValThrLysLeuMetAsp 196

Qy 38714 GCCAATTTCAATGAGCTTAGAAAGAGCTGACAGCCTGATTTTCAGCACTTACTTTAAA 38773
Db 197 GlyAlaPheArgGlyLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnAsnLeuThr 216

Qy 38774 AGGCTCAACAATTC----- 38788
Db 217 GluIleThrLysGlyTyLeuTyGlyLeuLeuMetLeuGlnGluLysLeuSerGln 236

Qy 38789 -----TCAGCGTTCTTATCCCTTGAAGAAAGTACTTACTT 38824
Db 237 AsnAlaIleAsnArgIleSerProAspAlaThrGluPheCysGlnLysLeuSerGluLeu 256

Qy 38825 GACATCTCTTATTAATAAC--ACCAAAATTTGACTTCAGTGTATTTCTTGGCTGACC 38881
Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275

Qy 38882 AGCTCAACAATTAATAAAGCGCTGCAATTTCTTCAAAAGCAACACCTTTCAAAATGTC 38941
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Qy 38942 TTTCGAAACACAACAATTTGACATTCCTGAGATCTTCTTAATGTCAATGGAACAATA 39001
Db 295 PheArgGlyLeuSerSerLeuLysrThrLeuAspLeuLysAsn-----AsnGluIle 311

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QY 39002 TCTTGG-----GGGGTATTGACACCTCCATAGACTTCAATTATTA 39043
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QY 39104 CTCAGCACTTGTGATTCGATTTCAATCGCATAGACATCTAAAGAAATATCGCAACAT 39163
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QY 39164 TTTCGAAAGAGTCTAGGCTTCTTAATCTTAACAATTCGTGTGTTGATATGTGAA 39223
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QY 39224 CATCAGAAATTCCTCGAGTGGTCAAGAAACAGAAAG--CAGTTCTTGTAATGTGAA 39280
Db 392 LeuIleTrpLeuProGluInlTrpValAlaGluAsnAsnGluInserPheValAsnAla--- 410
QY 39281 CAAATGACATGTGCAACACCT 39301
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RESULT 12
US-09-304-920A-290
/ Sequence 290, Application US/09904920A
/ Patent No. 6806352
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi.
/ APPLICANT: Botstein, David
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OR INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/904, 920A
/ CURRENT FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143, 048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145, 698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146, 222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090

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/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 290
/ LENGTH: 1059
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-304-920A-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15

US-09-396-985B-48 (1-50000) x US-09-304-920A-290 (1-1059)
QY 38390 GCGAATGTTCTGCAATGTCCTGCGAGAGTGATCTATTAATAATCTAGAAAGTTCCT 38449
Db 61 AlaAsnIleThrLeuLeuSerLeuAlaGlyAsnArgIle-----ValGluIleLeuPro 78
QY 38450 AAACATTTCAA---TGGCAATCCTTATCAATCATAGATGATCACTTAAGCAG----- 38500
Db 79 GluIleLeuGluSerLeuGluInserLeuGluThrLeuAspLeuSerSerAsnAlaIleSer 98
QY 38501 -----TTTCCACTCTGATCTACCTTTCTT----- 38527
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QY 38528 ----- 38545
Db 119 ValThrSerMetGluProGlyIlePheAspAsnLeuAlaAsnThrLeuValLeuIle 138
QY 38546 ATGACAAAGGCTCTACAGTTT-----AAAAAGTGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnTrpAsnArgIleSerAlaIleProProIleMetPheIleuProGluInleuGln 158
QY 38597 TATCTAGATCTTGTAGAAATGCACTGAGCTTGTAGTGTGCTGTCTTATTTGATTTG 38656
Db 159 HisLeuGluLeuAsnArgIleValIleValAsnValAspIleuThrPheGluInleu 178
QY 38657 GGAACAACAGCCTGAGACACTTACAGCTTCAATGAGTGCATC---ATTAGAGT 38713
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QY 38714 GCAATTTCAATGAGTCTAGAAAGAGCTGACAGCTGATTTTTCAGCACTTACTTAAAA 38773
Db 197 GlyAlaPheTrpIleuSerAsnMetGluIleuGluInleuAspHisAsnIleuThr 216
QY 38774 AGGATCAGCAAAATTC----- 38788
Db 217 GluIleThrIleGlyTrpLeuTyArgIleLeuMetLeuGluInleuHisLeuSerGln 236

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QY 38789 -----TCAGCTTCTTATCCCTTGAAGAGCTTACTTACCTT 38824
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QY 38825 GACATCTCTTAACTAAC--ACCAAAATGACTTCGATGATATTTCTTGCTGACC 38881
Db 257 AspLeuThrPheAsnIleLeuSerArgLeuAsp--AspSerSerPheLeuGlyLeuSer 275
QY 38882 AGTCTCAACATTTAAATGGCTGGCAATCTTTCAAAAGCAACACCCCTTCAAAATGC 38941
Db 276 LeuLeuAsnThrLeuHisIle--GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294
QY 38942 TTTCGCAAAACACACAAATGACATTCCTGATCTTTCTTAATGTCATTTGACAAATA 39001
Db 295 PheArgGlyLeuSerSerLeuIleuSerLeuAspLeuIleuAsp-----AsnGlnIle 311
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QY 39224 CATGAGAAATCCGACGATGGCTCAAGAAACAGAG--CAGTCTTGCTGTAATGTTGAA 39280
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QY 39281 CAATGACATGTGCAACACCT 39301
Db 411 -----SerCysAlaHisPro 415

RESULT 13
US-09-909-064-290
Sequence 290, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909, 064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 280
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-064-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15

US-09-396-985b-48 (1-5000) x US-09-909-064-290 (1-1059)
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QY 38450 AAACATTTCAA--TGCAATCCTTATCAATCATTAAGATGTCACATTAAGCAG----- 38500
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QY 38501 -----TTTCCAACTCTGGATCTACCTTTCTT----- 38527
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QY 38528 -----AAAATTGACTTTTACT 38545
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QY 38546 ATGACAAAGAGGTCTATCAAGTTT-----AAAAAGTGCCCTTACCAAGTCTCAGC 38596
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Db 411 -----SerCysAlaHisPro 415

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APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905, 381A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-381A-290
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US-09-396-985b-48 (1-50000) x US-09-905-381A-290 (1-1059)
QY 38390 GCCAATGTTTCTGCAATGCTTCTGGGCAAGTGATCTATATAAATATCTAGAAAGATGTTCTCT 38449
    ::::::::::::::::::::
Db 61 AlaAsnIleThrLeuLeuSerLeuAlaGlyAsnArgIle-----ValGluIleLeuPro 78

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QY 38450 AACATTTCAAA---TGGCAATTCCTTATCAATCATTAAGTCACTTAAGCAG----- 38500
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QY 38501 -----TTTCCAACTGCACTTACCTCTTT----- 38527
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuLysTyrLeuTyrLeuAsnSerAsnArg 118
QY 38528 -----AAAATTGACTTAACT 38545
Db 119 ValThrSerMetGluProGlyTyrPheAsnAsnLeuAlaAsnThrLeuLeuValLeuLys 138
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Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275
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Db 276 LeuLeuAsnThrLeuHisIle---GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294
QY 38942 TTTGCAAAACACAAACTTACATCTCTGATCTTTTAATGTCATTAAGCAATA 39001
Db 295 PheArgGlyLeuSerSerLeuLysThrLeuAspLeuLysAsn-----AsnGlnIle 311
QY 39002 TCTTGG-----GGGGTATTTGACACCTCCATAGACTTCAATTTA 39043
Db 312 SerThrThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuArgLeu 331
QY 39044 AATATGAGTCAACAATCTATTTGATTCATCCCATTAATAACCACTGTATTTCC 39103
Db 332 IleLeuGlnGlyAsnArgIleArgSerIleThrLysLysAlaPheThrGlyLeuAspAla 351
QY 39104 CTCGACACTCTTATTTGAGATTTCAATGCACTTAAGCATTAAGAATCTGCAACAT 39163
Db 352 LeuGlnHisLeuAspLeuSerSerAspAsnAlaIleMetSerLeuGlnGlyAsnAlaPheSer 371
QY 39164 TTTTCAAGAGTCAAGCTTCTTCAATCTTACTTAACATTTGTTGCTGATATGAGA 39223
Db 372 GlnMetLysLysLeuGlnGlnLeuHisLeuAsnThrSerSerLeuLysCysAspCysGln 391
QY 39224 CATAGAAATTCCTGAGTGGCTCAAGAGACAGAG---CAGTTCTTGATGATTTGAA 39280
Db 392 LeuLysThrLeuProGlnTyrValAlaGluLysAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTGACACCT 39301
Db 411 -----SerCysValHisPro 415

RESULT 15
US-09-906-618-290
Sequence 290, Application US/09906618
Patent No. 6628146
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT

ORGANISM: Homo Sapien
US-09-906-618-290

US-09-906-618-290

Alignment Scores:

1.35e-15

Length: 1059

Score:

269.50

Matches: 101

Percent Similarity

42.78%

Conservative: 56

Best Local Similarity Match:

27.52%

Mismatches: 135

Query Match:
DB:

0.31%

Indels: 75

DB:

4

Gaps: 15

US-09-396-985B-48 (1-50000) x US-09-906-618-290 (1-1059)

OY	38390	GCAGATGTTCTCGTACAGTCTCTCGACGGGTGATCTATATAAAATATACGAATGCTCT	38449
Db	61	AlaasnlethrleuleuserleuAlaaglyAsnArgile-----ValGluIleuPro	78
OY	38450	AAACATTTCAAA--TGCAATCCCTATATCAATCATTAGATGTCMACTTAAGCAG-----	38500
Db	79	GluIleuLeuysGluPheGlnSerleuGluThrLeuAspLeuSerSerAsnAsnIleSer	98
OY	38501	-----TTTCCACTCGGATCTACCCCTTCTT-----	38527
Db	99	GluLeuGlnThrAlaPheProAlaLeuGlnLeuLySerIleuLyIleuAsnSerAsnArg	118
OY	38528	-----AAAAGTTGACTTTAACT	38545
Db	119	ValThrSerMetGluProGlyIlyrPheAspAsnLeuAlaAsnThrLeuLeuValLeuLys	138
OY	38546	ATGAAACAAGGCTCTATCACTTT-----AAAAAAGTGCCCTACCAAGCTCAGC	38596
Db	139	LeuAsnArgAsnArgIleSerAlaIleProProlYMetPheLySerProGlnLeuGln	158
OY	38597	TATCTAATCATCTTAGTACAAATGCACGAGCTTGTAAGTGTTGCTGTCTTATCTGATTTG	38656
Db	159	HisleuGluLeuAsnArgAsnLysIleLyAsnValAspGlyLeuThrPheGlnIlyLeu	178
OY	38657	GGAACAAACAGCCTGAGACACTTAGACCTTCAGCTTCATGTGGCCATC---ATTATAGT	38713
Db	179	Gly-----AlaLeuLysSerIleuLysMetGlnArgAsnGlyValThrLysLeuMetAsp	196
OY	38714	GCCAAATTTCATGGCTCTGAGAAGAGCTGCAGACCTCGATTTTCAGACCTCTACTTAA	38773
Db	197	GlyAlaPheTrpGlyLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnAsnLeuThr	216
OY	38774	AGGCTCACAGAAATTC-----	38788
Db	217	GluIleThrLysGlyTrpLeuLyrglyLeuLeuMetLeuGlnGlnLeuHisIleuSerGln	236
OY	38789	-----TCAGCGTTTTCATCCCTTGAAAAGCTACTTAACTT	38824
Db	237	AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheCysGlnLysLeuSerGluLeu	256
OY	38825	GACATCTCTTAATACAC--ACCAAAATGACTGTCAGTGAATATTTTGGCTGTGAC	38881
Db	257	AspLeuThrPheAsnHisIleuSerAsnArgLeuAsp--AspSerSerPheLeuGlyLeuSer	275
OY	38882	AGTCTCAACACATTAAAAATAGCTGCGCAATCTTTTCAAGACACAACCCCTTCAATGTC	38941
Db	276	LeuLeuAsnThrIleuHisIle---GlyAsnAsnArgValSerLyrlleAlaAspCysAla	294
OY	38942	TTTGCAAAACAACAACCTTGACATTCCTCGAGATCTTCTTAATGTCAATTTGGAACAATA	39001
Db	295	PheArgGlyLeuSerSerIleuLysrThrLeuAspLeuLysAsn-----AsnGluIle	311
OY	39002	TCTTGG-----GGGTATTTGACACCCCTCATGACTACTATATATTA	39043
Db	312	SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuArgIrgLeu	331
OY	39044	AATATGAGTACAAACAATCTATTTGTTTGGATTCATCCCAATTATDACCAGCTGATTC	39103
Db	332	IleLeuGlnIlyAsnArgIleArgSerIleThrLyLysAlaPhePheArgIlyLeuAspAla	351

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QY 39104 CTGACGACCTTTGATTTGCAGTTTTCATTCGCATATGAGACATCTAAAGATATCTGCACACT 39153
Db 352 LeuGluuHisLeuAspSerLeuSerAspAlaAlaIleMetSerLeuGlnGlnYAsnAlaPheSer 371
QY 39164 TTTCCAAAGAGGTAGACCTCTCTTCATATCTTAACATTCCTGTGGCTGTATATGTGA 39223
Db 372 GlnMetLysLysLeuGlnGlnLeuHisLeuAlaThrHisSerSerLeuLeuCysAspGlySerGln 391
QY 39224 CATTGAGAAATTCCTGCAGTGGGTCAAGAGCAAGAG--CAGTCTTGTTGATGTTTGA 39280
Db 392 LeuLysTrpLeuProGlnTrpValAlaGlnAlaMetPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGATGCAACACT 39301
Db 411 -----SerCysAlaHisPro 415

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Search completed: March 30, 2005, 03:08:44
Job time : 2473 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:51:33 ; Search time 542 Seconds
(without alignments)
17752.170 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
Sequence: 1 ttccacatcgcagtagtc.....catttagatatttcaga 50000

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 1133664

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODL=frame+np2.model -DEV=xlh
-Q=/cgn_1/USPTO_spool/US09396985/runat_28032005_155743_21159/app_query.fasta-1.85098
-DB=PIR_79 -QFMT=fastan -SUFFIX=trp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODS=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CNC 1.1 1364 @runat_28032005_155743_21159 -NCPV=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	765.5	0.9	1281	1 GNMSTL	retrovirus-related
C 2	732	0.8	1275	2 S21348	probable pol polyp
C 3	680.5	0.8	1281	1 GNMSTL	retrovirus-related
C 4	568.5	0.7	1273	2 S21976	probable RNA-direc
C 5	575.5	0.7	1275	2 B28096	line-1 protein ORF
C 6	573.5	0.7	1280	2 B34087	hypothetical prote
C 7	572.5	0.7	1275	2 B34087	reverse transcript
C 8	567.5	0.7	1275	2 B34087	reverse transcript
C 9	567.5	0.7	1275	2 B34087	reverse transcript
C 10	547.5	0.6	1259	4 GNMSTL	retrovirus-related
C 11	491.5	0.6	1259	4 GNMSTL	retrovirus-related
C 12	492.5	0.6	1260	4 GNMSTL	reverse transcript
C 13	487	0.6	1260	4 GNMSTL	reverse transcript
C 14	482.5	0.6	1275	2 B28096	line-1 protein ORF

15	483	0.6	1275	2	138588	reverse transcript
16	480.5	0.6	1280	2	B34087	hypothetical prote
17	473.5	0.5	712	2	S23650	retrovirus-related
18	457.5	0.5	786	2	T08664	Toll protein-like
19	453	0.5	1259	4	GNMSTL	retrovirus-related
20	445	0.5	317	2	SL0151	transforming prote
21	441.5	0.5	1260	4	GNMSTL	retrovirus-related
22	393.5	0.5	143	2	B41925	hypothetical prote
23	391	0.4	112	2	S21351	hypothetical prote
24	381	0.4	126	2	S33477	hypothetical prote
25	396	0.5	275	2	S21348	probable pol polyp
26	375	0.4	1097	2	A29943	Toll protein precu
27	372.5	0.4	392	2	S57662	hypothetical prote
28	336.5	0.4	562	2	UJ0033	hypothetical prote
29	315.5	0.4	1389	2	T13852	chaoptin precursor
30	313.5	0.4	1385	2	T13887	insulin-like growt
31	318	0.4	392	2	S57662	hypothetical prote
32	301.5	0.3	99	2	S21350	hypothetical prote
33	292	0.3	1066	2	T15864	hypothetical prote
34	270	0.3	1134	1	A29944	chaoptin precursor
35	264.5	0.3	605	2	JC5239	insulin-like growt
36	263.5	0.3	2026	1	ORF	adenylate cyclase
37	261	0.3	1143	2	T10636	hypothetical prote
38	254.5	0.3	1051	2	T13174	gp150 protein - fr
39	251.5	0.3	603	2	T24315	hypothetical prote
40	252.5	0.3	994	2	H96510	probable disease r
41	245.5	0.3	603	2	JC6128	insulin-like growt
42	251.5	0.3	1112	2	T10504	disease resistance
43	244.5	0.3	983	2	G84524	probable disease r
44	249	0.3	409	2	E86336	hypothetical prote
45	242.5	0.3	741	2	T05250	probable disease r

ALIGNMENTS

RESULT 1
GNMSTL
retrovirus-related reverse transcriptase homolog - mouse retrotransposon
N:Alternate names: LMD repetitive element ORF-2; LINE-1 hypothetical protein; ORF 3900;
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence revision 08-Jan-1999 #text change 09-Jul-2004
C:Accession: B58927; B24906; I49130; A23772; B2430
R:Obob, D.D.; Padgett, R.W.; Hardies, S.C.; Shehee, W.R.; Comer, M.B.; Edgell, M.H.; Hut
Mol. Cell. Biol. 6, 168-182, 1986
A:Title: The sequence of a large LMD element reveals a tandemly repeated 5' end and sev
A:Reference number: A93072; MUID:87064284; PMID:3023821
A:Accession: B58927
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1281 <LOE1>
A:Cross-references: UNIPROT:P11369; UNIPROT:O60713; UNIPROT:O61787; GB:M13002; NID:g2008
A:Note: sequence constructed using the first potential start codon for ORF2
A:Accession: B24906
A:Molecule type: DNA
A:Residues: 'NNQESNHNSTNOKEDSHKNR', 1-1281 <LOE2>
A:Cross-references: GB:M13002; NID:g200849
A:Note: sequence shown in Fig. 2
R:Martin, S.L.; Martin, S.L.
Gene 153, 261-266, 1995
A:Title: Characterization of a LINE-1 cDNA that originated from RNA present in ribonucle
A:Reference number: 149129; MUID:95180729; PMID:7533116
A:Accession: 149130
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-85, 'L', 87-358, 'K', 360-706, 'F', 708-735, 'A', 737-760, 'W', 762-927, 'D', 929-1281
A:Cross-references: EMBL:U15647; NID:g558906; PIDN:AAA67727.1; PID:g558908
R:Moletz, E.; Rogan, P.K.; Manuelidis, L.
Nucleic Acids Res. 14, 3119-3136, 1986
A:Title: Conservation in the 5' region of the long interspersed mouse L1 repeat: implicat
A:Reference number: A23772; MUID:86176789; PMID:3008107
A:Accession: A23772
A:Molecule type: DNA
A:Residues: 'NNQESNHNSTNOKEDSHKNR', 1-245, 'K', 247-423, 'SYTQNMKTKTKTN', 439, 'WTDTRYQS' <MO

Oy 5465 GAATATTTGAACATGTTTATGCAATCAGAGAAAGGAAATGAAACCAACCGTGAAGAAAGTG 5524
 |||||
 Db 1100 SLVYSerThrSerIleuIleIleArgGluMetGlnIleLysThrThrIleuIlePheIle 1120
 |||||
 Oy 5525 TATTCCTCGAAGTGTGTTATGAAATAATGTCCTTAAACCTAATGACCTGAGAGAGTAAATCAG 5584
 :|||
 Db 1120 SLerThrProVal-----ArgMetAla-LysIleLysAlaMetSerG 1133
 |||||
 Oy 5585 AAACATCT-----GGGAATAACACATAT----- 5610
 |||||
 Db 1133 LysPserArgCysTTPArgGlyCysGlyGluIleArgGlyThrIleuLeuHisCysTTPArg 1153
 |||||
 Oy 5611 -----TTACATATTTAAATCTGAAGAAATGAGGAATATTTTAAATTTAAATTTTAA 5662
 |||||
 Db 1153 LysCysArgLeuValGlnProIleuThrLysSerValIleArgPheIleuArg-LysLeuAsp 1172
 |||||
 Oy 5663 ATC----- 5665
 |||||
 Db 1173 IleValLeuProGluAspProAlaIleProLeuIleuGlyIleTyrProGluAspAlaPro 1192
 |||||
 Oy 5666 -----ACATGTCTATCTTA----- 5680
 |||||
 Db 1193 ThrGlyLysLysAspThrCysSerThrMetPheIleAlaIleuPheIleIleAlaArg 1212
 |||||
 Oy 5681 -----AAATGCATTAACCATACCAACCAAGCTAATGATATATTAATG 5725
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 Db 1213 SerTTPylsGluProAlaArgCysProSerThrGluIle-----TPIleGlnLysMet 1229
 |||||
 Oy 5726 TGTATATGTATACCATGATGATTTTATAGACAGAA---AAAAAGTGAATAATACAAATT 5782
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 Db 1230 TTPylIleIleTyrThrMetGluTyrTyrSerAlaIleLysLysAsnGluPheMetLysPhe 1249
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 Oy 5783 TTPAGAAATGTCATGATTTTAAATAATTAACTCAGACTGGAATTAA 5830
 |||||
 Db 1250 LeuAlaLysTTPMetAspLeuGluGlyIleIleuSerGluValThr 1265
 |||||

RESULT 4
 S21976
 probable RNA-directed DNA polymerase (EC 2.7.7.49) (clone MH2C) - rat retrotransposon L1
 N/Alternate names: reverse transcriptase
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
 C/Accession: S21976
 R/Kahre, O.; Ilves, H.; Speck, M.
 submitted to the EMBL Data Library, August 1991
 A/Reference number: S16783
 A/Accession: S21976
 A/Molecule type: mRNA
 A/Residues: 1-513 <KAH>
 A/Cross-references: UNIPROT:Q61289; EMBL:X61295; NID:956521; PIDN:CAA43593.1; PID:956522
 A/Experimental source: clone MH2C
 C/Genetics:
 A/Mobile element: retrotransposon L1
 C/Superfamily: polI polypeptide
 C/Keywords: nucleotidyltransferase; polyprotein; reverse transcriptase

Alignment Scores:
 Pred. No.: 3,44e-36 Length: 513
 Score: 568.50 Matches: 115
 Percent Similarity: 82.28% Conservative: 15
 Best Local Similarity: 72.78% Mismatches: 24
 Query Match: 0.65% Indels: 5
 DB: 2 Gaps: 2

US-09-396-985B-48 (1-50000) x S21976 (1-513)

Oy 4937 CACTTGATCTTTGACAAGAGCTAAACCATACAGTTGAAAAAGACAGCATTTTAA 4996
 |||||
 Db 356 HistenulephesapylsGlyAlaLysAlaIleGlnTTP-LysLysAspSerIlePhe 375
 |||||
 Oy 4997 CAAATGTGCTGCTCACTGTCTGTGACGATGACAAAAATGCAATTGACCATCTTT 5056
 :|||

```

Db      375  llyetirpcyetrphreaenttrpargalathrcyalarqarqmetcniileaprcyble 395
Qy      5057  ATTCCTTAGGCAAGCTCAAGTCCAACTGATCAAGAACTTCACTATAAACCAAGATAC 5116
      |||||
Db      395  userProcyerthrlyleuylserylstrpdllyeayarpneuhisllelyspProaerth 415
Qy      5117  CCTGAAATTTATTAAGAGAGAGAGAGAGAGAGGCTTGAACACATGGGCAAAAGGGGAAA 5176
      |||||
Db      415  rleuylsleuileegluglyllylsynglylshlsleuclunlsmetgylthrdglyllybav 435
Qy      5177  ATTCCTGAGCAAGAACACAGTGGC-----TTAAGATCAAGAAATCTCAAAATGGGGCCT 5229
      |||||
Db      435  nphleuenuylshtrpmetcalatyrAlaleuudrgerstrgylleasplystrparple 455
Qy      5230  CATAAATATGCAAAAGCTTCTGTAAATGCAMAGACACTGTCTCAATAGACAAAAAGGCA-- 5287
      |||||
Db      455  uilleyeuleuclnserPhecyblysalalyasPthrValalrghthrlxysarGlnpr 475
Qy      5288  -ACGATTGGGAAAAGATCTTTACCAATCTTACATCCATATGAGGGCTTAATATTCAATAT 5346
      |||||
Db      475  othrasPtpglnlysllephetrAsnProthThrxasparGlyleuileSerlysl 495
Qy      5347  ATACAAACACTCAAGAGTGAAGTTCAGTCCAGAGAACCAATACCTTTAA 5398
      |||||
Db      495  elrylsglneuleuyllyblyleuaspargalglunthrxasnpProillelys 512

RESULT 5
line-1 protein ORF2 - human
B28096
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C:Accession: B28096
A:Skowronski, J., Fanning, T.G., Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A:Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A:Reference number: A28096; MUID:88246405; PMID:2453389
A:Accession: B28096
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1275 <SKO>
A:Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:Q00363; UNIPROT:Q9Y5K0; UNIPROT:Q00366; UNIPROT:Q8TE30; UNIPROT:Q00375
C:Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 7.77e-36 Length: 1275
Score: 575.50 Matches: 110
Percent Similarity: 72.73% Conservative: 34
Best Local Similarity: 55.56% Mismatch: 53
Query Match: 0.66% Indels: 2
DB: 2 Gaps: 1

US-09-396-985B-48 (1-50000) x B28096 (1-1275)
Qy      36378  ATTGAAAATGGGGGTACGAACATTAAGAAGAAATTCACACTGAGAAATCTGATGACT 36319
      |||||
Db      1069  lleyllystrpalalyasPmetcAsnArghslshPserlysgluasplleetyAlala 1088
Qy      36318  GAAAGATCCCTTAATAAAATGTTTAAACATCCCTTAAGCATCAGAGAAATGCAATCAAAACA 36259
      |||||
Db      1089  llysllyshlsmecllyblylcyserseerleualatlelavgglumeglnllelystr 1108
Qy      36258  ACCCGATATTCCTCACTTCCACACAGTCAGATGACTAAGATCAAAATCTCAAGTGACGC 36199
      |||||
Db      1109  ThreMetarGlyrlyleuethrProValarqmetcalatlellelyblyseGlyAsnAsn 1128
Qy      36198  AGATGCTTGGCAGA--TGTAAGAAAGAGAAACACTTTTCAATCTGTGGCAGAACTGTAA 36140
      |||||
Db      1129  ArgcysrtparGlylcyGglunlleglythrleuethlsCystrtparPcyblyls 1148
Qy      36139  CTGATATTAACAACCTTGGAAATCAGTTGGTGCTCTCGAATAATGGACATGGTACTA 36080
      |||||
Db      1149  leuValglnprleuethrlylseserValtrpArqPheleuAspaleuclnleuGlnle 1168

```

[illegible]

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Db 1194 TyrlysaapThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIyethrTrrp 1213
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1214 AenGlnProLysCysProMetIleAspTrpIleLysMetTrrpHisIleTrrp 1228
Oy 35902 GTGAGTACTATGACGCTATTAAAAACAGTGAATCTATGACATCTTACGCAAAATGAATG 35843
Db 1224 MetGlnTrrpTrrpAlaIleIleLysAsnAspGlnPheMetSerPheValGlyThrTrrpMet 1253
Oy 35842 GACCTGAGGCGATCATCTGATGAGGTAAACCCAGTCATATAAAGACACATGATATG 35783
Db 1254 LysLeuGlnTrrpIleIleLeuSerLysLeuSerGlnGlnGlnLysThrLysHisArgMet 1273
Oy 35782 CACTTAATCTG 35771
Db 1274 PheSerLeuIle 1277

RESULT 7
138588
reverse transcriptase homolog - human retrotransposon L1
N/Alternate names: ORF2 protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: J38588
R/Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
A/Title: A new retrotransposable human L1 element from the LINE2 locus on chromosome 1q
A/Reference number: J38587; MUID:95004577; PMID:7920631
A/Accession: J38588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:g483914; PIDN:AAB60345.1; PID:g4839
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 1 356-35 Length: 1275
Score: 572.50 Matches: 109
Percent Similarity: 72.73% Conservative: 35
Best Local Similarity: 55.05% Mismatches: 53
Query Match: 0.66% Indels: 2
Gaps: 1

US-09-396-985b-48 (1-50000) x J38588 (1-1275)
Oy 36378 ATTGAAAATGGGGTACAGAACTAAAGAAATTCACACTGAGAACTGATGACT 36319
Db 1069 IleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGlnAspIleTrrpAlaAla 1088
Oy 36318 GAAAGTACTAAAAAATGTTTAAATCTTACTGATCAGGGAATGCAATCAAAACA 36259
Db 1089 LysLysHisMetLysLysCysSerSerSerLeuAlaIleArgLysMetGlnIleLysThr 1108
Oy 36258 ACCCTGATATTCCTTCAACACCGTCGATGATGATCAAAATCAAGTACAGC 36199
Db 1109 ThrMetArgTrrpHisLeuThrProValArgMetAlaIleLysLysSerGlyAsnAsn 1128
Oy 36198 AGATGCTCGCAAGA-TGTAGAGAAAGAGAAACACTCTTCATTTGCTGCGAAGCTGTAA 36140
Db 1129 ArgCysTrpArgGlyCysGlyGlnIleLysThrLeuLeuHisCysTrpTrrpAspCysLys 1148
Oy 36139 CTGATATAACCACTCTGGAATATCAGTTGTGTTCTCTCAGAAAATTGACATGCTACTA 36080
Db 1149 LeuValGlnProLeuTrrpLysSerValTrrpArgPheLeuArgAspLeuGlnLeuGlnIle 1168
Oy 36079 CCTGAGATCCAGCAATACCACTCCAAAGCAAAATTCAGATGAT---GCTTACCTTGT 36023
Db 1169 ProPheAspProAlaIleProLeuLeuGlnIleTrrpProGlnAspTrrpLysSerCysLys 1188
Oy 36022 AATAAGACACATGCTCTACTACTGTTTCAATACAGTTTATTATTAATAGCCAGATGCTTG 35963
Db 1209 AsnGlnProLysCysProThrMetIleAspTrpIleLysLysMetTrrpHisIleTrrp 1228
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Db 1189 TyrlysaapThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIyethrTrrp 1208
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1209 AenGlnProLysCysProMetIleAspTrpIleLysMetTrrpHisIleTrrp 1228
Oy 35902 GTGAGTACTATGACGCTATTAAAAACAGTGAATCTATGACATCTTACGCAAAATGAATG 35843
Db 1229 MetGlnTrrpTrrpAlaIleIleLysAsnAspGlnPheMetSerPheValGlyThrTrrpMet 1248
Oy 35842 GACCTGAGGCGATCATCTGATGAGGTAAACCCAGTCATATAAAGACACAT 35789
Db 1249 LysLeuGlnTrrpIleIleLeuSerLysLeuSerGlnGlnGlnLysThrLysHis 1266

RESULT 8
S65824
reverse transcriptase homolog - human transposon L1.1
C/Species: Homo sapiens (man)
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S65824
R/Dombroski, B.A.
submitted to the EMBL Data Library, January 1992
A/Description: Isolation of an active human transposable element.
A/Reference number: S65823
A/Accession: S65824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1275 <DOM>
A/Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AA51622.1; PID:g3397
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 3 376-35 Length: 1275
Score: 567.50 Matches: 108
Percent Similarity: 72.73% Conservative: 36
Best Local Similarity: 54.55% Mismatches: 53
Query Match: 0.65% Indels: 2
Gaps: 1

US-09-396-985b-48 (1-50000) x S65824 (1-1275)
Oy 36378 ATTGAAAATGGGGTACAGAACTAAAGAAATTCACACTGAGAACTGATGACT 36319
Db 1069 IleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGlnAspIleTrrpAlaAla 1088
Oy 36318 GAAAGTACTAAAAAATGTTTAAATCTTACTGATCAGGGAATGCAATCAAAACA 36259
Db 1089 LysLysHisMetLysLysCysSerSerSerLeuAlaIleArgLysMetGlnIleLysThr 1108
Oy 36258 ACCCTGATATTCCTTCAACACCGTCGATGATGATCAAAATCAAGTACAGC 36199
Db 1109 ThrMetArgTrrpHisLeuThrProValArgMetAlaIleLysLysSerGlyAsnAsn 1128
Oy 36198 AGATGCTCGCAAGA-TGTAGAGAAAGAGAAACACTCTTCATTTGCTGCGAAGCTGTAA 36140
Db 1129 ArgCysTrpArgGlyCysGlyGlnIleLysThrLeuLeuHisCysTrpTrrpAspCysLys 1148
Oy 36139 CTGATATAACCACTCTGGAATATCAGTTGTGTTCTCTCAGAAAATTGACATGCTACTA 36080
Db 1149 LeuValGlnProLeuTrrpLysSerValTrrpArgPheLeuArgAspLeuGlnLeuGlnIle 1168
Oy 36079 CCTGAGATCCAGCAATACCACTCCAAAGCAAAATTCAGATGAT---GCTTACCTTGT 36023
Db 1169 ProPheAspProAlaIleProLeuLeuGlnIleTrrpProGlnAspTrrpLysSerCysLys 1188
Oy 36022 AATAAGACACATGCTCTACTACTGTTTCAATACAGTTTATTATTAATAGCCAGATGCTTG 35963
Db 1189 TyrlysaapThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIyethrTrrp 1208
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1209 AsnGlnProLysCysProThrMetIleAspTrpIleLysLysMetTrrpHisIleTrrp 1228
```

QY GTGGAGGACATAGAGTATTAAAAACAGGAATCTATAGACATCTTAGGCAAAATGAAAG 35843
35802
Db MetcLuryrYrYzaaAaAaIeYvshnaSpolpheiIseerhneValdIyhrTrpEc 1248
1229
QY GACCTGGAGGSCATCATCTCTGAGTGAAGTAACCAAGTCATATAAAGAAACACAT 35789
35842
Db LysLeuLthrTrIeIleuSeuLysLeuSeuGlnuGlnLysThrIyShs 1266
1249

RESULT 9

S23650
S23650
retrovirus-related hypothetical protein II - human retrotransposon LINE-1
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S23650
R:Hohjoh, H.; Minakami, R.; Sakaki, Y.
Nucleic Acids Res. 18, 4099-4104, 1990
A:Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences which
A:Reference number: S23649; MUID:90332398; PMID:2165587
A:Accession: S23650
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-712 <HCH>
A:Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:Q00363; UNIPROT:Q14754; UNIPROT:Q91YK0; UNIPROT:Q00366; UNIPROT:Q6T830; UNIPROT:Q00375; EMBL:X52233
Note: the nucleotide sequence was submitted to the EMBL Data library, March 1990

Alignment Scores:

Pred. No.:	5,54e-35	length:	712
Score:	563.50	Matches:	109
Percent Similarity:	71.72%	Conservative:	31
Best local Similarity:	55.05%	Mismatches:	55
Query Match:	0.65%	Indels:	2
DB:	2	Gaps:	1

US-09-396-985B-48 (1-50000) x S23650 (1-712)

QY	36378	ATTGAAAAATGGGGATCAAGAACTAAAGAAGAAATTTCTACTAGAGAAATACTGAATGACT	36319
Db	506	l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	525
QY	36318	GAAGAAGTCTPAAAAAAATGTTTAAACATCTCTTAGCATCAGAGAAATGCAATCAAAACA	36259
Db	526	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	545
QY	36258	ACCCTGATATTTCCACTTCAACACCGTCAGATGAAATGACTAAATCAAAACTCAAGTCACAGC	36199
Db	546	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	565
QY	36198	AGATGCTGCACAGA-TGTAGAAGAGAGAAACACTCTTCATTTGCTGCACAGACGTGAAA	36140
Db	566	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	585
QY	36139	CTGATATTAACAACCTCTGGAATTCAGTTTGATGGTTCCTCAGAAAAATTGACATGGTACTA	36080
Db	586	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	605
QY	36079	CCTGAGATTCAGCAAAATCCACTCCAGGCAAAATTCAGATGATGCT--TCACTTGT	36023
Db	606	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	625
QY	36022	AATAGACACATGCTCTACTACTATGTTTCATAGCAGTTTATTTATATATACGACATGCTTG	35963
Db	626	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	645
QY	35962	AAAGAACCTTAATGTCTCTCAACAGAGAAATGGAATCAAAAAAATATGTAATTTGGACA	35903
Db	646	l l l l l s t t p a l a l y a s p e t a n a r g h s p e s e r l y s g u a s p l e t y t a a l a	665
QY	35902	GTGAGTACTATGACGATTTAAAAACAGTGAATCTATGACATTTCTTGAGCAAAATGAAATG	35843

[illegible]

RESULT 10

GNHUU1
retrovirus-related reverse transcriptase pseudogene - human
C|Species: Homo sapiens (man)
C|Date: 31-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
C|Accession: A25313
R|Hattori, M.; Kubara, S.; Takenaka, O.; Sakaki, Y.
N|ature 321, 625-628, 1986
A|Title: Ll family of repetitive DNA sequences in primates may be derived from a sequence
A|Reference number: A93381; MUID:86230917; PMID:2423883
A|Accession: A25313
A|Status: conceptual translation of pseudogene
A|Molecule type: DNA
A|Residues: 1-1259 <HAT>
A|Cross-references: UNIPROT:P08547
A|Note: this sequence was constructed from an alignment of published and unpublished seq
C|Keywords: reverse transcriptase; pseudogene

Alignment Scores:

Pred. No.:	1,1e-33	Length:	1259
Score:	547.50	Matches:	106
Percent Similarity:	72.40%	Conservative:	32
Best local Similarity:	55.21%	Mismatches:	52
Query Match:	0.63%	Indels:	2
DB:	4	Gaps:	1

US-09-396-985B-48 (1-50000) X GNHUL1 (1-1259)

[illegible]

Db 1248 LysleuGIuThrllelleLeuSerlyLeuSerGln 1259

RESULT 11

156258 mouse

RPI05 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56258

R:Myake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.

J. Immunol. 154, 3333-3340, 1995

A:Title: RPI05, a novel B cell surface molecule implicated in B cell activation, is a me

A:Reference number: I56258; MUID:95204928; PMID:7897216

A:Accession: I56258

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-661 <RES>

A:Cross-references: UNIPROT:Q62192; GB:DJ37797; NID:9761711; PIDN:BAA07043.1; PID:9761712

Alignment Scores:

Pred. No.:	4,74e-30	Length:	661
Score:	491.50	Matches:	155
Percent Similarity:	44.48%	Conservative:	115
Best Local Similarity:	25.54%	Mismatches:	288
Query Match:	0.57%	Indels:	49
DB:	2	Gaps:	15

US-09-396-985b-48 (1-50000) x I56258 (1-661)

QY 37706 ATATTGGTATCTCTTTGGCCAT-----AGGTGTAATTTGAAACATTTGAAACAG 37759

Db 76 LeuIleAsnLeuThrlPheLeuAspLeuThrlArgCysGlnIleYrYrIleIleGluAsp 95

QY 37760 GCATGGCATGGCTTACACACCTGCAAACTGTACAGACAGAAACCTTACAGAGT 37819

Db 96 ThrlheGlnSerGlnHisArgLeuAspThrlLeuValLeuThrIleAsnProLeuIlePhe 115

QY 37820 TTTTCCCGAGAGAGTTCTCTGCACTAACAGTTTGAAGATCTGTGGCTGTGGAGACA 37879

Db 116 MetIleGluThrlAlaLeuSerGlyProlysalLeuIleuHisLeuPheIleGlnThr 135

QY 37880 AAATTGGCCTCTTGAAGAAAGCTTCCCTATTTGACAGCTTATTAACCTTAAAGAACTCAAT 37939

Db 136 GlyIleSerSerIleAspPheIleProleuHisAsnGlnIleuThrlLeuGlnSerLeuIlyr 155

QY 37940 GTGGCTCAACATTTTATATACATCTCTGTAAGTTACCTGATATTTTCCAACTTACAGAC 37999

Db 156 LeuGlySerAsnHisIleSerSerIleLeuLeuProlysglyPheProth--GluIys 174

QY 38000 CTAGTACATGTGATCTTTCTTATATATATATCAAACTATTAAGTACAGACTTACAG 38059

Db 175 LeuIleValLeuAspPheGlnAsnAsnAlaIleHisIleuSerIlyGluAspMetSer 194

QY 38060 TTTTCTAGTGAAGAAATCCCAAGTCAATCTCTTTAGACATGTCTTTGAACCCATTTGAC 38119

Db 195 SerIleuGlnGln-----AlaThrAsnLeuSerLeuAsnGlnIlyAsnAspIleAla 212

QY 38120 TTCAATTAAGACCAAGCCTTTACAGGAATTAAGTCCATGACATGACCTTAAGAGTAAAT 38179

Db 213 GlyIleLeuProGlyAlaPheAspSerAlaValPheGlnSerLeu-----Asn 228

QY 38180 TTTTAATAGCTCAATATATATGAAGAAATTTGCTTCAAACTGTGGCTTATACAGTCCAT 38239

Db 229 PheIleGlyIleThrlGlnAsnLeuValIlePheIleGlyLeuIlysaAsnSerThrlIleGln 246

QY 38240 CCGTTGATCTTTGGAGAAATTTAAAGATGAAGAAATCTGCAAAATTTTGAACCTCTATC 38299

Db 249 SerIleuThrlPheGlnIlyThrlPheGlnAspMetAspAspGluAspIle-----SerProAlaVal 267

QY 38300 ATGGAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38359

Db 268 PheGlnIleuIlyCysGlnMetSerValGlnSerIleAsnLeuGlnIlyHisIleYrPhePhe 287

QY 38360 TCAGATGATATTTGTAAGTTCCATGCTGTGGCAATGTTTCTGCAATGTCTCTGGCAGGT 38419

Db 288 AsnIleSerSerAsnThrlPheHisCysPheSerGlyLeuGlnIleuAspLeuThrlAla 307

QY 38420 GTATCTATAAAATCTTGAAGATGTTCTTAAACATTTTC----- 38458

Db 308 Thr-----HisLeuSerGlnLeuProSerGlyLeuValGlyLeuSerThrlLeuIys 324

QY 38459 -----AAATGGCAATCTTATCAATCATATGATGCAACTT--- 38494

Db 325 LysLeuValLeuSerAlaAsnIlyPheGluAsnLeu-----CysGlnIleSer 340

QY 38495 ---AAGAGTTTCCAACTGTGATCTAACCTTTTAAAGTTGACTTAACTTAAGAC 38551

Db 341 AlaserAsnPheProSerLeuThrlHisLeuSerIleIlysglyAsnThrlYrArgLeuGlu 360

QY 38552 AAAGGCTCTACGTTTAAAAAGTGCCCTTACCAAGTCTCAGACTATCTGATCTTAACT 38611

Db 361 LeuIlyThrlGlyCysLeuGluAsn-----LeuGluAsnLeuArgGluLeuAspLeuSer 378

QY 38612 AGAATGCACTGACCTTAAAGTGTGCTGTCTTATTTCTGATTTGGGAAACAAAGCCTG 38671

Db 379 HisAspAspIleGluThrlPheSerCysCysAsnLeuGlnLeuArgAsnLeuSerHisLeu 398

QY 38672 AGACACTTGAACCTCAGCTTCAATGATGACATTAATGAGTGCCAAAT--TTCAATGGGT 38728

Db 399 GlnSerLeuAsnLeuSerIlyYrAsnGluProLeuSerLeuIlyThrlAlaPheIlyGlu 418

QY 38729 CTAGAAGCTGCGACGACCTGATTTTACAGACTCTTATTAAGAGGTGACAGAACTTC 38788

Db 419 CysProGlnLeuGlnIleuLeuAspLeuAlaPheThrlArgLeuValIlyAspAlaGln 438

QY 38789 TCAGCGTTTCTTATCCCTTGAAGAGTCTTAACTTACATCTCTTATTAACACCAAA 38848

Db 439 SerProPheGlnAsnIleuHisIleuIlyValLeuAsnLeuSerHisIleuLeuAsp 458

QY 38849 ATTGACTTGAAGTATATTTCTTGGCTTGAACAGCTTCAACATTAATAAATGCTGTGC 38908

Db 459 IleSerSerGlnIleuPheAspGlyLeuProAlaLeuGlnHisIleuAsnLeuGlnIly 478

QY 38909 AATTCTTTCAAAAGCAACACCCCTT-----TCAATGTCTTTGCAACACAAACACTTG 38962

Db 479 AsnHisPheProIlysglyAsnIleGlnIlySerHisIleuGlnIlyArgLeu 498

QY 38963 ACATCTCGATCTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39022

Db 499 GluIleLeuValLeuSerPheCysAspLeuSerSerIleAspGlnHisAlaPheThrlSer 518

QY 39023 CTCATAGACTCAATATTAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 39076

Db 519 LeuIlyMetMetAsnHisValAspLeuSerHisAsnArgLeuThrlSerSerIleGlu 538

QY 39077 ---TCATCCATTAATACACAGCTGATTCCTCAGACACTTGTGATTCAGTTCAATGCC 39133

Db 539 AlaLeuSerHisIleuIlysglyIleYr-----LeuAsnLeuAlaSerAsnHis 554

QY 39134 ATAGAGACATCTAAAGAAATATGCAAACTTTTCCAAAGGTGAGCTTCTTCAATCTT 39193

Db 555 IleSerIleIleLeuProSerLeuLeuProIleuSerGlnGlnIlyThrlIleAsnLeu 574

QY 39194 ACTTAACATCTGTGTCTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 39253

Db 575 ArgGlnAsnProLeuAspCysThrlPheSerAsnIleYrPheLeuGluIlyPryIlyGlu 594

QY 39254 CAGAAGCAGTTCTTGGATGATTTGAACAAATGATGATGATGATGATGATGATGATGATGAT 39313

Db 595 AsnMetGlnIlyLeuGluAspThrlGluAspThrlLeuIlysglyAsnProProLeuLeuArg 614

QY 39314 -----ACCTCTTAAGTGTGATTTTAATATCTTACCTGTATATGATGATGATGATGAT 39361

Db 615 GlyValArgLeuSerAspValThrlLeuSerCysSerMetCysAlaValGlyIlePhePhe 634

QY 39362 ACAATCATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39421

Db 635 leu1eValpheu1eValphe1a1le1eu1eU1eph1eal1aVal1yStYrPhe1eu 654
 QY 39422 TACCACTTCTATTTCACCTG 39442
 Db 655 ArgTrp1yStYrGlnHis1le 661

RESULT 12
 S65824
 Reverse transcriptase homolog - human transposon Ll.1
 C/Species: Homo sapiens (man)
 C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S65824
 R/Dombroski, B.A.
 Submitted to the EMBL Data Library, January 1992
 A/Description: Isolation of an active human transposable element.
 A/Reference number: S65823
 A/Accession: S65824
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1275 <DOM>
 A/Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:G339767; PIDN:AAA51622.1; PID:G3397
 C/Superfamily: pol polypotein

Alignment Scores:
 Pred. No.: 1.66e-29 Length: 1275
 Score: 492.50 Matches: 153
 Percent Similarity: 48.20% Conservative: 74
 Best Local Similarity: 32.48% Mismatches: 141
 Query Match: 0.57% Indels: 106
 Gaps: 15

US-09-396-985b-48 (1-50000) x S65824 (1-1275)

QY 4711 AAAATTAAACAATTATTTGTCAGTCAATTAGTAAAGTAATATAGCTTTTTCAC--- 4767
 Db 831 LysLeuProMetThrPhePheThrGlnLeuGlnLysThrThrLeuLysPhe1leTrpAsn 850
 QY 4768 -----ATTTTCCTTAAGTCAGT----- 4785
 Db 851 GlnLysArgAlaAg1leAlaLysSer1leLeuSerGlnLysAsnLysAlaGlyGly1le 870
 QY 4786 -----CCTTAGATTTTCTTAAGTACAAATTTGATAGATCTTAAGCTTTGTTTCTTTT 4839
 Db 871 ThrLeuProAspPheLysLeuLysTrpLysAlaThrValThrLysThrAlaTrpLysTrp 890
 QY 4840 CAAAGCAATTGACAAATATTTTGAACCTGGAGAAAGAGATGCTTTGTTACTCAGGT 4899
 Db 891 TyrGlnAsn-----ArgAsp1leAspGlnTrpAsnArg----- 901
 QY 4900 TAAATGCTGACAGTGAAGTCTTAATTCATGTCATC---CACTTGATCTTTGACAAAG 4956
 Db 902 ---ThrgLuproSerGln1leMetPro-His1leTyrAsnTrpLeu1lePheAspLysPr 920
 QY 4957 AGCTAAACCATACAGTTGAAAAAAGACAGCATTTTAAACAAATGGTGTGCTCAACT 5016
 Db 920 GGLuLysAsnLysGlnTrp-GlyLysAspSerLeuPheAsnLysTrpCystrpGlnAsn 940
 QY 5017 GTCTGTGAGCATGTACAAAAATGCAATTCACCATTTTATCTTCCTTAGCAAGCAAGCTCA 5076
 Db 940 TrpLeuAla1leCystrArgLysLeuLysLeuAspProPheLeuThrProLysThrLys1leA 960
 QY 5077 AGTCAAGTGTAGTCAAGACCTCTACATAAACAGATACCTGAAATTTTAAAGAGGA 5136
 Db 960 snSerArgTrp1leLysAspLeuAsnValLysProLysThr1leLysThrLeuGlnGluA 980
 QY 5137 GAGTGGAGAGAGAGGCTTGACACATGGGCAAGGGGAAAAATTCCTGACGAGAACACCA- 5195
 Db 980 snLeuGly1leThr1leGlnAsp1leGlyValGlyLysAspPheMetSerLysThrProL 1000
 QY 5196 -----GTGGCTTA-AGATCAAGATCTACAAATGGGGCTCATTAATTTGCAAAAGCTTTCT 5249
 Db 1000 ysa1aMetAlaThrLysAspLys1leAspLysTrpAspLeu1leLysLeuLysSerPheC 1020

QY 5250 GTAATGCAAGAGCACTGTCATAGGACAAAGGCA---ACAGATTGGGAAAGATCT 5306
 Db 1020 ysrThrAlaLysGlnTrpThr1leArgValAsnArgGlnProThrTrpGlnLys1leB 1040
 QY 5307 TTACCAATCTACATTCATAGAGGCTAATATTCAATTATTTACAAACCACTTAAGAG 5366
 Db 1040 hea1aThrYsrSerSerAspLysGlyLeu1leSerArg1leTyrAsnGlnLeuLysGln 1060
 QY 5367 TAGACTCCAGAACCAATTAACCTATTAA--AAATGGGGTAC--AAGCTAAACAAAGAA 5424
 Db 1060 1eTyrLysLysLysTrpAsnAsnPro1leLysLysTrpAlaLysAspMetAsnArgHis 1080
 QY 5425 TTTCAGCTGAGGAATATTGAATGGCCAGAAATCACCTAAAGAAATATGACATTGTAG 5484
 Db 1080 heserLysGlnAsp1leTyrAla1leLysLysHisMetLysLysCyserSerSerLeuA 1100
 QY 5485 TCATCAGGGAATATGCAATTCAAACCAACCTGAGAAAGTATCTCTGAAGT----- 5537
 Db 1100 1a1leArgGlnMetGln1leLysThrThrMetArgTrpHisLeuThrProValArgMet 1120
 QY 5538 --TTATTAATAATGTCCTTAAACCTAATGACCTGAGAGAGTAATACAGAAACATCTGGG 5595
 Db 1120 1a1le1leLysLysSerGlyAsn-----AsnArgCystrpArgGly-CysGly 1135
 QY 5596 GAAATACCAACATAT-----TTACTATTTAATAACTGAG 5631
 Db 1136 Gln1leGlyThrLeuLeuHisCystrTrpAspCyLysLeuValGlnProLeuTrpLys 1155
 QY 5632 AAAATGCAATATTTTAATTTAATTTTAAATC----- 5665
 Db 1156 SerValTrpArgPheLeuArg-AspLeuGlnLeuGln1leProPheAspProAla1lePr 1175
 QY 5665 ----- 5665
 Db 1175 oLeuLeuGly1leTyrProAsnGlnLysSerCyserLysLysAspThrCystrHar 1195
 QY 5666 -----ACCAGTCTAATCTTAATGTCATTA 5691
 Db 1195 gmetPhe1leAla1leuPheThr1leAlaLysThrTrpAsnGlnProLysCysProth 1215
 QY 5692 AACTATCACCAAGGCTAATGATTAATAAAGTGTATATGATATACCTAGATTTTA 5751
 Db 1215 rmet1leAsp-----Trp1leLysLysMetTrpHis1leTyrThrMetGlnLysTrp 1232
 QY 5752 GACAGAA---AAAAAAGTGAATATACAAATTTTGAAGATGATGATTTAAAAA 5808
 Db 1232 rAlaAla1leLysAsnAspGlnPhe1leSerPheValGlyThrTrpMetLysLeuGln 1252
 QY 5809 TTATCTCAGACTGGAATTAACAATAATTTCAAGACTGACCAATAGTCTTATTCAGAA 5868
 Db 1252 r1le1le-----LeuSerLysLeuSerGlnGlu-----GlnLys 1263
 QY 5869 GACAAATCTATATATATATATCTC 5893
 Db 1263 strLysHisArg1lePheSerLeu 1271

RESULT 13
 GNRRL1
 retrovirus-related reverse transcriptase pseudogene - slow loris
 C/Species: Nycticebus coucang (slow loris)
 C/Date: 31-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
 C/Accession: B25313
 R/Hatori, M.; Kuhara, S.; Takenaka, O.; Sakaki, Y.
 Nature 321, 625-628, 1986
 A/Title: Ll family of repetitive DNA sequences in primates may be derived from a sequence
 A/Reference number: A9381; M01D:86230917; PMID:2423883
 A/Accession: B25313
 A/Status: conceptual translation of pseudogene
 A/Molecule type: DNA
 A/Residues: 1-1260 <HAT>
 A/Cross-references: UNIPROT:P08548
 A/Note: this sequence was constructed from an alignment of six sequences, determined by r
 C/Keywords: reverse transcriptase; pseudogene

Alignment Scores:

Pred. No.: 7,18e-29 Length: 1260
 Score: 487.00 Matches: 99
 Percent Similarity: 65.28% Conservative: 27
 Best Local Similarity: 51.30% Mismatches: 65
 Query Match: 0.56% Indels: 3
 Gaps: 2

US-09-396-985b-48 (1-50000) x GNLRL1 (1-1260)

QY 36378 ATTGAAAATGGGGTACGAACTAAAGAAATTTCTCACTGAGGAATTAAGTAACT 36319
 Db 1068 Tlserglttptalaaargspdeuylsarganpheserlysgluasparghistrille 1087
 QY 36318 GAAAGTACCTAAATAATGTTTAACTCTTACATCAGCAGAAATCAATCAATCAATCA 36259
 Db 1088 Tyrlvshsmetylserserserserleulleargglumecghilleysthr 1107
 QY 36258 ACCCTGATATTCACCTTCACAGCAGTCAAGTCAATGATCAATCAATCAATGACAGC 36199
 Db 1108 ThrlenuaglytrhlsleuthProvalargvalaahlslethrlyseserProhsegin 1127
 QY 36198 AGATGCTGCAGAA-TGTAGAGAGAGAGAACTCTTTCATTCCTGTCGAGAACTGTAAA 36140
 Db 1128 Argcystpargglycysglygllylsglythrlenuelhscystptptgltucyspro 1147
 QY 36139 CTGATATTAACCACTCTGGAATCACTGTGTGCTTCCTCAGAAATTTGACATGTA 36080
 Db 1148 Leulleargserphetppllyasprvaltrparglleuargapdeulleysleasprle 1167
 QY 36079 CCTGAGATCCAGCAATACCACTCCAGCAATATTCAGATGAT--GCTTCACTCTGT 36023
 Db 1168 ProheasprcoilleleleProleuenciyleuthrProgluabpghllyserglntyr 1187
 QY 36022 AATAAGACACACTCTCTACTATGTTCATACAGTTTATTTATTAATGACAGATGCTTG 35963
 Db 1188 AsnlyasprllecysttharMetPheillelaahlnpheillelaialyserttrp 1207
 QY 35962 AAAAAGCTAGATCCCTCCTCAAGAGAAATGATACAAATATGTTACATTTGCACA 35903
 Db 1208 LyslyspPolysCysProserThrhisgluttrpThrSerlyleuthrlypMettyrthr 1227
 QY 35902 GTGAGTACTATGAGTATTAATAAACAAGTAACTATGACA--TTCTTAGGCAATGA 35846
 Db 1228 MetgluttrpTyrAlaAlaLeuylsaspolyasprphetrSerPheMetPheThrtrp 1247
 QY 35845 ATGAGACCTGAGGAGCATCTGAGTGAAGTAAACCCAG 35807
 Db 1248 MetgluLeuGluHilelleLeuSerlyValSerGln 1260

RESULT 14

B28096 line-1 protein ORF2 - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Nov-1998 #sequence_revision 03-Nov-1998 #text_change 09-Jul-2004
 R/Accession: B28096
 R/SKOWRONSKI, J.; Fanning, T.G.; Singer, M.F.
 Mol. Cell. Biol. 8, 1385-1397, 1988
 A/Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
 A/Reference number: A28096; MUID:88246405; PMID:2454389
 A/Accession: B28096
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-1275 <SKO>
 A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:Q00363; UNIPROT:Q9Y5K0; UNIPROT:Q00366; UNIPROT:Q8TE30; UNIPROT:Q00375
 C/Superfamily: pol polyprotein

Alignment Scores: 1.04e-28 Length: 1275
 Score: 482.50 Matches: 134
 Percent Similarity: 52.25% Conservative: 63

Best Local Similarity: 35.54% Mismatches: 106
 Query Match: 0.56% Indels: 77
 Gaps: 10

US-09-396-985b-48 (1-50000) x B28096 (1-1275)

QY 4937 CACTTGATCTTTGACAAAGAGCTAAACCATACAGTTGAAAAAGACACATTTTAA 4996
 Db 914 TyrlleulepheasprlyserProglulysasnlysglnttrp-gllyasprserleuPheas 933
 QY 4997 CAATGTCGTGCTCAATCTCTGTCAAGATGTCACAAATGCAATGCAATGCAATGCTT 5056
 Db 933 nlystrpCysstrpplubsntrpleuallileCysarglyleuylsvalasprProPhe 953
 QY 5057 ATTCCTTAGGCAAGAGCTCAAGTGCATGAGATGATGATGATGATGATGATGATGATGAT 5116
 Db 953 utrProtyrThrlyslleasnserllystrpLysaspdeuasnvalasprProPhe 973
 QY 5117 CCTGAAATTTATTAAGAGAGAGTGAAGAGAGAGCTTGAACATGAGGCAAGGAGAAA 5176
 Db 973 TllelythrleuenglulsnleuyllethrTlleghlnasprllegllyValgllyas 993
 QY 5177 ATTCCTGAGCAACACCA-----GTGGCTTA-AGATCAAGATTCACAAATGGGCTT 5229
 Db 993 pPheMetSerlyserThrProlysalametalathlysalaleysleasprlystrpPhe 1013
 QY 5230 CATTAATTTGCAAGCTTCGTGTAATGCAAGAGACAGTGCATCAATGCAAGAGCAAA 5287
 Db 1013 uilleyleuylserPheCysThrAlalyglutThrTlleargvalasndarglnpr 1033
 QY 5288 -ACAGATTTGCAAGAGATCTTTACCAATCTTACATCCATGAGAGGCTAATTTCAATAT 5346
 Db 1033 othrThrtrpGluThrlePheThrThrlyrserSerAsprlysglyleuileserArgil 1053
 QY 5347 ATACAAACAACTCAAGAGATTTAGACTCCAGAGAAACAAATTAACCTTATTA-AAATGGGG 5405
 Db 1053 elyAsnGluLeuylsGlnlelyrlysllystrPheAsnProillelysllystrpAl 1073
 QY 5406 TAC-AGCTAAACAAAGATTTTCAGCTGAGGAATTTGAATGAGCCAGAAATCCCTAAA 5464
 Db 1073 alysaspMetAsnarghlsPheSerlysgluasprlletyrAlaAlalyshsmely 1093
 QY 5465 GAAATATTTGACATTTAGTATCATCAGGAGAAATCAATCAACAAACCTGAGAAATG 5524
 Db 1093 elysCysSerSerleuallileargglumecghilleysthrThrMetAlglyrhi 1113
 QY 5525 TATTCCTGAAGTG-----TTATAAAATGGCTCTTAACCTTAATGACCTGAGAGA 5575
 Db 1113 sleuthrProvalargMetAlallellelysllyserGlyasn-----AsnAr 1129
 QY 5576 GTATACGAAACATCTGGGGAATTAACACATAT-----T 5611
 Db 1129 gCysstrpArggly-CysglyglulilegllythrleuasnlyscystpttrpAsprCyslyyl 1149
 QY 5612 TACTATTAAATATCTAGAGAAATGAGATATTTTAAATTTTAAATC----- 5665
 Db 1149 euvalGlnProleuthrlysllyserValtrpargPheleuarg-AsprleuGluLeuGluile 1168
 QY 5665 ----- 5665
 Db 1169 ProheasprProalalleProleuLeuGlylletyrProasndasprlylyserCys 1188
 QY 5666 -----ACCATG 5671
 Db 1189 TyrlasprThrCysThrargMetPheilleAlaAlaLeuPheThrilleAlalystrtrp 1208
 QY 5672 TCATCTTAATATCTCATTAACATCATACCAAGGCTAATGATTAATTAATGCTTAT 5731
 Db 1209 AsnGlnProlysCysProthMetilleaspr-----trpilleyslysmettrpHis 1225
 QY 5732 ATGTATACCATGAGATTTTGAAGCAAA--AAAAAAAGTAAATATATCAAAATTTTGA 5788
 Db 1226 lletyrThrMetGluTyrTyrAlaAlaAlaLeuylsasnargpghlupPheMetSerPheValGly 1245

QY 5789 ATGCGATGATTTAAATAATTAATCTACAGCTGGAATTAACAAAATTTGCAAGACTGGA 5848
DB 1246 ThrtPrpLeuLysLeuGluThrIlele-----LeuSerLysLeuSerGlnGlu--- 1261
QY 5849 CCAATAGCTCTTATTCAGAGACCAATTAATTAATTAATACCC 5893
DB 1262 -----GlnLysThrLysHisArgLlePheSerLeu 1271
RESULT 15
138588
reverse transcriptase homolog - human retrotransposon L1
N:Alternate names: ORF2 protein
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I38588
R:Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazanietz, H.H.
Nature Genet. 7, 143-148, 1994
A:Title: A new retrotransposable human L1 element from the LME2 locus on chromosome 1q p
A/Accession: I38587; MUID:9504577; PMID:7920631
A:Reference number: I38587; translated from GB/EMBL/DBJ
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:9483914; PIDN:AA60345.1; PID:94839
C:Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 9.46e-29 Length: 1275
Score: 483.00 Matches: 175
Percent Similarity: 44.19% Conservative: 95
Best Local Similarity: 28.64% Mismatches: 196
Query Match: 0.56% Indels: 148
DB: 2 Gaps: 20

US-09-396-985B-48 (1-50000) x I38588 (1-1275)

QY 4398 GCACTGTTGCTGACGCTTGGATAGCTTACTACATTAACATTC----- 4442
DB 698 SerLeuPheAlaAspPheMetCileValIyLeuGlnAsnProIleValSerAlGlnAsn 717
QY 4443 CTATTAAGGCTCAGAGCAATTAACAGAGAGTGGGTAAGAATGTTGAAGCCATTGAC 4502
DB 718 LeuLeuLysLeuLleSerAsnPheserIyValSerGlyTyLysIleAsnValGlnLys 737
QY 4503 TTGGAGAACTACTGCAAAACAGTGAAGTTCAGACACACTCTCTTCAATGTGGTCT 4562
DB 738 SerGlnAlaPheLeuTyThrAsnAsnArgLlnThrGlnSerGlnIleMetGlyGlnLeu 757
QY 4563 CCTTGATATTTA-----ATCCCATACCTCAACCAACCAACATC 4601
DB 758 ProPheThrIleAlaSerLysArgLleLysTyLeuGlnIleGlnLeuThrArgAspVal 777
QY 4602 -----TTTCAACACTCTGTTCCCAATTAACATTAATAGCTTGAT 4640
DB 778 LysAspLeuPheLysGlnAsnTyLysPheLeuLeuLysGlnIleLysGlnAspThrAsn 797
QY 4641 TAAATTAAGACATATCAAGTGTCTACTAGAGACTTCCTGCAATTAATAATGATGTTACA 4700
DB 798 LysTrpLysAsn-IleProCysSerTrpValGlyArgLleAsn----- 811
QY 4701 CATTTATTAAG-----AA 4712
DB 812 -IleValLysMetAlaIleLeuProLysValIleTyArgPheAsnAlaIleProLleLly 831
QY 4713 AATTAAACAATTAATTTGATGCAATTAAGTAAAGTAAATTAAGCTTTTATAC----- 4767
DB 831 GluLeuProMetThrPhePheThrGlnLeuGlnLysThrThrLeuLysPheIleTrpAsnG 851
QY 4768 -----ATTTTCTTAAGCTGAT----- 4785
DB 851 nLysArgAlaArgIleAlaLysSerIleLeuSerGlnLysAsnLysAlaGlyIleTh 871

QY 4786 -----CCTTAGATTTTCTTAAGTACAAATTTGATGATCTTAATCTGTGTTCTTTTGA 4841
DB 871 rLeuProTyrrPheLysLeuTyTyTyLysAlaThrValThrLysThrAlaTrpTyrrPry 891
QY 4842 AAGCAATTAAGCAATTAATTTGAAATCGAGAAAGATGCTGTTTACTCAGATTA 4901
DB 891 rGlnAsn-----ArgAspIleAspGlnTrpAsnArg----- 901
QY 4902 AATGCTGACAAATGAGAGCTTAATTCATGTCATC---CACTGATCTTTGACAAAGAG 4958
DB 902 -ThrGlnProSerGlnIleMetPro-HisIleTyrrAsnTyrrLeuIlePheAspLysProG 921
QY 4959 CTTAAACCATACAGTTGAAAAAAGACAGCATTTTAAACAAATGCTGCTCAACTGT 5018
DB 921 LysLysAsnLysGlnTrp-GlyLysAspSerLeuPheAsnLysTyrrCysTrpGlnAsnTrp 940
QY 5019 CTGTGAGCATGTACAAATGCAATTCACCAATCTTATCTCTTAAAGCAAGCTCAAG 5078
DB 941 LeuAlaIleCysArgLysLeuLysLeuAspLeuPheLeuThrProTyrrThrLysIleAsn 960
QY 5079 TCCAAATGATACAAAGACCTCTACATTAACCGATACCTGAAATTTTAAAGAGAGA 5138
DB 961 SerArgTrpIleLysAspLeuAsnValLysProLysThrIleLysThrLeuGlnLysAsn 980
QY 5139 GTGAGAGAGAGGCTTGAACATGAGGCAAGGAGAAATTCCTGACAGAACACA--- 5195
DB 981 LeuGlyIleThrIleGlnAspIleGlyValGlyAspPheMetSerLysThrProLys 1000
QY 5196 ---GTGGCTTA-AGATCAAGATCTCAATGGGGCTCTAAATTTGCAAACTTCTGT 5251
DB 1001 AlMetAlaThrLysAspLysIleAspLysTrpAspLeuLleLysLeuLysSerPheCys 1020
QY 5252 AATGCAAGACAGCTGTCAATAGACAAAGGCA---ACAGATGGGAAAAAGATCTT 5308
DB 1021 ThrAlaLysGlnThrThrIleArgValAsnArgLlnProThrThrTrpGlnLysIlePhe 1040
QY 5309 ACCAATCTTACATCAATGAGGAGGCTAATTTCAATATATACAAACACTCAAGAGTTA 5368
DB 1041 AlaThrLysSerSerAspLysGlnLysLeuIleSerArgIleTyrrAsnGlnLeuLysGlnIle 1060
QY 5369 GACTCCAGAACCAATTAACCTTATTA-AAATGGGGTTC-AAAGCTAAACAAAGATT 5426
DB 1061 TyrrLysLysThrAsnAsnProIleLysLysTrpAlaLysAspMetAsnArgHisPhe 1080
QY 5427 TCGCTGAGAAATTAATGAATGGCCAGAAATCACCTTAAGAAATTAATGATGTTATGTC 5486
DB 1081 SerLysGlnAspIleTyrrAlaAlaLysLysHisMetLysLysCysSerSerSerLeuAla 1100
QY 5487 ATCAGGAAATGCAAAATCAAAACACCTGAGAAAGTATTCCTGAAGTG----- 5537
DB 1101 IleArgGlnMetGlnIleLysThrThrMetCArgTyrrHisLeuThrProValArgMetAla 1120
QY 5538 TTATTAATAATGTCTTAAACCTTAATGACCTGAGAGAGATTAACAGAAACATCTGGGGA 5597
DB 1121 IleLleLysLysSerGlnAsn-----AsnArgCysTrpArgGly-CysGlyG 1136
QY 5598 AATTAACAACATAT-----TTACTTTTAAATTAATGAGAA 5633
DB 1136 uLleGlyThrLeuLeuHisCysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSe 1156
QY 5634 AATGTGAATATTTTAATTAATTTTAATATC----- 5665
DB 1156 rValTrpArgPheLeuArg-AspLeuGlnLeuGlnIleProPheAspProAlaIleProL 1176
QY 5665 ----- 5665
DB 1176 euLeuGlyIleTyrrProGlnAspTyrrLysSerCysTyrrLysAspThrCysThrArgm 1196
QY 5666 -----ACCATGCTCATTTAAATGTCATTA 5693
DB 1196 etPheIleAlaAlaLeuPheThrIleAlaLysThrTrpAsnGlnProLysCysSerProThm 1216
QY 5694 CTATACCAAAAGGCTAATGATTAATAAAATGTGTTATGATTAACATGATTTTGA 5753

Db	1216	ettlleasp-----	trpilleuylsmeuttrphtsilelytthrtmetglutyr	1233
Qy	5754	CAGAA-----	AAAAAAGTAAGTAATTAATACAAATTTTGGAAATGTCATGGATTTAAAAAT	5810
Db	1233	laaiailelyasnsgrplubheileserephevalglythtrptwelyslenguthrt	1253	
Qy	5811	ATACTCGACGTGAATTACAAAATTTTCAAGACTGACCAATAGTCCTTATTCAGAAAG	5870	
Db	1253	lelle-----	leuserlyslseuserglu-----	gluylvt 1264
Qy	5871	ACAATACTATATATATACCTC	5893	
Db	1264	hrlyshleatgillepheserleu	1271	

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 2837 Seconds
(without alignments)

18050.024 Million cell updates/sec

Title: US-09-396-985B-48

Perfect score: 86900

Sequence: 1 ttccacatcatgatagtc.....catttagtattattccaga 50000

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6449512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DRV=xlh

-O=/cgm2_1/USFPO.spool/US09396985/rnatc_28032005_155743_21146/app_query.fasta_1.85098

-DB=uniprot_03 -QMT=faasta -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45

-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USRR=US09396985 @CGN 1.1 5213 @rnatc_28032005_155743_21146 -NCPU=6 -ICPU=3

-NO_MMAP -LARGEOUTPUT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TTIMEOUT=120 -WARN_TTIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : uniprot_03:*

UniProt_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	3895	4.5	835	TIR4_MOUSE	Q9GUK6 mus musculus
2	3876	4.5	835	Q8K2T5	Q8K2T5 mus musculus
3	3382	3.9	835	TIR4_RAT	Q9GUK6 ratulus norv
4	3155	3.6	838	TIR4_CRIGR	Q9W822 cricetus
5	2607	3.0	839	TIR4_HUMAN	Q00206 homo sapien
6	2607	3.0	839	TIR4_HUMAN	Q00206 homo sapien
7	2597	3.0	826	TIR4_PANPA	Q9T822 pan paniscu
8	2582	3.0	837	Q8SPF8	Q8SPF8 gorilla gor
9	2580	3.0	828	TIR4_PONPY	Q8SPF8 pongo pygma
10	2578	3.0	841	TIR4_BOVIN	Q9G166 bos taurus
11	2575	3.0	841	Q8S0S5	Q8S0S5 bos taurus
12	2573	3.0	841	Q6WCD5	Q6WCD5 bos taurus
13	2571	3.0	841	Q6WCD4	Q6WCD4 bos taurus
14	2567	3.0	843	TIR4_HORSE	Q6WY43 equus cabal
15	2522.5	2.9	833	TIR4_FELCA	Q88727 felis silve
16	2507	2.9	841	TIR4_PIG	Q68Y56 sus scrofa

17	2374	2.7	839	2	Q8MIQ2	Q8MIQ2 oryctolagus
18	1967	2.3	636	2	Q8SCH3	Q8SCH3 canis famli
19	1576.5	1.8	843	2	Q7ZTGS	Q7ZTGS gallus galli
20	1118	1.3	819	2	Q6T541	Q6T541 brachydanio
21	1107	1.3	817	2	Q6NV08	Q6NV08 brachydanio
22	897	1.0	1015	2	Q7TMA9	Q7TMA9 ratulus norv
23	767.5	0.9	477	2	Q7R857	Q7R857 plasmodium
24	765.5	0.9	1281	2	Q91288	Q91288 mus musculus
25	765.5	0.9	1281	2	Q91289	Q91289 mus musculus
26	765.5	0.9	1300	1	BOL2_MOUSE	P11369 mus musculus
27	765.5	0.9	1300	2	Q61785	Q61785 mus musculus
28	764	0.9	432	2	Q7R714	Q7R714 plasmodium
29	762	0.9	1281	2	Q88915	Q88915 mus musculus
30	769.5	0.9	258	2	Q70EKA	Q70EKA sus scrofa
31	760.5	0.9	627	2	Q7RAY6	Q7RAY6 plasmodium
32	761	0.9	1300	2	Q08906	Q08906 mus musculus
33	756	0.9	1219	2	Q9QIM3	Q9QIM3 mus musculus
34	756	0.9	1281	2	Q54850	Q54850 mus musculus
35	756	0.9	1281	2	Q88913	Q88913 mus musculus
36	756	0.9	1281	2	Q88914	Q88914 mus musculus
37	756	0.9	1281	2	Q79219	Q79219 mus musculus
38	756	0.9	1281	2	Q9QI72	Q9QI72 mus musculus
39	756	0.9	1281	2	Q9QWY0	Q9QWY0 mus musculus
40	756	0.9	1281	2	Q9QWY3	Q9QWY3 mus musculus
41	751	0.9	1714	2	Q6Q178	Q6Q178 ratulus norv
42	745	0.9	1446	2	Q7TP07	Q7TP07 ratulus norv
43	743	0.9	621	2	Q6Q153	Q6Q153 ratulus norv
44	741	0.9	516	2	Q6Q192	Q6Q192 ratulus norv
45	738.5	0.9	1217	2	Q6TUP6	Q6TUP6 ratulus norv

ALIGNMENTS

RESULT 1	TIR4_MOUSE	STANDARD; Q9Z203; PRT; 835 AA.
ID	TIR4_MOUSE	
AC	Q9GUK6; Q9D691; Q9QZFS; Q9Z203;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Toll-like receptor 4 precursor.	
GN	Name="Tlr4"; Synonyms=Lps;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C3H/HeJ;	
RX	MEDLINE=99167984; PubMed=10087992; DOI=10.1006/bcmd.1998.0201;	
RA	Poltorak A., Smirnova I., He X., Liu M.-Y., Van Huffel C., Du X.,	
RA	Birdwell D., Alejos E., Silva M., Thompson P., Chan E.K.L.,	
RA	Ledesma J., Roe B., Clifton S., Vogel S.N., Beutler B.,	
RT	"Genetic and physical mapping of the lps locus: identification of the	
RT	Toll-4 receptor as a candidate gene in the critical region.";	
RT	Blood Cells Mol. Dis. 24:340-355(1998).	
RL	[2]	
RN	SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.	
RP	STRAIN=C3H/HeJ;	
RC	MEDLINE=99059627; PubMed=9851930; DOI=10.1126/science.282.5396.2085;	
RX	Poltorak A., He X., Smirnova I., Liu M.-Y., Van Huffel C., Du X.,	
RA	Birdwell D., Alejos E., Silva M., Galanos C., Freudenberg M.,	
RA	Ricciardi-Castagnoli P., Layton B., Beutler B.,	
RT	"Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: mutations	
RT	in Tlr4 gene.";	
RT	Science 282:2085-2088(1998).	
RL	[3]	
RN	SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.	
RP	STRAIN=C57BL/6J;	
RC	MEDLINE=99145502; PubMed=9989976;	
RX	Qureshi S.T., Laviere L., Leveque G., Clermont S., Moore K.U.,	
RA	Gros P., Malo D.;	
RT	"Endotoxin-tolerant mice have mutations in Toll-like receptor 4	

RT (Tlr4).";

RL J. Exp. Med. 189:615-625(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX TISSUE=Macrophage;

MDLINE=20014145; PubMed=10548109; DOI=10.1038/44605;

RA Underhill D.M., Ozolsky A., Hajjar A.M., Stevens A., Wilson C.B.,

RA Bassetti M., Adereas A.;

RT "The Toll-like receptor 2 is recruited to macrophage phagosomes and

RT discriminates between pathogens.";

RL Nature 401:811-815(1999).

RN [5]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-94; ILE-209; GLY-219; ILE-254;

RP LRU-423; SER-477; ALA-516; ASP-593; ILE-600; VAL-607; ILE-637; HIS-761

RP AND LYS-811.

RC STRAIN=Various strains;

RX MEDLINE=20558910; PubMed=11104518;

RA Shinnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4

RT locus (TLR4).";

RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).

RN [6]

RP SEQUENCE OF 1-154 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki I., Furuno M., Kaenkawa T., Adachi J., Bono H., Kondo S.,

RA Nikaiko I., Osato N., Saico R., Suzuki H., Yamana K., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schindach C., Gojohori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirral L.M., Kanapin A., Matcoda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmeron S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,

RA Meglout D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider Y., Seiple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wainstedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yaumateh A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [7]

RP FUNCTION.

RX MEDLINE=20507837; PubMed=10952994; DOI=10.1074/jbc.M007386200;

RA Rhee S.H., Hwang D.;

RT "Murine Toll-like receptor 4 confers lipopolysaccharide responsiveness

RT as determined by activation of NF kappa B and expression of the

RT inducible cyclooxygenase.";

RL J. Biol. Chem. 275:34035-34040(2000).

RN [8]

RP FUNCTION: Cooperates with Lys6 and CD14 to mediate the innate

RP Immune response to bacterial lipopolysaccharide (LPS). Acts via

RP MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine

RP secretion and the inflammatory response (By similarity).

CC -1 SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a

CC multi-protein complex containing at least CD14, Lys6 and TIRAP.

CC Binds Lys6 via the extracellular domain. Binds MyD88 and TIRAP via

CC their respective TIR domains.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1 TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and

CC muscle. Lower levels are found in liver and kidney.

CC -1 POLYMORPHISM: Interstrain analysis reveals that TLR4 is a

CC polymorphic protein and that the extracellular domain is far more

CC variable than the cytoplasmic domain, which is variable at the C-

CC terminal.

CC -1 DISEASE: The protein is encoded by the Lps locus, an important

CC susceptibility locus, influencing the propensity to develop a

CC disseminated Gram-negative infection.

CC -1 SIMILARITY: Belongs to the Toll-like receptor family.

CC -1 SIMILARITY: Contains 19 leucine-rich (LRR) repeats.

CC -1 SIMILARITY: Contains 1 TIR domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: AF095353; AAC9411.1; -;

DR EMBL: AF185285; AAF04278.1; -;

DR EMBL: AF110133; AAD2972.1; -;

DR EMBL: AF17767; AAF05317.1; -;

DR EMBL: AK014533; -; NOT_ANNOTATED_CDS.

DR HSSP: Q15399; 1FVY.

DR MGD: MGI:96824; Tlr4.

DR GO: GO:0046596; C:lipopolysaccharide receptor complex; ISS.

DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO: GO:0004888; F:transmembrane receptor activity; ISS.

DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.

DR GO: GO:0016046; P:detection of fungi; ISS.

DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO: GO:0042116; P:macrophage activation; ISS.

DR GO: GO:0045576; P:osteoclast activation; NAS.

DR GO: GO:0045711; P:negative regulation of osteoclast different. . . ; ISS.

DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; NAS.

DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.

DR GO: GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; NAS.

DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; NAS.

DR GO: GO:0042088; P:positive regulation of immune response; ISS.

DR InterPro: IPR001611; LRR.

DR InterPro: IPR000483; LRR_Cterm.

DR InterPro: IPR00157; TIR.

DR Pfam: PF00560; LRR; 10.

DR Pfam: PF01582; TIR; 1.

DR PRINTS: PR00019; LEURICRPT.

DR SMART: SM00082; LRRCT; 1.

DR SMART: SM00255; TIR; 1.

DR PROSITE: PS50104; TIR; 1.

DR Disease mutation: Glycoprotein; Immune response;

KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;

KW Repeat; Signal; Transmembrane.

FT SIGNAL 1 25 Potential.

FT CHAIN 26 835 Toll-like receptor 4.

FT DOMAIN 26 638 Extracellular (Potential).

FT TRANSMEM 639 659 Potential.

FT DOMAIN 660 835 Cytoplasmic (Potential).

FT REPEAT 29 52 LRR 1.

FT REPEAT 53 75 LRR 2.

FT REPEAT 76 99 LRR 3.

FT REPEAT 100 123 LRR 4.

FT REPEAT 127 148 LRR 5.

FT REPEAT 149 172 LRR 6.

FT REPEAT 173 196 LRR 7.

FT REPEAT 201 224 LRR 8.

FT REPEAT 227 251 LRR 9.

FT REPEAT 305 330 LRR 10.

FT REPEAT 348 370 LRR 11.

FT REPEAT 371 393 LRR 12.

FT REPEAT 396 413 LRR 13.

FT REPEAT 420 443 LRR 14.

FT REPEAT 468 492 LRR 15.

FT REPEAT 494 516 LRR 16.

FT REPEAT 517 540 LRR 17.
 FT REPEAT 542 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 75 75 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 172 172 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 204 204 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 237 237 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 492 492 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 572 572 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 613 613 N-linked (G1cNAc. . .) (Potential).

Alignment Scores:

Pred. No.: 3.76e-277 Length: 835
 Score: 3895.00 Matches: 750
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.48% Indels: 0
 DB: 1 Gaps: 0

US-09-396-985b-48 (1-50000) x TLR4_MOUSE (1-835)

QY 37730 AGGTGTGAATTTGAACAATTTGAAGACAGGACATGGCTTACACACCTTCTCAAC 37789
 DB ArgGySglnIleGlnThrIleGlnAspLysAlaTrpHisGlyLeuHisSLeuSerAsn 105
 QY 37790 TTGTATGACAGGAAACCCATCCAGAGTTTCCACAGAGTTTCTCGACTACA 37849
 DB LeuIleuThrGlyAsnProIleGlnSerPheSerProGlySerPheSerGlyLeuThr 125
 QY 37850 AGTTAGAGATCTGTGCTGTGTGAGACAAATTTGCGCTCTAGAAAGCTTCCCTATT 37909
 DB SerLeuIleuAsnLeuValAlaValGlnThrIleuAsnLeuLeuSerLeuGlyLeuSerPheProIle 145
 QY 37910 GGACAGCTTTACCTTAAGAACTCAATGTGGCTCAACAATTTTATACATTTCTGTAG 37969
 DB GlyIleuIleuThrIleuValLeuAsnValAlaHisAsnPheIleHisSerCysLeu 165
 QY 37970 TTACCTGCATATTTTCCATCTGACGACCTAGATGATGATCTTTCTTAACTAT 38029
 DB LeuProAlaTrpPheSerAsnLeuThrAsnLeuValHisValAspLeuSerTrpAsnTrp 185
 QY 38030 ATTCAACTATTAAGTCAAGACTTACAGTTTCTAGCTGAAATTCACAAGTCAATCTC 38089
 DB IleGlnThrIleThrValAsnAspLeuGlnPheLeuArgLeuAsnProGlnValAsnLeu 205
 QY 38090 TCTTTAGACATGTCTTTGAACCCAAATGACTCTTCAACAACCAAGCTTTACAGGAATT 38149
 DB SerLeuAspMetSerLeuAsnProIleAspPheIleGlnAspGlnAlaPheGlnGlyIle 225
 QY 38150 AAGTTCATGAATGAGCTTAAGAGTAATTTTAAATGCTCAATTAATGAAGAACTTGC 38209
 DB LysLeuHisSerLeuLeuThrLeuArgGlyAsnPheAsnSerSerAsnIleMetLysThrCys 245
 QY 38210 CTTCAAAACCTGTGCTGTTTACAGCTCAATCGATGATCTTTGGAGAGATTTAAAGATGAA 38269
 DB LeuGlnAsnLeuHisGlyLeuHisValHisArgLeuIleLeuGlyGlnPheLysAspGln 265
 QY 38270 AGGAATCTGAATTTTGAACCTCTATCATGAGAGACTATGTGATGACCATTTGAT 38329
 DB ArgAsnLeuGlnIlePheGlnProSerIleMetGlnGlyLeuCysAspValThrIleAsp 285
 QY 38330 GAGTTCAGGTTAATATATACAAATGATTTTCAATATATGTTAGTCCATGCTTG 38389
 DB GluPheArgLeuThrTrpAsnAspPheSerAspIleValLysPheHisCysLeu 305
 QY 38390 GCGAATGTTTCTGCAATGTCTGTGGCAGTGTATCTTAAATATCTAGAAAGATGTTCT 38449
 DB

DB 306 AlaAsnValSerAlaMetSerLeuAlaGlyValSerIleLeuGlyAspValPro 325
 QY 38450 AAACATTTCAAAAGCGCAATCTTATATCATATGATGATGCACTTAAGCACTTCCAACT 38509
 DB LysHisPheLeuTrpGlnSerLeuSerIleIleArgCysGlnLeuLysGlnPheProThr 345
 QY 38510 CTGGATCTACCCCTTTCTTAAAGTTTGACTTTAACTATGAACAAAGGCTCATGAGTTT 38569
 DB LeuAspLeuProPheLeuLysSerLeuThrLeuThrMetAsnLysGlySerIleSerPhe 365
 QY 38570 AAAAAGTGGCCCTTACCAAGTCTTCACTATGATCTTATGATGAAATGACATGAGCTTT 38629
 DB LysLeuValAlaLeuProSerLeuSerTrpLeuAspLeuSerArgAsnAlaLeuSerPhe 385
 QY 38630 AGTGTGCTGTTCTTATTTGATTTTGGGAAACAAAGCCTTGAGACACTTAAGACTTGAC 38689
 DB SerCysCysSerTrpSerAspLeuGlyThrAsnSerLeuArgHisLeuAspLeuSer 405
 QY 38690 TTCAATGTGCTCATATATGATGAGTGCATTTTCAAGAGCTGACACCTG 38749
 DB PheAsnGlyAlaIleIleMetSerAlaAsnPheMetCysLeuGlnLysLeuGlnHisLeu 425
 QY 38750 GATTTTCAGCACTCTTATTTAAAGGTCACAGAAATTCAGCGTTCTTATCCCTTGA 38809
 DB AspPheGlnHisSerThrLeuLysArgValThrGlnPheSerAlaPheLeuSerLeuGln 445
 QY 38810 AAGCTACTTATCTTATCATCTTATATCAACCAAAATTTGACTTCGATGATATTT 38869
 DB LysLeuLeuTrpLeuAspIleSerTrpAsnThrLysIleAspPheAspGlyIlePhe 465
 QY 38870 CTTGGCTTGACAGCTCAACATTAATAAATGGCTGGCAATCTTCAAGAACACAC 38929
 DB LeuGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSerPheLysAspAsnThr 485
 QY 38930 CTTTCAATGTCTTTGCAACACACAACTTGACATTTCTGTGATCTTTTAAATGTCAA 38989
 DB LeuSerAsnValPheAlaAsnThrTrpAsnLeuThrPheLeuAspLeuSerLysCysGln 505
 QY 38990 TTGGAACAAATATCTTGGGGGGATTTTGAACACCTCATAGACTTCAATTTAAATATG 39049
 DB LeuGlnGlnIleSerTrpGlyValPheAspThrLeuHisArgLeuGlnLeuLeuAsnMet 525
 QY 39050 AGTCACAAATCATATGTTTGGATTTTCAATCCATTAACAGAGCTGTATCCCTCAGC 39109
 DB SerHisAsnAsnLeuLeuPheLeuAspSerSerHisTrpAsnGlnLeuTrpSerLeuSer 545
 QY 39110 ACTCTTGATTTGACATTCGATAGACATCTTAAGAAATCTGACAACTTTTCCA 39169
 DB ThrLeuAspCysSerPheAsnArgIleGlnThrSerLysGlyIleLeuGlnHisPhePro 565
 QY 39170 AAGAGTCTAGCCTTTCTTCAATCTTACTACAAATTCGTGCTGTGATATGTGAACATCAG 39229
 DB LysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCysIleCysGlnHisGln 585
 QY 39230 AAATTCCTGAGTGGGCAAGAAACAGACAGCTTGTGTAATGTTGAACAAATGACA 39289
 DB LysPheLeuGlnTrpValLysGlnGlnLysGlnPheLeuValAsnValGlnGlnMetThr 605
 QY 39290 TGTGCAACCTGTAGAGATGAAATACCTCTTATGTTGATTTTAAATTTCACTGT 39349
 DB CysAlaThrProValGlnMetAsnThrSerLeuValLeuAspPheAsnAsnSerThrCys 625
 QY 39350 TATATGTACAAACATCATCATGTGTGTCAAGTGTGATGTGATGTGATGATGATGATG 39409
 DB TyrMetTrpArgThrIleIleSerValSerValValSerValIleValAlaSerThrVal 645
 QY 39410 GCATTTCTGATATACCACTTCTTATTTTCACTGATCTTATTTGCTGGCTGTAAGATAC 39469
 DB AlaPheLeuIleTrpHisPheTrpPheHisSLeuIleuIleAlaGlyCysLysLysTrp 665
 QY 39470 AGCAGAGAGAAAGCATATGATGATTTGTGATCTATCGATCGAGTCAAGATGAGACTGG 39529
 DB SerArgGlyGlnSerIleTrpAspAlaPheValIleTyrSerSerGlnAsnGlnAspTrp 685

QY 39530 GTGGAATGAGCTGTAAGATTTTGAAGAAGAGCGCCGCTTCACTCTGCTT 39589
| | | | |
DB 686 ValArgsnGluLeuValIysAsnLeuGluGluValAlaProArgPheHisLeuCySLeu 705
QY 39590 CACTACAGAGACTTATCTCTGTGTAGCCATTGCTCCCAATCATCCAGAAAGCTTC 39649
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DB 706 HisArgArgAspPheIleProGluValAlaIleHisAlaHisIleIleGluGluPhe 725
QY 39650 CACAAAGCCCGAAGGTTATTTGTGTAGTGTCTGACACTTTATTCAGAGCCGTTGCTGT 39709
| | | | |
DB 726 HisLysSerArgLysValIleValValSerArgHisPheIleGlnSerArgTyrCys 745
QY 39710 ATCTTGAATATGATGATTCCTCAACATGCGAGTTCTTGACAGCCGCTCTGACATATC 39769
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DB 746 IlePheGluTyrGluIleHisGlnThrTyrPheIleHisLysSerArgSerGlyIleIle 765
QY 39770 TTCATTGCTTGAAGAGTTGAGAGTCCCTGCTGAGCGACAGGTGGAATGTATCGC 39829
| | | | |
DB 766 PheIleValLeuGluLysValGluLysSerLeuArgGlnGlnValGluLeuTyrArg 785
QY 39830 CTTTGTGACAGAAACACTTACTGATGAGAGACATCTCTGGGAGGACATCTTC 39889
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DB 786 LeuLeuSerArgAsnThrTyrLeuGluTyrPheLysAsnProLeuGlyArgHisIlePhe 805
QY 39890 TGGAGAGAGCTTAAATAATGCCCTTGTGATGAGAAAGCTCTGATCTGAGCAACAGCA 39949
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DB 806 TyrArgArgLeuLysAsnAlaLeuLeuAspGlyLysAlaSerAsnProGluGlnThrAla 825
QY 39950 GAGGAGAGCAAGAAACGGCACTTGAGCC 39979
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DB 826 GluGluGluGluGluThrAlaThrTyrThr 835
RESULT 2
QY 08K2T5 PRELIMINARY; PRT; 835 AA.
ID 08K2T5;
AC 08K2T5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein J., Ustin T.B., Toshlyuk S., Canninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska J., Smalins D.E., Schnerch A., Schein J.R.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029856; AAH29856.1; -.
DR HSSP: O60603; 1077.
DR MGD: MGI:96824; TLR4.
DR GO: GO:0005615; C:extracellular space; TMS.
DR GO: GO:0016021; C:integral to membrane; TMS.
DR GO: GO:004872; F:receptor activity; IDA.
DR GO: GO:0007249; P:1-kappaB kinase/NF-kappaB cascade; IDA.
DR GO: GO:0008063; P:Toll signaling pathway; IDA.
DR InterPro: IPR000867; AldIsr_KDPe_KHG.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00560; LRR_1; 10.
DR Pfam: PF01582; TIR_1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00159; ALDOLASE_KDPe_KHG_1; UNKNOWN_1.
DR PROSITE: PS50104; TIR; 1.
KM RECEPTOR.
SQ SEQUENCE 835 AA, 95488 MW, A103C3997A59CF5B CRC64;
Alignment Scores:
Pred. No.: 9,41e-276 Length: 835
Score: 3876.00 Matches: 745
Percent Similarity: 99.87% Conservative: 4
Best Local Similarity: 99.33% Mismatches: 1
Query Match: 4.46% Indels: 0
Gaps: 0
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DB 86 ArgCysGluIleGluThrIleGluAspLysAlaTyrHisGluLeuHisLeuSerAsn 105
QY 37790 TTGATCTGACAGAAACCCATCCAGAGTTTTCACGAGAGTTTCTGTGACATPACA 37849
| | | | |
DB 106 LeuIleLeuThrGlyAsnProIleGlnSerPheSerProGlySerPheSerGlyLeuThr 125
QY 37850 AGTTGAGAGATCGTGCGCTGTGAGACAAATTTGCGCTCTAGAAAGCTTCCCTATT 37909
| | | | |
DB 126 SerLeuGluAsnLeuValAlaValGluThrLysLeuAlaSerLeuGlnSerPheProIle 145
QY 37910 GAGACGCTTAAACCTTAAAGAACTCAATGCGCTCAACATTTTATACATTCCTGTAG 37969
| | | | |
DB 146 GlyGlnLeuIleThrLeuLysLysLeuAsnValAlaHisAsnPheIleHisSerCysLys 165
QY 37970 TTACCTGCATATTTTCCCATCTGAGAACCTTATCATGTGATCTTCTTAATATAT 38029
| | | | |
DB 166 LeuProLalArgPheSerAsnLeuThrAsnLeuValHisValAspLeuSerTyrAsnTyr 185
QY 38030 ATTCAACTTATCTGTCAACGACTTACAGTTTCTAGGTAAATCCAAAGTCAATCTC 38089
| | | | |
DB 186 IleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGluAsnProGlnValAsnLeu 205
QY 38090 TCTTTAGACATGTCTTGAACCCCAATGTGATCTTATTCACAAACGCTTTCAGGAAAT 38149
| | | | |
DB 206 SerLeuAspLysSerLeuAsnProIleAspPheIleGlnAspGlnAlaPheGlnGlyLe 225
QY 38150 AAGTCATGATGATCTGCTCAAGAGGTAATTTAATAGCTCAATATTAAGAAAGTTCG 38209
| | | | |
DB 226 LysLeuHisGluLeuThrLeuArgLysAsnPheAsnSerSerAsnIleLeuLysTrpHisCys 245
QY 38210 CTTCAAAACCTGCGCTGTATACAGCTCCATCGGTTGATCTTGGAGAGATTTAAGATGAA 38269
| | | | |
DB 246 LeuGlnAsnLeuAlaGlyLeuHisValHisArgLeuIleLeuGlyGluPheLysAspGlu 265
QY 38270 AGGAATCGAAATTTTGAACCTCTATCATGAGAGACTATGTGATGACCATTTGAT 38329
| | | | |
DB 266 ArgAsnLeuGluIlePheGluProSerIleMetGluGlyLeuGlyAspValThrIleAsp 285

QY 38330 GAGTTGAGTTAACAATATACAAATGATTTTTCAGATGATATATGTTAGTTCCATGCTTG 38389
 DB 286 GlubheaurgleuthrhiethrAsnAspSerSerAspArgIleValLysPheHisCysLeu 305
 QY 38390 GCGAATGTTTTCGAATGCTCTGCGACGGTGTATCTATTAATAATATCTAAGAAGATGTTCT 38449
 DB 306 AlaAsnValSerIleMetSerLeuAlaGlyValSerIleLysTyrLeuGlnAspValPro 325
 QY 38450 AAAAATTCAATAGGCAATCTTTATTCATCATATGATGTCATCTTAAGCACTTTCACACT 38509
 DB 326 LysHisPheLysTyrPginSerLeuSerIleLeuArgCysGlnLeuLysGlnPheProThr 345
 QY 38510 CTGATCTACCTCTTCTTAAAGTTTGACTTAATATGACAAAGGGCTATGACGTTT 38569
 DB 346 LeuAspLeuProPheLeuLysSerLeuThrLeuThrMetAsnLysGlySerIleSerPhe 365
 QY 38570 AAAAAAGTGGCCCTACCAAGTCTCAGCTATGATCTTAAGTGAATGCACTGAGCTTT 38629
 DB 366 LysLysValAlaLeuProSerLeuSerTyrLeuAspLeuSerArgAsnAlaLeuSerPhe 385
 QY 38630 AGTGGTGTCTTCTTATTTCTGATTTGGGAAACAAAGCCTGAGACACTTGACCTCAGC 38689
 DB 386 SerGlyCysCysSerTyrSerAspLeuGlyThrAsnSerLeuArgHisLeuAspLeuSer 405
 QY 38690 TTCAATGGTGCATCATATATGAGTGCCTCAATTCAGGGCTGAGAAGAGCTGACGACCTG 38749
 DB 406 PheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGlnGlnLeuGlnHisLeu 425
 QY 38750 GATTTTGAAGCACTGCTACTTTAAAAAGGTCACAGAAATCTCAGCGTTTATCCCTTGA 38809
 DB 426 AspheGlnHisSerThrLeuLysArgValLhrGlnPheSerAlaPheLeuSerLeuGln 445
 QY 38810 AAGCTACTTACCTTGAATCTCTTACTTAACACCAAAATGACCTTGATGATATTT 38869
 DB 446 LysLeuLeuTyrLeuAspIleSerTyrThrAsnThrLysIleAspPheAspGlyIlePhe 465
 QY 38870 CTTGGCTTGACCACTGCTCAACACATTTAAATGCGTGCATCTTCTTCAAGACACACC 38929
 DB 466 LeuGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSerPheLysAspAsnThr 485
 QY 38930 CTTTCAATGCTCTTGGCAACACAACTGACATTCCTGATCTTCTTCAATGTCAC 38989
 DB 486 LeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAspLeuSerLysCysGln 505
 QY 38990 TTGGAACAAATATCTTGGGGGGTATTGACACCTCCATACATTCATTTTAAATATG 39049
 DB 506 LeuGlnGlnIleSerTyrGlyValPheAspThrLeuHisArgLeuGlnLeuLeuAsnMet 525
 QY 39050 AGTCACAACATCTATGTTTGGATTTCATCCCATTAACCAAGCTGATTCCTCAGC 39109
 DB 526 SerHisAsnAsnLeuLeuPheLeuAspSerSerHisTyrAsnGlnLeuTyrSerLeuSer 545
 QY 39110 ACTCTGATTCAGTTTCAATCGCATAGACATCTAAGAAATCTGCAACATTTTCCA 39169
 DB 546 ThrLeuAspCysSerPheAsnArgIleGlnThrSerLysGlyIleLeuGlnHisPhePro 565
 QY 39170 AAGAGCTAGCCTTCTTCAATCTTACTAACAATTCGTGCTGTATATATGAAATCAG 39229
 DB 566 LysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCysIleCysGlnHisGln 585
 QY 39230 AAAATCTGAGTGGTGCACAGAACAGACAGATCTTGGTGATGTTGAAACAATGACA 39289
 DB 586 LysPheLeuGlnThrValLysAspGlnLysGlnPheLeuValAsnValGlnGlnMetThr 605
 QY 39290 TGTGCAACACCTGTAGATGAATACCTCTTAGTGTGATTTAAATTTTACCTGT 39349
 DB 606 CysAlaThrProValGlnMetAsnThrSerLeuValLeuAspPheAsnSerThrCys 625
 QY 39350 TATATGACAAACAATATATAGTGTGTGATGCTGAGTGTGATGTTGGTATCCACTGA 39409
 DB 626 TyrMetTyrLysThrIleIleSerValSerValIleSerValIleValIleValSerThrVal 645

QY 39410 GCATTTCTGATATACACCTTCTATTTTACCTGATATCTATGCTGCTGTAAGATAC 39469
 DB 646 AlaPheLeuIleTyrHisPheTyrPheHisLeuIleLeuIleAlaGlyCysLysLeuTyr 665
 QY 39470 AGCAGAGAGAAAGACATCTATGATGCACTTTGTGATCTTACTGAGTCAAGATGAGACTCG 39529
 DB 666 SerArgGlyGlnSerIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyr 685
 QY 39530 GTGGAAGAATGAGCTGGTAAAGATTTTGAAGAAGAGAGTGGCCGCTTTCACCTGCGCTT 39589
 DB 686 ValArgAsnGlnLeuValLysAsnLeuGlnGlnIleValProArgPheHisLeuCysLeu 705
 QY 39590 CACTACAGACATTTATCTGCTGTAGCCATTCCTGCTGCAACATCATTCAGAAAGCTTC 39649
 DB 706 HisTyrThrAspPheIleProGlyValAlaIleAlaHisIleIleGlnGlnLysPhe 725
 QY 39650 CACAAGACCGGAGATTTATGCTGAGTGTCTTACACATTTATTCAGAGCGTGGTGT 39709
 DB 726 HisLysSerArgLysValIleValValSerArgHisPheIleGlnSerArgTyrCys 745
 QY 39710 ATCTTGAATATGATGATTTGCTCAACATGCGACATTCCTGAGACGCGCTGCGATATC 39769
 DB 746 IlePheGlnTyrGlnIleAlaGlnThrTyrPginPheLeuSerSerArgSerGlyIleIle 765
 QY 39770 TTCAATGCTCTGAGAGTGTGAGAAAGTCCCTGCTGAGCAGCAGTGAATTTATCGC 39829
 DB 766 PheIleValLeuGlnLysValGlnLysSerLeuLeuArgGlnGlnValGlnLeuTyrArg 785
 QY 39830 CTTTGAACAAACACCTTACCTGGAATGGAGACAAATCTCTGGGAGGACATCTTC 39889
 DB 786 LeuLeuSerArgAsnThrTyrLeuGlnTyrPginLysPheLeuSerProLeuGlyArgHisIlePhe 805
 QY 39890 TGGAGAGACTTAAATGGCCCTTATGATGAGAAAGCCTCGATCTCTGAGCAACGCA 39949
 DB 806 TyrArgArgLeuLysLysValAlaLeuLeuAspGlyLysAlaSerAsnProGlnGlnThrAla 825
 QY 39950 GAGGAAGAACAGAAACGCAACTTGAGCC 39979
 DB 826 GlnGlnGlnGlnGlnThrAlaThrTyrThr 835

RESULT 3
 TLR4 RAT ID TLR4 RAT STANDARD; PRT; 835 AA.
 AC 09X05;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor (Toll14).
 GN Name:TLR4;
 OS Rattus norvegicus (Rat).
 CC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, TISSUE=Heart;
 RK MEDLINE=99362487; PubMed=10430608;
 RA Frenzt S., Kobzik L., Kim Y.-D., Fukazawa R., Medzhitov R., Lee R.T.,
 RA Kelly R.A.;
 RT "Toll14 (TLR4) expression in cardiac myocytes in normal and failing
 myocardium";
 RL J. Clin. Invest. 104:271-280(1999).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.

CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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CC -----
 DR EMBL; AF057025; AAC13313.1; -.
 DR HSSP; Q15399; 1FV.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000157; TIR_Cterm.
 DR Pfam; PF00560; LRR; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KM Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 638 Extracellular (Potential).
 FT DOMAIN 26 639 Potential.
 FT TRANSMEM 639 659 Potential.
 FT DOMAIN 660 835 Cytoplasmic (Potential).
 FT REPEAT 32 52 LRR 1.
 FT REPEAT 53 75 LRR 2.
 FT REPEAT 76 99 LRR 3.
 FT REPEAT 100 123 LRR 4.
 FT REPEAT 148 172 LRR 5.
 FT REPEAT 173 196 LRR 6.
 FT REPEAT 201 224 LRR 7.
 FT REPEAT 227 251 LRR 8.
 FT REPEAT 305 330 LRR 9.
 FT REPEAT 370 393 LRR 10.
 FT REPEAT 396 419 LRR 11.
 FT REPEAT 420 443 LRR 12.
 FT REPEAT 468 492 LRR 13.
 FT REPEAT 493 516 LRR 14.
 FT REPEAT 518 540 LRR 15.
 FT REPEAT 542 563 LRR 16.
 FT REPEAT 565 589 LRR 17.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 237 237 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 281 281 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 835 AA; 96071 MW; DFSE16A30851B3A0 CRC64;

Alignment Scores:
 Pred. No.: 2.18e-239
 Score: 3382.00
 Percent Similarity: 86.79%
 Best Local Similarity: 80.12%
 Query Match: 3.89%
 DB: 1

Length: 835
 Matches: 661
 Conservative: 55
 Mismatches: 90
 Indels: 19
 Gaps: 3

US-09-396-985B-48 (1-50000) x TLR4_RAT (1-835)

QY 37555 GCAGAGTCTCTCTCTGCTACACATCAACCTGTTTCTGTCAGATTTCTCT 37614
 DB 14 ALLeuPheLeuSerCysLeuArgProGlySerLeuAsnProCysIleGlu-----Val 31
 QY 37615 TACAAATACATGGTAAATATCATATCTGT-----TTGATATCATAGTATG 37656
 DB 32 LeuProAsnIleThrTyGlnCysMetAspGlnAsnLeuSerIysIleProHIsAspIle 51
 QY 37657 GTAGGGACGTGTTATGTCATTAAGAGGTTTCTTTCAGCAAAATATACATAATGGTAT 37716
 DB 52 ProTySerThrIysAsnLeuAspLeuSerPheAsnProLeuIlyIleLeuAspSerTy 71
 QY 37717 CTCTTTTGCCCAT-----AGGTGTGAAATGAAC 37746
 DB 72 -SerPheThrAsnPheSerGlnLeuGlnTrpLeuAspLeuSerArgCysGluIleGluTh 91
 QY 37747 AATTGAAGACAGGATGGCATGGCTTTACACACCTCTCAAACTTGATATGTCAGAGAA 37806
 DB 91 rIleGluAspIysAlaTrpHisGlyLeuAsnGlnLeuSerThrLeuValLeuThrGlyAs 111
 QY 37807 CCTATCCAGATTTTCCCAAGAAAGTTTCTGAGCTAAAGTTTAGAATCTGT 37866
 DB 111 nProIleLysSerPheSerProGlySerPheSerGlyLeuThrAsnLeuGlnAsnLeuVa 131
 QY 37867 GGCTGTGAGACAAAATGGCCTCTGTAGAAAGCTTCCCTATTGACAGCTTATTAACCTT 37926
 DB 131 lAlaValGluThrLysMetThrSerLeuGlnGlyPheHisIleGlyGlnLeuIleSerLe 151
 QY 37927 AAAGAAATCAATGTGGCTCAAAATTTTATKATCTCTGTAACTTACCTGCAATTTTTC 37986
 DB 151 uLysLysLeuAsnValAlaHisAsnLeuIleHisSerPheLysLeuProGluTyPheSe 171
 QY 37987 CAATTCAGCAACCTAGTACATGTGATCTTTCTTAACTATATCAACTATTACTGT 38046
 DB 171 rAsnLeuThrAsnLeuGlnHisValAspLeuSerTyPheAsnTyIleGlnThrIleSerVa 191
 QY 38047 CAACGACTTACAGTTTCTACGTGAAATCCAAAGTCAATCTCTTTAGACATGTCTTT 38106
 DB 191 lLysAspLeuGlnPheLeuArgGluAsnProGlnValAsnLeuSerLeuAspSerLe 211
 QY 38107 GAACCCATTCATCTTCAATCAACCAAGCTTTCAGGAAATTAAGTCCATTAACCTGAC 38166
 DB 211 uAsnProIleAspSerIleGlnAlaGlnAlaPheGlnGlyLeuArgLeuHisGluLeuTh 231
 QY 38167 TCTAAGAGTAAATTTTAAATAGCTCAAAATATATGAAATCTGCTCAAAACCTGGCTGG 38226
 DB 231 rLeuAsnSerAsnPheAsnSerSerAsnValIleuLysMetCysLeuGlnAsnMetThrGl 251
 QY 38227 TTTACAGTCCATCGTGTGATCTTGGAGAAATTTAAAGATGAAAGAAATCTGAAATTTT 38286
 DB 251 yLeuHisValHisArgLeuIleLeuGlyGluPheLysAsnGluArgAsnLeuGlnUserPh 271
 QY 38287 TGAACCTTCATCATGGAAGAGCATGTGATGACCATTTGATGATGATTCAGGTTAAATA 38346
 DB 271 eAspArgSerValMetGluGlyLeuCysAsnValSerIleAspGluPheArgLeuThrTy 291
 QY 38347 TACAAATGATTTTCAAGATGATTTGTAAGTTCAATGCTGGCGCAATGTTTGTGCAAT 38406
 DB 291 rIleAsnHisPheSerAspAspIleTyPheAsnLeuAsnCysLeuAlaAsnIleSerAlaMe 311
 QY 38407 GTCTCTGCGAGGTGTATCTATAAATATCTAGAGATGTTCTTAAACATTTCAATGGCA 38466
 DB 311 tSerPheThrGlyValHisIleLysHisIleAlaAspValProArgHisPheLysTrpGl 331
 QY 38467 ATCTTTATCAATCATTTGATGATGTCACACTTTCGAAGCTTTCGATCTTACCCCTTTCT 38526
 DB 331 nSerLeuSerIleIleArgCysHisIleuLysProPheProLysLeuSerLeuProPheLe 351
 QY 38527 TAAAGTTTGACTTATCACTAATGAACAAAGGCTTATCAGTTTAAAAAGTGGCCCTTACC 38586
 DB 351 uLysSerTrpThrLeuThrAsnArgGluAspIleSerPheGlyGlnLeuAlaLeuPr 371
 QY 38587 AAGTCTCAGCTATCTAGATCTTATAGAAATGCACTGAGCTTTAGTGTTGCTGTCTTA 38646

DR	InterPro: IPR003591; LRR_tyr.
DR	InterPro: IPR000157; TIR.
DR	Pfam: PF00560; LRR; 8.
DR	Pfam: PF01582; TIR; 1.
DR	PRINTS: PR00019; LEURICHRPT.
DR	SMART: SM00082; LRCT; 1.
DR	SMART: SM00369; LRR_TYR; 1.
DR	SMART: SM00255; TIR; 1..
DR	PROSITE: PSS0104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response; Receptor; Signal; Transmembrane.
KW	Leucine-rich repeat; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 25 Potential.
FT	CHAIN 26 838 Toll-like receptor 4.
FT	DOMAIN 26 629 Extracellular (Potential).
FT	TRANSMEM 630 650 Potential.
FT	DOMAIN 651 838 Cytoplasmic (Potential).
FT	REPEAT 31 52 LRR 1.
FT	REPEAT 53 75 LRR 2.
FT	REPEAT 76 99 LRR 3.
FT	REPEAT 100 123 LRR 4.
FT	REPEAT 127 148 LRR 5.
FT	REPEAT 149 172 LRR 6.
FT	REPEAT 173 196 LRR 7.
FT	REPEAT 200 224 LRR 8.
FT	REPEAT 227 251 LRR 9.
FT	REPEAT 305 330 LRR 10.
FT	REPEAT 351 370 LRR 11.
FT	REPEAT 371 393 LRR 12.
FT	REPEAT 396 419 LRR 13.
FT	REPEAT 420 443 LRR 14.
FT	REPEAT 468 492 LRR 15.
FT	REPEAT 494 516 LRR 16.
FT	REPEAT 517 538 LRR 17.
FT	REPEAT 541 563 LRR 18.
FT	REPEAT 565 589 LRR 19.
FT	DOMAIN TIR.
FT	CARBOHYD 34 34 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 115 115 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 172 172 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 204 204 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 237 237 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 307 307 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 492 492 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 495 495 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 524 524 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 572 572 N-linked (GlcNAc . .) (Potential) .
FT	CARBOHYD 622 622 N-linked (GlcNAc . .) (Potential) .
QO	838 AA; 96277 MW; 129533596E08B48 CRC64;

Alignment Scores:	
Pred. No.:	1.12e-222
Score:	3155.00
Percent Similarity:	81.90%
Best Local Similarity:	72.14%
Query Match:	3.63%
DB:	1
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	Matches: 619
	Conservative: 76
	Mismatches: 111
	Indels: 52
	Gaps: 8
US-09-396-985B-48 (1-50000) x TLR4_CRIGR (1-838)	

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OY 37409 TGCATAAATTAATTAAGACTACTACATATCAACGTCTTTATGTATGCCCAAGTTATGATC 37468
      |||:::|      |||:::|
Db 28 CysValGluValaIseSerAsnThrSerGlyL-----CysMetArg 41
      |||:::|      |||:::|
OY 37469 TTGAATTGATTTTTTTTCATAGATTCCTGCGCTGACATAGTGTGATGTTTATCATCACT 37528
      |||      |||:::|
Db 42 ArgAsn-----LeuAsnLysIleProAspAsnIle----- 51
      |||      |||:::|
OY 37529 GTACCAAGTGTGAATAATGACAAATCTGCAGAGTTCTCTCTGCTACACCATCATCACC 37588
      |||:::|      |||:::|
Db 52 ProSerSerVallySHisLeuAspLeu---SerPheAsnProLeuLysThrLeu----- 68
      |||:::|      |||:::|
OY 37589 TGTTTTGTCTGTACAGTTTCTCTTACCAATAACATGTATATCATATCTGTTGTATAC 37648
      |||:::|      |||:::|

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Db	69	-----Glyserhisserphe-----	73
Qy	37649	ATAGTATGTGAGGACTGTATGTCAATTGAAAGGTTTTTTTTTCAGCAAAAATACATA	37708
Db	74	-----Pheasnphprodiuleuylsueu	81
Qy	37709	ATTGGATCTCTTTTGCCCATAGGTGTGAAATTGAAACAATTGAGACACAGGATGGCAT	37768
Db	82	Leuaspseuser-----AGCySgIuilegIuthrileGluaspIyalaIatrgIn	98
Qy	37769	GCGTTACACCACTCTCCAACTTGATAGTACGAGAAACCCTATCCAGATTTTTCCCCA	37828
Db	99	GlyeuhIegIeuthrThrleuileleuthrGlyAsnProileGlnAsnleuserIys	118
Qy	37829	GGAAGTTCTCTGGACTTAACAGTTTAGAAGATCTGTGGCTGTGGAGACAAATTGGCC	37888
Db	119	GlyThrpheSerGlyleuAlaAsnleuGlnAsnleuValAlaValaGluIleIysleuAla	138
Qy	37889	TTCCTGGAAGGCTTCCCTATATGGACGCTTATACCTTAAAGAACTCAATGGCTCAC	37948
Db	139	SerleuaspserleuProileGlyHisleuValThrleuIyIsleuAsnValAlaHis	158
Qy	37949	AATTTTATACATTCCTGTAGTACCTCGCATATATTTTCCAACTCGACGAACTAGACAT	38008
Db	159	AsnleuileHisSerThelysleuProGluIyThrpheSerAsnleuThrsnleuGluHis	178
Qy	38009	GTCGATCTTTCTTATATACCTATATTCACACTATTACTGTCAACGACTTACAGTTTCTACGT	38068
Db	179	LeuaspseuserAsnleuIyIleGlnIthrIleTyIyThraspIeugInIthrleuArg	198
Qy	38069	GAATAATCCAAATCCATCTCTCTTTAGACATGTCTTGAACCCATAGCACTTCATTCOA	38128
Db	199	GluasnProIleuAsnleuSerleuGluIleuSerleuAsnProileaspheIleGln	218
Qy	38129	GACCAACCTTTCAGGGAATTGAAGTTCACATGAACTACTCTAAGAGGTATTTTAAATAC	38188
Db	219	ProGlyAlaIahelGlnGlyIleArgleuHisIegIeuthrleuArgSerAsnphensSer	238
Qy	38189	TCAAATATTAATGAAAACTTGCCCTTCAAACTGTGGCTGTGTTTACACGTCATCGGTTGATC	38248
Db	239	ThrasnValMetIyStrIyCysIleHisAsnleuAspGlyleuGlnValHisArgleuIle	258
Qy	38249	TTGGGAAATATTTAAAGATGAAGAATCTGGAAATTTTGAACCCCTCATCATGGAAGA	38308
Db	259	LeuGlyIuIphelysAsnGluAspAsnValaGluArgphAspArgIyValIleGluGly	278
Qy	38309	CTATGATCATGTGACCAATGATGAGTTCAGGTTTACATATACAAATGATTTTTCAGATGAT	38368
Db	279	LeuCyAlaIyValIthrIleGluGluIuIphArgphethrThyAlaAsnIuIpheserGluAsp	298
Qy	38369	ATTGTTAAGTTCATGTCCTTGCGGAATGTTTTCGCAATGTCTCTGGCAGGTGATCTATA	38428
Db	299	IleThraspheAspCysleuAlaAsnValSerAlaMetSerleuIlaAsnValIyIleu	318
Qy	38429	AAATATTTAGAAGATGTTCTTAACAATTTCAATGGCAATCCCTATCATCATTAGATGT	38488
Db	319	LysArgleuGluIuIspIleProIyIyThrpheIyItrGlnIthrleuAlaValIleArgCys	338
Qy	38489	CAACTTGAAGAGTTTCCAACTCGCAATCACCTTTCTTAAAGTTCATTAACTTAACTAAG	38548
Db	339	GluIleuIySgInIphProIProIeGluIuIleuIProIphleuIyArgleuIleIheIlethr	358
Qy	38549	AACAAAGGCTCATCATGTTTAAAAAAAGTGCCCTTACCAAGTCTCAGCATCTCATGTTT	38608
Db	359	AsnIySgIyAlaIthrSerThrpheProGluValaAsnleuProSerleuThrpheIuAspIleu	378
Qy	38609	AGTAGAAATSCATGACCTTTAGTGTGTGTGTTTATTTCTGATTTGGGAAACAAACAGC	38668
Db	379	SerGlyAsnGlyMetSerThrpheArgIyCysCysSerIyThraspIeugIyAlaArgSer	398
Qy	38669	CTGAGACACTTAAGACCTCAGACTTCATATGGGCAATCATATATAGTGCCAAATTCAGGT	38728
Db	399	LeuIyHisleuAspIeuserIphAsnGlyValIleSerMetSerIeIuAsnIphMetGly	418

QY	38729	CTGAAGACGCTGAGACACCGTGAATTTTTCAGCACTGACTTAAATAAAAGGCTCAAAATTC	38729
	419	LeuGIuGIuLeuGIuTyrLeuAapRheGlnHisSerThrLeuLysValaThrGIuRhe	438
QY	38789	TCAAGCTTTTATTCCTTTGAAAAGTACTTTACCTTGACATCTTATATCAACCAAA	38848
	439	SerMetRheLeuProLeuGIuLysLeuLeuTyrLeuAspLysSerTyrThrAsnThrLys	458
QY	38849	ATTGACTTGCATGAGTAAATTTCTTGGCTTGACCAAGTCAACCACTTAAATTAATGGCTGGC	38908
	459	IleAspRheAsnGIuLysIlePhePheGIuLeuThrSerLeuAsnThrLeuLysPheCalaGIu	478
QY	38909	AATTTCTTCAAGACCAACACCCCTTTCAAATGCTTTTGCAACCAACAACTTGACATTC	38968
	479	AsnSerRheLysAspAsnLysIleLeuSerAsnValPheThrAsnThrThrAsnLeuThrPhe	498
QY	38969	CTGACTTTTCTTAAATGTCAATTTGAACAAATATCTTGGGGGATATTGACACCTCCAT	39028
	499	LeuAspLysSerLysCysGIuLeuGIuGIuValSerTrpGIuValPheAspThrLeuHis	518
QY	39029	AGACTTCAATTAATTAATATGAGCAACAACATCTATGTTTGGATTCAATCCCACTTAT	39088
	519	ArgLeuGIuLeuLeuAsnMetSerHisAsnAsnLeuLeuLeuAspLeuPheHisTyr	538
QY	39089	AACCAAGCTGATTTCCCTCAGACACTCTTGATTGCAAGTTTCAATGCAATAGACATCTAA	39148
	539	LysGIuLeuHisSerLeuLeuLysThrLeuAspCysSerPheAsnHisIleGIuThrSerLys	558
QY	39149	GGAAATCTGCAACATTTTCCAAAGAGTCTAGCCTTCTTCAATTTTACTAAACATTTCTGT	39208
	559	GIuLysMetGlnHisPheProLysSerLeuValaPheLeuAsnLeuThrAsnProPhe	578
QY	39209	GCTGTATATGTAACAATCAAGAAATTCCTCAGTGGTCAAGAACAGACAGAGCTTCTTG	39268
	579	AlaCysIleCysGIuHisGIuAsnPheLeuGIuTrpValLysAspGlnArgLeuPheLeu	598
QY	39269	GTCGATCTTGAACAATGACATGTGCAACCTCTGAGATGTAATCTCTTATGTGTG	39328
	599	ValLysThrGIuGIuMetThrCysValaThrProValGIuMetLysAspSerLeuValLeu	618
QY	39329	GATTTTAAATTAATCTTACCTGTATATATATCAACAACATCATCTAGTGTGACAGGCTAGT	39388
	619	AspPheArgAsnAlaThrCysTyrValGIuLysThrIleIleSerValSerValIleSer	638
QY	39389	GTCATTTGATTCACCTGATGACATTTCTGATATACCACTTATTTTCACTGATATCTT	39448
	639	ValLeuValValSerThrIleAlaPheLeuValTyrLysPheTyrPheHisLeuIleLeu	658
QY	39449	ATTGCTTGGCTGTAAAAAGTACACAGACAGGAAGAAAGCATCTATGATGCAATTTTGATCTAC	39508
	659	IleAlaGIuCysLysLysTyrSerAlaGlyGIuHisSerIleLysArgAlaPheValIleTyr	678
QY	39509	TTCGATCAGATATGAGACTGGGTGAGAAATGACTGGTAAAGAAATTTAGAAAGAGAGTG	39568
	679	SerSerGIuAspGIuAspTrpValArgAsnGIuLeuValLysAsnLeuGIuGIuVal	698
QY	39569	CCCCGCTTTCACCTTCTGCTTCACTACAGACACTTATTTCTGTGTAGCATTGCTGCC	39628
	699	ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGIuAlaIleAlaIle	718
QY	39629	AACATATTCAGAGAGGCTCCCAAGAGCCGAAGGTTATCTGTGTAAGTCTACAC	39688
	719	AsnIleIleGIuGIuPheHisLysSerAlaLysValIleValValValSerArgHis	738
QY	39689	TTTATTCAGAGCCGTTGGTGTATCTTTGAAATATGAGATTGCTCAACATGGCAGTTTCTG	39748
	739	PheIleGIuSerArgTrpCysIlePheGIuTyrGIuIleAlaGlnThrTrpGIuPheLeu	758
QY	39749	AGCAGCCGCTGGCAGACATTTCAATTTGCTTGAAGAGTTTGAAGAGTTCAGAGTCCCTGCTGAG	39808
	759	SerSerHisSerGIuLysIleIlePheIleValLeuGIuLysValGIuLysSerLeuLeuLys	778

QY 39809 CACACAGTGAATTTGATGCGCTTCTTACAGAAACACTTACTGGAATGGAGACAT 39868
Db 779 GINGINVAIGIUNUUYRZRGLEUENUSERRAGSATHRTYLUENGLUTPOLUNSPHAN 798
QY 39869 CCCTCTGGGGGAGCATCTTCTTGAGAAAGACTTTAAATGCCCTATTTGAGTGAAGAACCC 39928
Db 799 AIALEUGLYARIGHIETIEPHERTPARGAGLEUUYLYALALEUENUSPGLYRGAIA 818
QY 39929 TCGAATCTGAGCAAAACAGCAGCAGAA-----CAAGAAAGGCAACT 39973
Db 819 TRPASNPROGLUQLYALATHRGUALAGUAENANGINGLUHRTHR 836
RESULT 5
TLR4_HUMAN STANDARD; PRT; 839 AA.
ID TLR4_HUMAN
AC O00206; Q9UK78; Q9UM57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll-like receptor 4 precursor (hToll).
GN Name=TLR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RX MEDLINE=97379437; PubMed=92337759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlburt P., Janeway C.A. Jr.;
RT "A human homologue of the Drosophila Toll protein signals activation
RT of adaptive immunity.";
RL Nature 368:394-397(1997).
RN [2]
RP SEQUENCE OF 41-839 FROM N.A.
RP TISSUE=Fetal liver, lung, and placenta;
RX MEDLINE=8118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
RA Rock F.L., Hardman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;
RA Arbour N.C., Lorenz E., Schutte B.C., Zabner J., Kline J.N., Jones M.,
RA Freese K., Mett J.L., Schwartz D.A.;
RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in
RT humans.";
RL Nat. Genet. 25:187-191(2000).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP MUTAGENESIS OF GLU-697, ARG-710, ASP-711 AND PRO-714.
RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RA Xu Y., Rao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domain.";
RL Nature 408:111-115(2000).
RN [7]
RP CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
RX MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;

QY 39494 GCATTGTGATCTACTGAGTCAGATAGAGTGGTGGAGAAATGAGCTGTGAAGAT 39553
 DB 676 AlahetValletIerIserIserGlnApGlnuAhrIahrgangluuValIahBn 695
 QY 39554 TTGAAGAGAGAGTGGCCCGCTTACCTTGCCTTCACTACAGAGACTTTATCTGGT 39613
 DB 696 LengludluglyValIProProPhGlnIeucYseruHsIryrAargapPheilleProGly 715
 QY 39614 GTAGCCATTCGTCACATCATCATCAGAGGCTTCCACAGAGCGGAGGATATGTG 39673
 DB 716 ValAlaIlealaaIaaanIleIleHieGlnIyPheHsIySserAargLysValIleVal 735
 QY 39674 GTAGTGTCTAGACACTTATTCAGAGCGGTGTGTATCTTTGAATATGAGATTCTCAA 39733
 DB 736 ValValserGlnHsPheIleGlnIserAargIryrPheIlePheGlnIyrgluIleAlGln 755
 QY 39734 ACATGCGAGTTTCTGAGAGCGCGCTTGGCATCATCTTCTGCTTGAAGAGTTGAG 39793
 DB 756 ThrIrypGlnPheIleuSserAargIyIleIlePheIleValIleGlnIyValGln 775
 QY 39794 AAGCCCTGCTGAGGAGCGAGTGGATTTGATGCTTCTTACAGAAACACTACCTG 39853
 DB 776 LysThrIleuValGlnIValGlnIleuIyIryrIleuSserAargAthrIryIleu 795
 QY 39854 GAATGAGAGGACATCTCTTGGAGGACATCTTCTGAGAGACTTAAATGCCCTA 39913
 DB 796 GluIrypGlnuApsrValIleGlnIyAryHsIleIlePheIryAargLysValIleu 815
 QY 39914 TTGGATGAAAAGCCTCGAATCTTGGAGAACCA 39946
 DB 816 LeuApsIyIySserIryPasnProGlnIyIyThr 826
 RESULT 6
 TLR4_PANPA STANDARD; PRT; 839 AA.
 ID TLR4_PANPA
 AC Q9TTN0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NX NCBI_TaxID=9597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20558910; PubMed=11104518;
 RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 locus (TLR4)".
 RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MYD88, IRAK and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TLR4.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and IRAK via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@ebi.ac.uk).

DR EMBL; AF179220; AAF05320.1; -.
 DR EMBL; AF179219; AAF05320.1; JOINED.
 DR EMBL; AF179219; AAF05320.1; JOINED.
 DR HSSP; Q15399; 1FVY.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macrophage activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 DR KX Glycoprotein; Immune response; Inflammatory response;
 DR Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT CHAIN 1..23
 FT DOMAIN 24..839
 FT TRANSMEM 632..652
 FT DOMAIN 653..839
 FT REPEAT 52..76
 FT REPEAT 77..100
 FT REPEAT 101..124
 FT REPEAT 128..149
 FT REPEAT 150..173
 FT REPEAT 174..197
 FT REPEAT 203..225
 FT REPEAT 228..252
 FT REPEAT 277..303
 FT REPEAT 307..330
 FT REPEAT 332..350
 FT REPEAT 351..372
 FT REPEAT 373..398
 FT REPEAT 400..421
 FT REPEAT 422..445
 FT REPEAT 447..469
 FT REPEAT 470..494
 FT REPEAT 495..518
 FT REPEAT 520..541
 FT REPEAT 543..566
 FT REPEAT 568..592
 FT REPEAT 672..818
 FT DOMAIN 819..839
 FT CARBOHYD 173..173
 FT CARBOHYD 205..205
 FT CARBOHYD 282..282
 FT CARBOHYD 309..309
 FT CARBOHYD 497..497
 FT CARBOHYD 526..526
 FT CARBOHYD 575..575
 FT CARBOHYD 624..624
 FT CARBOHYD 630..630
 FT SEQUENCE 839 AA; 95637 MW; 3B328C5682127D57 CRC64;
 Alignment Scores: 2,46e-182 Length: 839
 Pred. No.:

QY	39934	TTTACCGGTAACCTTATTGCTGGCGCTGTAAAAAGTACAGCAGACGAGAAAGCACTTATGAT	39943
Db	656	PhehiIvneuectleueuAlaaglyCySlelyetyrGlyArgGlyGluSenlIetyrAsp	675
QY	39494	GCATTGTGATCTCTCTGAGTCAGAAATGAGAGACTGGGTGGAGAAATAGCTGGTAAAGAT	39553
Db	676	AlaheValIleIetyrIserSerGlnaSpGluInpTrpValAlaGsnIuIeuVallyIaSn	695
QY	39554	TTAGAGAGAGAGTGGCCCGCTTACCTCTGCTTCCTTACCTACAGAGACTTTATTCCTGAT	39613
Db	696	LeuGIuGIuGIyValProProPheGlnLeuCySleuhtIetyrArgaSpheIleProGly	715
QY	39614	GTAGCCATTTGGTGGCAATCATTCACGAGAGCGCTTCACAGAGCCGGAAGCTTATTCG	39673
Db	716	ValAlaIleAlaAlaSenIleIehtIeSgIuGlyPhehtIeSySerArguValIleVal	735
QY	39674	GTACTGTCTAGACACTTATTTACAGAGCGCTGGTGTATCTTTGAATATGAGATTGCTCA	39733
Db	736	ValValSerGlnhtIeSphelIeGlnSerArgTrpCyleIeheIuIyTrGluIleAlaGln	755
QY	39734	ACATGGCAGTTTCTGAGCAGCCGCTCTGGCATCATCTTCAATTGCTCTTGAGAAAGTTGAG	39793
Db	756	ThrTrpGlnPheIeuSerSerArgAlaGlyIleIleIePheIleValLeuGlnlyValGlu	775
QY	39794	AAGTCCTGCTGAGCAGCAGGTGGAATTGTATGCGCTTTTGCGAAACACCTACTCG	39853
Db	776	LysThrIeuLeuArgGlnGlnValGluLeuIyArgIeuLeuSerArgaSnThrIyIleu	795
QY	39854	GAATGGAGAGCAATCCTCTGGGGAGCAGCATCTTCTGAGAGAGACTTAAATAGCCCTA	39913
Db	796	GIuTrpGluIeSpSerValIeGlyGlnhtIlePhehtIyArgArgIeuArglySAlaIeu	815
QY	39914	TTGGATGAAAAAGCCTCAATCTCGAGCAA	39943
Db	816	LeuAepGlyArgSerTrpAenProGluGlu	825
RESULT 8			
ID	Q8SPER	PREDIMINARY;	PRT; 837 AA.
AC	Q8SPER;		
DT	01-JUN-2002 (TREMblrel. 21, Created)		
DT	01-JUN-2002 (TREMblrel. 21, Last sequence update)		
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)		
DE	Toll-like receptor 4.		
GN	Name=TLR4;		
OS	Gorilla gorilla (gorilla).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.		
OX	NCBI_TaxID=9593;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21405531; PubMed=11514453;		
RA	Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;		
RT	"Excess of rare amino acid polymorphisms in the Toll-like receptor 4		
RT	in humans.";		
RL	Genetics 158:1657-1664(2001).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF497565; AAM18617.1; -		
DR	EMBL; AF497563; AAM18617.1; JOINED.		
DR	EMBL; AF497564; AAM18617.1; JOINED.		
DR	HSSP; O60603; 1077.		
DR	GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.		
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.		
DR	GO; GO:0004888; F:transmembrane receptor activity; ISS.		
DR	GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.		
DR	GO; GO:0016046; P:detection of fungi; ISS.		
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.		
DR	GO; GO:0042116; P:macrophage activation; ISS.		
DR	GO; GO:0045576; P:mast cell activation; ISS.		
DR	GO; GO:0045671; P:negative regulation of osteoclast different. .; ISS.		

DB	Accession	Gene	Protein	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
DR	GO:00465362	P:positive regulation of interleukin-1 biosyn.	ISS.							
DR	GO:0045084	P:positive regulation of interleukin-12 biosyn.	ISS.							
DR	GO:0045368	P:positive regulation of interleukin-13 biosyn.	ISS.							
DR	GO:0045410	P:positive regulation of interleukin-6 biosyn.	ISS.							
DR	GO:0042088	P:T-helper 1 type immune response, ISS.								
DR	InterPro: IPR001611	LRR.								
DR	InterPro: IPR000483	LRR_Cterm.								
DR	InterPro: IPR003591	LRR_Cyp.								
DR	InterPro: IPR001571	TIR.								
DR	Pfam: PF01463	LRRCT1.								
DR	Pfam: PF00560	LRR_1.	10.							
DR	Pfam: PF01582	TIR_1.								
DR	PRINTS: PR00019	LEU1CHRT.								
DR	SMART: SM0082	LRRCT1.								
DR	SMART: SM00369	LRR_TYP.	2.							
DR	SMART: SM00255	TIR_1.								
DR	PROSITE: PS50104	TIR_1.								
KM	Receptor									
SEQ	SEQUENCE	837 AA;	95497 MW;	5A177BAB341396DD	CRG64;					
Alignment Scores:										
Pred. No.:	1,7e-180	Length:	837							
Score:	2582.00	Matches:	523							
Percent Similarity:	73.44%	Conservative:	102							
Best Local Similarity:	61.46%	Mismatches:	172							
Query Match:	2.97%	Indels:	54							
DB:	2	Gaps:	9							
US-09-396-985B-48 (1-50000) x Q8SPB8 (1-837)										
QY	37400	TGAAAAAATGCATAATTAATCTAAGACTACATCACTGCTTATATGATACCCCA	37455							
DB	26	TripLupProcyVal1-----ValProAsnIleThrTrgIn-----	37							
QY	37460	GTTATGATCTGGATGATGATTTTCTTAATGAGATTTGCTGCTGACATAGTGTGATGTTT	37519							
DB	38	CysMetGluLeuAsnPhenylTrpYsIleProAspAsnLeuPro-----	51							
QY	37520	ATCATCACTGTAGCAAGTGTGAATAATGACAAATCTGACAGTTCCTCTGCTGACACC	37579							
DB	52	-----PheSerThrIlybAsnLeuAspLeuSerPheAsnProLeuAlrghs---	66							
QY	37580	ATCATCACTGTTTGTCTGTACAGTTCCTTCTTACAAATACATGATATCATATCT	37639							
DB	67	-----LeuGlySerTyrSerPhe-----	72							
QY	37640	GTTTGATCATTAGTATGATGAGGACCTGTATATGATTAAAGAGGTTTTTTTTCAGCA	37699							
DB	73	-----PheSerPheProGlu---	77							
QY	37700	AAATACATAATGGATATCTCTTTGGCCATAGGTGTAATGAACAATGAAGAACAAG	37758							
DB	78	LeuGlnValLeuAspLeuSer-----ArgCysGluIleGlnThrIleGluAspGly	94							
QY	37760	GCATGAGCATGGCTTACACACACCTCTCAAACTTGATATCTGACAGAAACCTTATCCAGCT	37819							
DB	95	AlaIlyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrClybAsnProIleGlnSer	114							
QY	37820	TTTTCCCAAGAAATTTCTCTGACATCAAGATTTGAGAATCTGGTGGCTGTGAGACA	37879							
DB	115	LeuValLeuIlyAlaPheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGluThr	134							
QY	37880	AAATGGACCTCTGAGAAAGCTTCCATTTGAGCAGCTTATATACCTTAAGAAAGCTCAAT	37939							

QY	39137	GAGGACATCT---	AAAGGAAATACATCGCAACATTTTCCAAAGAGTGTAGCCTTCTTCATCTT	39193
Db	555	MetThieriselysilysgingulubegulinhisphreProSeSerleudialpheleudinhieu	574	
QY	39194	ACTAACAAATTCGTGGCTTGATATATGTGAACATCAGAAATTCCTGCAGTGGGTCAAGAA	39253	
Db	575	ThirGiniambsrphnealacysThrCysGulinhisGInserPheleudIntPrilleybaer	594	
QY	39254	CAGAAAGCATTTCTTGCGAATGTTTGAACCAATGACATGACATGTGGCAACACCTGTAAAGATGAAT	39313	
Db	595	GlnarGclnleueulvalGluvalGluarGmetGulCysalathrProSeKspsrlysgln	614	
QY	39314	ACGTCCTTAGNGTGGATTTTAATTAATTCACCTGTTATATGATTAACAGACATTCATCACT	39373	
Db	615	GlymetProValleuSerleu---AmlllethrCysGlnmetKasnllystrlillellegly	633	
QY	39374	GTCGCACTGGTCAGTGTGATTTGTGTATCCATGTAAGCATTTTCTGATATACCACTTCTAT	39433	
Db	634	ValSerlialleuSerValleuValValSerValValalValleuVallyllyrlysrphetyr	653	
QY	39434	TTTCACTGATTAATTTATGCTGCTGTAAAGTACAGACAGAGAAAGCATTTATGAT	39493	
Db	654	PhehisleuemetleuadlaglyCyslylelytyrGlyArGglyGlnuambValtyrAsp	673	
QY	39494	GCATTTTGATTCATCTGACATGACATGACAGACTGGGTGAGAAATAGCTGGTAAAGAT	39553	
Db	674	AlaIheValillelyrSerSerGlnasrPrlyValAlaGasnGluuVallylsbaen	693	
QY	39554	TTAGAAACAGAGTGGCCCGCTTTCACCTGCTGCTTCACTACAGAGACTTTATTCCTGGT	39613	
Db	694	LeuglunGlnlyValProPorphieGlnleuCysleuhistyrAlrAsrPheilleProGly	713	
QY	39614	GTAAGCATCTGCTCCACATCATCCAGAAAGGCTTCCACAAGAGCCGAGAGTTATGTG	39673	
Db	714	ValAlaIleAlaIleAlaAsnIlellethlsGlnGlyPhehislelySerAlrGlyValilleval	733	
QY	39674	GTAATGCTAGACACTTTATTCAGACACCGTGGTGTATCTTTGAATATATGAATTCGTCA	39733	
Db	734	ValValSerGlnhisphreilleGlnSerAlrGlyrCysAllephGlnlyrGlnillealagln	753	
QY	39734	ACATGAGCAAGTTTCTGAGACAGCCGCTGGCATCATCTTCATTTGCTTGAGAAAGGTGAG	39793	
Db	754	ThirTrpGlnpheleuSerSerAlrGlnlyllellelpherilleValleuGlnlysrValGln	773	
QY	39794	AAATCCCTGCTGAGGACGACAGGTGGAATGTATCGCTTCTTAGAGAAACAACCTTAACCTG	39853	
Db	774	lysrThrieleuKnrGlnGlnGlnValGlnleuTyrAlrGlnleuSerAlrGAsnThrlyrleu	793	
QY	39854	GAATGGAGAGCAATCTCTGTGGGAGGACACATCTTGTGGAGAAAGCTTAAAAATGCCCTA	39913	
Db	794	GlnTrpGlnAsrPheValleuGlnlyArGlnhisillepherTrAlrGAsrGlnuArGlysrAlaleu	813	
QY	39914	TTGGATGGAAAGACCTCGAATCCTTAGGCAAAACA	39946	
Db	814	LeuAspGlylysrSerTrpAsnProGlnGlyThr	824	
RESULT 9				
TLR4_PONPY				
ID	TLR4_PONPY	STANDARD:	PRT:	828 AA.
AC	Q8SPB9;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor.			
GN	Name=TLR4;			
OS	Pongo pygmaeus (Orangutan).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.			
OX	NCBI_Taxid=9600;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=21405531; PubMed=11514453;			
RA	Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;			

Db 175 LeuGluHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyrCysLeuAspLeuGln 194
 Qy 38060 TTCTTACAGTGAATAATCCACAATGCAATCTCTTATGACATGCTTTTAAACCAATGAC 38119
 Db 195 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnIleMetAsn 214
 Qy 38120 TTCAATTCAGAACCAAGCCTTTGAGGAAATTAAAGCTCCAGTAACTGACTCTTAAGAGTAA 38179
 Db 215 PheIleGlnProGlyAlaPheLeuSerGlnIleArgLeuHisLysLeuThrLeuArgAsnSer 234
 Qy 38180 TTTAAATGCTCAATATATATAAAATCTGCTTCAAAATCTGGCTGGTTTACAGTCCAT 38239
 Db 235 PheAspSerLeuAsnValMetLysThrCysIleGlnLysLeuAlaGlyLeuGlnValHis 254
 Qy 38240 CGGTGATCTTGGGGAATTTAAAGATGAAGAATGGAATTTGGAACCCCTATC 38299
 Db 255 HisLeuValLeuGlnLysPheArgAsnGlnLysAsnLeuGlnLysPheAspThrSerAla 274
 Qy 38300 ATGGAAGACTATGATGATGACCAATGATGAGTTGAGGTTTAAACATATATATATTT 38359
 Db 275 LeuGlnLysLeuCysAsnLeuThrIleGlnLysPheArgLeuAlaTyrLeuAspTyrTyr 294
 Qy 38360 TCAAGTATATTTTAAAG---TTCCATTGCTTGGCGAATGTTTTCGCAATGCTTGGCA 38416
 Db 295 LeuAspAspIleIleAspLeuPheAsnLysLeuAlaAsnValSerSerPheSerLeuVal 314
 Qy 38417 GGTGATCTATATATATATCTAAGAGATGTCCTTAACTTCAATGGCAATCCTTATCA 38476
 Db 315 SerValThrIleLysSerValLysPheSerTyrAsnPheGlyTyrGlnHisLeuGln 334
 Qy 38477 ATCATAGATGCAACTTAACAGTTTCCAACTGATGATCACTTCTTAAAGTTT 38536
 Db 335 LeuValAsnLysCysPheGlyGlnPheProThrLeuGlnLysSerLeuLysArgLeu 354
 Qy 38537 ACTTTAATGAAACAAGGCTTATCACTTTTAAAAAGTGGCCCTTCAAGTCTCAAC 38596
 Db 355 ThrPheThrAlaAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGln 374
 Qy 38597 TATCTAGATCTTAGAGAAATGACCTGAGCTTGTGCTGCTTCTTATCTTATGATTG 38656
 Db 375 PheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysPheSerGlnSerAspPhe 394
 Qy 38657 GGAACAACAGCCTGAGACCTTGAAGCTTCAATGATGATGATGATGATGATGATGATG 38716
 Db 395 GlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnAspValIleThrMetGlySer 414
 Qy 38717 AATTTCATGGCTTGAAGAGCTGACAGCTGATTTTCAAGCTTCACTTAAAGAG 38776
 Db 415 AsnPheLeuGlnLysLeuGlnLysLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGln 434
 Qy 38777 GTACAGAAATCTGAGGCTTCTTATCCTTGAAGAACTTCTTGAATCTTAT 38836
 Db 435 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 454
 Qy 38837 ACTTAACCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 38896
 Db 455 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuLysValLeu 474
 Qy 38897 AAAATGCTGGCAATCTTTCAAAAGACCAACCTTTCAATGCTTTGCAAAACACA 38956
 Db 475 LysMetIleGlyAsnSerPheGlnLysAsnPheLeuProAspIlePheThrGlnLeuArg 494
 Qy 38957 AACTTGACATTCGAGATCTTCTTAATGATGATGATGATGATGATGATGATGATGATG 39016
 Db 495 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLysSerProThrAlaPhe 514
 Qy 39017 GACACCTTCATAGACTTCAATTAATTAATGATGATGATGATGATGATGATGATGATG 39076
 Db 515 AsnSerLeuSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp 534
 Qy 39077 TCATCCATTAATTAACAGCTGATTTCCCTGACAGCTTGTGATGATGATGATGATG 39136
 Db 535 ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 554

Qy 39137 GAGACATCT---AAGAATACTGCAACATTTTCCAAAGATGATGATGATGATGATGATG 39193
 Db 555 MetHisSerLysLysGlnLysLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 574
 Qy 39194 ACTTAACATTTCTGCTGCTTGTATATGTTGAACATGATAAATTTCTGACAGTGGCTCA 39253
 Db 575 ThrGlnAsnAspPheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnTyrIleLysAsp 594
 Qy 39254 CAGAGAGATTTCTGGGGAATGTTGAACAATGACATGTCGAACACCTGATGATGATGAT 39313
 Db 595 GlnArgGlnLeuLeuValGlnValGlnArgMetLysCysAlaThrProSerAspLysGln 614
 Qy 39314 ACTCTCTAGTTGTTGATTTTAAATTTTCACTGATTAATTTGTTCAACAACATCACT 39373
 Db 615 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnLysThrValIleGly 633
 Qy 39374 GTGTCAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 39433
 Db 634 ValSerValPheSerValLeuValValSerValValAlaValLeuValTyrLysPheTyr 653
 Qy 39434 TTTTACCTGATCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 39493
 Db 654 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnThrTyrAsp 673
 Qy 39494 GCATTTGATCTTACTGAGTCAAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 39553
 Db 674 AlaPheValIleTyrSerSerGlnAspGlnAspIleTyrValArgAsnGlnLeuValLysAsn 693
 Qy 39554 TTGAGAAGAGATGCCCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 39613
 Db 694 LeuGlnLysValProThrPheGlnLeuLysCysLeuHisTyrArgAspPheIleProGly 713
 Qy 39614 GTAGCATTGCTGCGCAATCATCATGACAGAGAGCTTCCACAAGAGCCGGAAGATTATG 39673
 Db 714 ValAlaIleAlaAlaAsnIleIleHisGlnLysPheHisLysSerArgLysValIleVal 733
 Qy 39674 GTAGTCTCTGACACTTATTTACAGAGCGTGGTGGTATCTTTGAATGATGATGATGAT 39733
 Db 734 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlyTyrGlnIleAlaGln 753
 Qy 39734 ACATGAGATTTCTGACAGCCGCTGTCGATCATCTTCAATGCTTGAAGAGTGGAG 39793
 Db 754 ThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 773
 Qy 39794 AAGTCCCTGCTGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 39853
 Db 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
 Qy 39854 GAATGGAGGACATCCTTGGGGAGGACATCTTCTGGAAGACCTTAAATGAGCCCTA 39913
 Db 794 GlnTyrGlnAspSerValLeuGlyArgHisIlePheThrArgLeuArgLysAlaLeu 813
 Qy 39914 TTGATGAAAAGCTTGAATCTTGAACAACA 39946
 Db 814 LeuAspGlyLysSerTyrAsnProGlnLysTyr 824

RESULT 10
 TLR4_BOVIN
 ID TLR4_BOVIN STANDARD; PRT; 841 AA.
 AC 09GL65;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-1ike receptor 4 precursor.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eupleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Guionaud C.T., Dubey C., Jungi T.W.;
 RT "Ovine Toll-like receptor 4 (TLR4).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>/
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: AF310952; AAC32061.2; -.
 DR HSSP: O60603; LFYX.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:macrophage activation; ISS.
 DR GO: GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR004833; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF00560; LRR: 13.
 DR Pfam: PF01463; LRRCT: 1.
 DR Pfam: PF01582; TIR: 1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00369; LRR_TYP: 1.
 DR SMART: SM00082; LRRCT: 1.
 DR SMART: SM00255; TIR: 1.
 DR PROSITE: PS50104; TIR: 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 841 Toll-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 841 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 102 124 LRR 3.
 FT REPEAT 149 173 LRR 4.
 FT REPEAT 174 197 LRR 5.
 FT REPEAT 203 225 LRR 6.
 FT REPEAT 277 300 LRR 7.
 FT REPEAT 310 334 LRR 8.
 FT REPEAT 350 372 LRR 9.
 FT REPEAT 373 398 LRR 10.
 FT REPEAT 400 421 LRR 11.
 FT REPEAT 422 445 LRR 12.
 FT REPEAT 446 469 LRR 13.
 FT REPEAT 471 494 LRR 14.

FT REPEAT 495 518 LRR 15.
 FT REPEAT 520 542 LRR 16.
 FT REPEAT 544 566 LRR 17.
 FT REPEAT 568 592 LRR 18.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 841 AA; 96026 MW; C5E17CB9C798CD16 CRC64;
 Alignment Scores:
 Pred. No.: 3,36e-180 Length: 841
 Score: 2578.00 Matches: 520
 Percent Similarity: 72.02% Conservative: 103
 Best Local Similarity: 60.12% Mismatches: 188
 Query Match: 2.97% Indels: 54
 DB: 1 Gaps: 8
 US-09-396-985b-48 (1-50000) x TLR4_BOVIN (1-841)
 QY 37400 TGGAAAAAATGTAATTAATTAAGACTACATATCAATGCTTTATGTACCCCA 37459
 DB 26 TIRAPProcyvalGlnValProaenIleSerToln----- 39
 QY 37460 GTTATGATCTTGAATGATTTTCTTAATGATTTCTGCGTCGACATAGTATGTTT 37519
 DB 40 CyMeGlnLeuSsnLeuTyrlsleProaBsnIlePro----- 53
 QY 37520 ATGATCATCTGACGAAGTGAATAATGACAAATCTGACAGTTCCTCTGCTACACC 37579
 DB 54 -----IleSerThrIysMetLeuAspLeuSerPheAsnTyrlLeuAArgHis--- 68
 QY 37580 ATGATCACCGTTTGGCTGCTGATAGTTTCTGTTTCAATTAACATGATATCATATCT 37639
 DB 69 -----LeuGlySerHisAsnPheSer----- 75
 QY 37640 GTTGTATCATAGTATGATGAGGACTGTATGTCATTAAGAAAGGTTTTCACGAA 37699
 DB 76 -----SerPheProGlu 79
 QY 37700 AAATPACATTAATGATATCTTTTGGCCATAGTGGAATTAACATTAAGACACAG 37759
 DB 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleLeuIleIleGlnAspAsp 96
 QY 37760 GCATGCGATGCTTACACCAACCTCTGAATTAATCTGACAGAAACCTATCCAGAGT 37819
 DB 97 ThnPheGlnIleLeuSsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 116
 QY 37820 TTTTCCCGAAGATTTCTTGAGACTPACAGTTTGAAGATCTGAGTGGCTGAGAGACA 37879
 DB 117 LeuAlaIrrpGlnAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThr 136
 QY 37880 AAATGGCTCTCTAGAAAGCTTCCCTATTGACAGCTTAAACCTTAAGAAATGCAAT 37939
 DB 137 AsnLeuValSerLeuAsnAspPheProIleGlyHisLeuIleAsnLeuIleGlnLeuAsn 156
 QY 37940 GTGGCTCACAATTTTATACATCTCTGTAATTAACCTGACATATTTTCCATTCGACGAC 37999
 DB 157 ValAlaHisAsnPheIleHisSerPheIleProGlnIleTyrlPheSerAsnLeuProAsn 176
 QY 38000 CTATGATCATGATCTTTCTTATACATATTAATTAATCTATCTGACACGACTTACAG 38059
 DB 177 LeuGlnHisLeuAspLeuSerAsnAsnIleIleGlnAsnIleTyrlTyrlAspValIys 196
 QY 38060 TTTCATGTAATAATCCACAAGTCAATCTCTTTTACACATGCTTTGAAACCAATTTGAC 38119
 DB 177 LeuGlnHisLeuAspLeuSerAsnAsnIleIleGlnAsnIleTyrlTyrlAspValIys 196

Db 197 ValLeuHhSgLMecProLeuLeuSerLeuAspSerLeuAsnProLeuAsp 216
 QY 38120 TTCATTCAGAACCAAGCCTTTCAGGGAATTAGCTCCATGACTGACTCTTAAGAGTAA 38179
 Db 217 PheIleGluProGlyThrPheLeuSgUileuSLeuAsnGlyLeuThrLeuArgSerAsn 236
 QY 38180 TTTAATAGCTCAATATATAATGAAAACCTTGCTCAAAACCTGGCTGGTTTACACGTCAT 38239
 Db 237 PheAsnSerSerHValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuSerThrAsn 256
 QY 38240 CGGTGATCTTGGGGAATTTAAAGATGAAAGAACTTGGAATTTTGAACCCCTCTATC 38299
 Db 257 ArgLeuValLeuGlyGluPheLeuSasngluArgVleuGlnArgPheAspArgSerPhe 276
 QY 38300 ATGAAGAGCTATGATGATGACCAATGATGAGTTCAGGTAACTATACAAATGATTTT 38359
 Db 277 LeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgIleAlaTyLeuAspArgPhe 296
 QY 38360 TCA---GATGATATTTGTTAAGTTCCATTTGCTGGCAATGTTTGCACATGCTTGCA 38416
 Db 297 SerGlyAspAspThrAspLeuPheAsnGlyLeuAlaAsnValSerValIleSerLeuLeu 316
 QY 38417 GGTGATCTATATAATATCTAGAAGATGTTCTTAACATTTTGAATGGCAATCCTTATCA 38476
 Db 317 SerIleSerLeuGlySerLeuGlnAlaLeuLeuVAspPheArgTrpGlnHISLeuGlu 336
 QY 38477 ATCATTAAGATGCACTTAAGCAGCTTCCCACTGATCTGATCTACCTTTCTTAAAGTTTG 38536
 Db 337 IleIleAsnGlyAspPheAspArgPheProAlaLeuVleuSerSerLeuValSerPhe 356
 QY 38537 ACTTTAATATGAAACAAAGGCTCTATCAGTTTAAAAAAGGCCCTTACCAAGTCTCAGC 38596
 Db 357 ValPheThrAspAsnLeuAspIleSerThrPheThrGluPheGlnLeuProSerLeuGln 376
 QY 38597 TATCTAGATCTTAGAGNAAAGCACTGAGCTTATGAGTGGTGTCTTCTTATTCGATTTG 38656
 Db 377 TyrLeuAspLeuValArgAsnHISLeuSerPheValGlyCysSerHISThrAspPhe 396
 QY 38657 GAAACAAACAGCCTGAGACACTTAGACCTTCAATGGTGCATGATCATTAATGAGTCC 38716
 Db 397 GlyThrThrAsnLeuValHISLeuAspLeuSerPheAsnAspValIleThrLeuValSer 416
 QY 38717 AATTGATGGCTTGAAGAAGCTGAGACCTGATTTTCAAGCACTTACTTAATTAAGAA 38776
 Db 417 AsnPheMetGlyLeuGlnGlnLeuGlnHISLeuAspPheGlnHISerThrLeuValSgIn 436
 QY 38777 GTCAAGAAATTCAGCCTTCTTATCCCTTGAAGAAAGCTTACTTACCTTGAATCTTAT 38836
 Db 437 IleAsnAlaPheSerAlaPheLeuSerLeuArgAsnLeuArgTyLeuAspIleSerTyx 456
 QY 38837 ACTAACAACCAAAATGATCGATGATATTTCTTGCTTGAACCAAGTCTCAACCATTA 38896
 Db 457 ThrAsnIleArgIleValAlaPheHISGlyIlePheThrGlyLeuValSerLeuGlnThrLeu 476
 QY 38897 AAAATGGCTGCAATCTTTCAAGAACAAACCCCTTTCAAATGCTTTGCAAAACACAA 38956
 Db 477 LysMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAlaIlePheThrGlnLeuThr 496
 QY 38957 AACTTGACATTCCTGATCTTTCTTAATGATGATTTGCAACAAATATCTTGGGGGATTT 39016
 Db 497 AsnLeuThrValLeuAspLeuSerTyCysGlnLeuGlnGlnValAlaGlnThrAlaPhe 516
 QY 39017 GACACCTCCATAGACTCAATTAATTAATGATGACCAACATCTATGTTTGGAT 39076
 Db 517 HisSerLeuSerSerLeuGlnGlnLeuAsnMetSerHISAsnVleuLeuSerLeuAsp 536
 QY 39077 TCATCCCATTAATAACAGCTGATATTCCTCAGCACTTTGATGCAAGTTTCAATCGATA 39136
 Db 537 ThrPheLeuTyrgluProLeuHISerLeuArgIleLeuAspCysSerPheAsnArgIle 556
 QY 39137 GAGACATCTAA---GGAATCTGCAACATTTTCCAAAGATCTAGCCTTCTTCAATCTT 39193
 Db 557 MetAlaSerTyrgluGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsnLeu 576

QY 39194 ACTAACAATCTGTTGCTTGTATATGTAACATCAGAAATTCCTGAGGGGTCAAGGA 39253
 Db 577 ThrGlnAsnAlaPheAlaCysValCysGlnHISglnSerPheLeuGlnTrpValLysAsp 596
 QY 39254 CAGAAAGACTTCTTGATGAAATGTTGAACAAATGACATGTGCAACACTGAGAGATGAAT 39313
 Db 597 GlnArgGlnLeuLeuValGlyValGlnGlnMetMetCysAlaGlnProLeuAspMetGln 616
 QY 39314 ACCTCCTTAGTGGTGAATTTAATATCTTACCTGTATATGATACAAACATCTACGT 39373
 Db 617 AspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerTyThrIleLeSer 636
 QY 39374 GTGTGAGTGCAGGATGATGATATTCACCTGAGCAATTTGATATACCACTTAT 39433
 Db 637 ValSerValValThrValLeuLeuValSerValValGlyValLeuValTyLeuPheTyx 656
 QY 39434 TTTCACTGATATCTTATTTGCTGGCTGTAAAGTAACAGCAGAGAGAAAGCATCTATGAT 39493
 Db 657 PheHISLeuMetLeuLeuAlaGlyCysValSerTyrglyArgGlyGluSerIleTyxAsp 676
 QY 39494 GCATTTGTGATCTTACTGAGTCAGATCAGAAATGAGACTGGGTGAGAAATGACTGTAAAGAT 39553
 Db 677 AlaPheValIleTyxSerSerGlnAspGluAspTrpValArgAsnGlnLeuValLysAsn 696
 QY 39554 TTAGAAGAGAGTGGCCCGCTTACCTGCTGACCTTCACTGACAGACTTATATTCCTGCT 39613
 Db 697 LeuGlnGlnGlyValAlaProProPheGlnLeuCysLeuHISTyxArgAspPheIleProGly 716
 QY 39614 GTAGCATTGCTGCAACATCATCATCAGAAAGCTTCCACAAAGCCGGAAGTTATGCTG 39673
 Db 717 ValAlaIleAlaAlaAsnIleIleGlnGlnGlyPheHISTyxSerArgGlyValIleVal 736
 QY 39674 GTAGTGTCTAAGCACTTATATCAAGCCGTTGGTGTATCTTGAATATGAGATTGCTCA 39733
 Db 737 ValValSerGlnHISpheIleGlnSerArgTrpCysIlePheGlnTyrgluAlaGln 756
 QY 39734 ACATGGAGGTTTTCAGAGAGCCGCTGAGCACTCATCTTCAATGCTTGAAGAGTTGAG 39793
 Db 757 ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGln 776
 QY 39794 AAGTCCCTGTGAGCAGCAGAGTGAATGTATGACCTTCTTACAGAAACACTTACCTG 39853
 Db 777 LysSerLeuLeuArgGlnGlnValGlnLeuTyxArgLeuLeuSerArgAsnThrTyxLeu 796
 QY 39854 GAATGGAGAGCAATCCTCTGGGAGGACCATCTTCTGAGAAACATTAAATGCCCTTA 39913
 Db 797 GluTrpGluAspSerValLeuGlyArgHISValAlaPheTrpArgLeuArgGlyAlaLeu 816
 QY 39914 TTGATGGAAGAAAGCCTGGAATCCTGAGCAACAGCAGAGGAAGAA-----CAAGAA 39964
 Db 817 LeuAlaGlyLysProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGln 836
 QY 39965 ACGGCAACTTGAGCC 39979
 Db 837 AlaThrThrSerThr 841

RESULT 11
 Q8S055 ID Q8S055 PRELIMINARY; PRJ: 841 AA.
 AC Q8S055;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Toll-Like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.


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Db 477 LysMetAlaGlyAenSerPheGlnAsnAsnLeuProAspIlePheThrGluLeuThr 496
QY 38957 AACTGACATCTCGATCTTTTAATGATTCATATGGAACAATATCTGGGGGATATT 39016
Db 497 AsnLeuThrValLeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPhe 516
QY 39017 GACACCTCCATAGATCAATATTAATATGATGACAAACAATCTATTGTTTGGAT 39076
Db 517 HisSerLeuSerLeuGlnValLeuAsnMetSerHisAsnLeuLysLeuSerLeuAsp 536
QY 39077 TCATCCCATATTAACAGCTGTATTCCTCAGCACTGTGATTCGAGTTTAAATCCGATA 39136
Db 537 ThrPheLeuYrGluProLeuHisSerLeuArgIleLeuMetCysSerPheAsnArgIle 556
QY 39137 GAGACATCTAA---GGAACTACTGCAACATTTCCAAAGATCTGAGCTTCTTCAATCTT 39193
Db 557 MetAlaSerLysGlnGlnGlnLeuGlnHisLeuProArgSerLysThrTrpLeuAsnLeu 576
QY 39194 ACTACAAATCTGTGCTGTGATATGATGACATGACAAATTCCTGCAAGTGGTCAGGAA 39253
Db 577 ThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnTrpValLysAsp 596
QY 39254 CAGACAGATCTTGGTGGAATGTTGAACAATGACATGTCGACAACTGTAGAGATGAT 39313
Db 597 GlnArgGlnLeuLeuValGlyAlaGlnMetMetCysAlaGlnProLeuAspMetGln 616
QY 39314 ACCTCCTTAGTGTGATTTTAATTAATCTACCTGATATGATGACAAACAATCATAGT 39373
Db 617 AspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleIleSer 636
QY 39374 GTGTCAGTGTGCTGATGATGTTGATGATCCACTGTAGCATTTCTGATATACACTTCTAT 39433
Db 637 ValSerValValThrValLeuLeuValSerValValGlyValLeuValTyrLysPheTyr 656
QY 39434 TTTCACCTGATCTTATTGCTGCTGCTGTAAGAAAGTACAGCAGAGAGAAAGCATTTAGAT 39493
Db 657 PheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyGlnSerIleTyrAsp 676
QY 39494 GCATTTGTGATCTACGTGAGTACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39553
Db 677 AlaPheValIleTyrSerSerGlnAspGlnAspIleAspTrpAlaArgAsnGlnLeuValLysAsn 696
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QY 39614 GTAGCCATTTGCTGCCAATCATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39673
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QY 39674 GTAGTGTCTAGACATTTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39733
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QY 39794 AAGTCCCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39853
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QY 39854 GAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39913
Db 797 GlnTrpGlnAspSerValLeuGlyArgHisIleValAlaPheTrpArgLeuArgLysAlaLeu 816
QY 39914 TTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39964
Db 817 LeuAlaIleLysProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGln 836
QY 39965 ACGGCAACTTGAGAC 39979
Db 837 AlaThrThrSerThr 841

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RESULT 12
06WCDS PRELIMINARY; PRT; 841 AA.
ID 06WCDS
AC 06WCDS
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecorida; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
RT "Haplotype variation in bovine Toll-like receptor 4 and computational
RT prediction of a positively selected ligand-binding domain.";
PL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
DR EMBL; AY297040; AA062700.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001611; IRR.
DR InterPro; IPR000483; IRR_Cterm.
DR InterPro; IPR003885; IRR_Cyst.
DR InterPro; IPR003591; IRR_Cyp.
DR InterPro; IPR000157; TIR.
DR Pfam; PF01463; LRCT; 1.
DR Pfam; PF00560; LRR_1; 12.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00365; LRR_SD2; 6.
DR SMART; SM00369; LRR_TYP; 13.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
DR Receptor.
DR SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;
SQ
Alignment Scores:
Pred. No.: 7.83e-180 Length: 841
Score: 2573.00 Matches: 519
Percent Similarity: 71.91% Conservative: 103
Best Local Similarity: 60.00% Mismatches: 189
Query Match: 2.96% Indels: 54
DB: Gaps: 8
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QY 37400 TGAAGAAATGCAATTAATGATTAAGATCAATGACTGCTTATGATGCCCA 37459
Db 26 TrpAspProCysValGlnValAlaProAsnIleSerTyrGln----- 39
QY 37460 GTTATGATCTGGAATGATTTTTCATAGGATTTTGTGCTGACATAGTGTGATGTT 37519
Db 40 CysMetGlnLeuAsnLeuTyrLysIleProAsnIlePro----- 53
QY 37520 ATCATCACTGACAGAGTGAAGAAATGACAAATCTGACAGAGTTCCTCTGACACAC 37579
Db 54 -----IleSerThrLysMetLeuAspLeuSerPheAsnTyrLeuAlaGlnHis--- 68
QY 37580 ATCATCACTGTTTGTCTGTGACAGTTTCTCTTACAAATTAACATGATATCATATCT 37639
Db 69 -----LeuGlySerHisAsnPheSer----- 75
QY 37640 GTTTGATCATATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 37699
Db 76 -----SerPheProGln 79
QY 37700 AATATCATATGATATCTCTTTTGGCCATAGAGTGAATGAAACAATTAAGAGACAG 37759

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Db	80	LeuGIvalLeuaspLeuSer-----ArgCySGluIleuysIleIleGIuasp	96
Qy	37760	GCATGGCATGCTTATACACCACTCTCAAACTTGATATCTGACAGAAACCTTATCCAGAGT	37819
Db	97	ThrheGIingIleuAsnIhIleuSerThrIleuIleIeuThrGIyAsnProIleGIser	116
Qy	37820	TTTTCCCAAGAAAGTTCTCTGGACATPACAGATTGAGAAATCTGGTGGCTGTGGAGCA	37879
Db	117	LeuIaITrpgIyIaPheSerGIyLeuSerSerIeGIuIyLeuValaIaValGIuThx	136
Qy	37880	AAATGGCCCTCTGACAAAGCTTCCATTTGACACCTTATATACCTTAAGAAGCTCAAT	37939
Db	137	AsnIeuValSerIeuAsnAspPheProIleGIyIhIleuIyAsnIeuIySGIuIeuysn	156
Qy	37940	GTGGCTCACAATTTATACATCTCTGTAGTTCCTGCAATATTTTCCAACTGTACGAAAC	37999
Db	157	ValaIaIhAsnPheIleIhIseSerPheIyIeuProGIuTyPheSerAsnIeuProAsn	176
Qy	38000	CTAGTACATGATGATCTTTCTTATACATATATTCAAACTATTAAGTCTGACAGCTTACAG	38059
Db	177	LeuGIuIhISeuAspIeuSerAsnAsnIyIleGIaAsnIleTyTyGIuAspValIys	196
Qy	38060	TTTTCTAGTGAATAATCCACAAGTCATCTCTTTGACATGCTTTGAACCCATTTGAC	38119
Db	197	ValIeuIhISGIuMetProIleuAsnIeuSerIeuAspIeuSerIeuAsnProIeuAsp	216
Qy	38120	TTTCATTCAGAACCAAGCCCTTACAGGGAATTAAGCTCCATGAACCTGACCTTAAGAGTAT	38179
Db	217	PheIleGIuProGIyThrPheIySGIuIleIyLeuAsnGIyIeuThrIeuAspIySerAsn	236
Qy	38180	TTTATATAGCTCAATATATATGAAAACTGCTCCATCAAAACCTGGCTGGTTTACACGTCCAT	38239
Db	237	PheAsnSerSerhIhIValMetIySThrCyIleGIuIyLeuIaGIyIeuIyThrAsn	256
Qy	38240	CGGTTATCTTGGAGAAATTTAAGATGAAGAACTCTGGAATTTTGAACCCCTATAC	38299
Db	257	ArgIeuValIeuGIyGIuPheIyAsnGIuATyGIyLeuGIuATyPheAspIySerPhe	276
Qy	38300	ATGGAGAGCATATGTGATGACACCATTTGAGATGAGTATCAATATCAATATATTTT	38359
Db	277	LeuGIuGIyIeuCyAsnIeuThrIleGIuGIuPheATyIeIaIyIeuAspIySph	296
Qy	38360	TCA--GATGATATGTTAAGTTCATGCTGGTGGCAATGTTTCTGCAATGTCTCTGGCA	38416
Db	297	SerGIyAspAspIhIAspIeuPheAsnCyLeuIaIAsnValSerValIleSerIeuIeu	316
Qy	38417	GGTATATCTATAAAATATCTAGAAAGATGTTCTTAAACATTTCAAAATGGCAATCTTATCA	38476
Db	317	SerIleSerIeuGIySerIeuGIuIaIeIuIyAspPheATyPheGIuIhIAspIeuGIu	336
Qy	38477	ATCATTTAGATGATCAACTTAAGCAAGTTTCCAACTCTGATCTACCTTCTTAAAGTTTG	38536
Db	337	IleIleAsnCyAspPheAspIySphPheProIaIeIuIyIeuSerSerIeuIySphPhe	356
Qy	38537	ACTTTAATCTAGACAAAGGGCTTATACATGTTTAAAAAAGTGCCCTTACCAAGTCTCAGC	38596
Db	357	ValPheThrAspAsnIyAspIleSerThrPheThrGIuPheIhIeuProSerIeuGIu	376
Qy	38597	TATCTAGATCTTATGAAATGCACTGAGCTTTAGTGGTGTCTGTCTTATTTCTGAATTG	38656
Db	377	TyTleuAspIeuIyAspAsnIhIleuSerPheIyGIyCySeuSerhIhIAspPhe	396
Qy	38657	GGAAACAAAGCCSGACGACCTTAAACCTGACCTGACCTGAAGTGGTCCATTTAGAGTGCC	38716
Db	397	GIyIhThrAsnIeuIyAsnIleuAspIeuSerPheAsnAspValIleThrIeuGIySer	416
Qy	38717	AATTTCAATGGCTTAGAGAAAGCTGACACCTGATTTTTCAGACCTTATTAAGAG	38776
Db	417	AsnIhIeuGIyIeuGIuIhIeuGIuIhIleuAspPheGIuIhIseSerThrIeuIySGIu	436
Qy	38777	GTCACAGAAATTCAGCGTTCTTATCCCTTGAAGGCTACTTACCTTGACATCTTAT	38836

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QY	37640	GTATTGATCATAGATAGTGGAGGACGTGTATGTCAATTAGAAAGGGTTTTTTTTCAGCAA	37699
Db	76	-----SerheProGlu79	
QY	37700	AAATACATAATGGGTATCTCTTTTGCCCAATAGGTGAAATTGAAACAAATTGAACAAG	37759
Db	80	LeuGlnValLeuAspLeuSer-----ArgCysGluIleLysIleIleGluAsp	96
QY	37760	GCATGGCATGGCTTTACACCAACCTTCGAACCTTGATCTGACACGAAACCTTTCAGAGT	37819
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QY	38060	TTTCTACGTGAAATTCACAAGTCATCTCTCTTTAGACATCTTTGAACCCAAATTGAC	38119
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Db	217	PhelIleGluProGlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuLysSerHisn	236
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Db	257	ArgLeuValLeuGlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSerPhe	276
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QY	38417	GGTGTCATCTATAAATAATATAGAAAGATGTTCTTAAACATTTGAAATGGCAATCTTATCA	38476
Db	317	SerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgTrpGlnHisLeuGlu	336
QY	38477	ATCATTAGATGTCAACTTAAGAGGTTTGCACCTCGAGATCTACCCCTTCTTAAAGTTTG	38536
Db	337	IleIleAsnCysAspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPhe	356
QY	38537	ACTTTAATCTATGAAACAAGGTCATACGATTTTAAAAAAGTGCCCTTACCAAGTCTCAGC	38596
Db	357	ValPheThrAspAsnLysAspIleSerThrPheThrGlnPheGlnLeuProSerLeuGln	376
QY	38597	TATCTGATCTTAGTGAAGAAATGACATGACCTTATGAGTGCTGTGTTCTTATTCGATTTG	38656
Db	377	TyLeuAspLeuLysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAspPhe	396

QY	38557	GGAA	CAAA	CAGC	CTTGAG	CA	CTTAA	AG	CTTG	CA	TATTA	TAG	AG	TGCC	38716
Db	397	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	416
QY	38717	AAT	TG	CA	TGG	GT	CTA	GA	AG	CTG	CA	CTG	GA	CA	38776
Db	417	Asn	Phe	Met	Gly	Leu	Glu	Leu	Glu	His	Asp	Phe	Gln	His	436
QY	38777	GTC	A	G	A	A	A	A	A	A	A	A	A	A	38836
Db	437	Ile	Asn	Ala	Phe	Ser	Ala	Phe	Leu	Ser	Leu	Ala	Gly	Leu	456
QY	38837	ACT	TA	CA	CA	C	CA	AA	A	A	A	A	A	A	38896
Db	457	Thr	Ser	Asn	Ile	Arg	Val	Phe	His	Arg	Val	Phe	Thr	Gly	476
QY	38897	AAA	TG	G	CTG	CA	AT	TCT	T	CTT	CA	AA	A	A	38956
Db	477	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Asn	Ser	Leu	Pro	Asp	496
QY	38957	AAC	TG	CA	AT	TCT	CTG	AT	CTT	T	TAA	TGT	CA	A	39016
Db	497	Asn	Leu	Thr	Val	Leu	Asp	Ser	Val	Cys	Glu	Leu	Gln	Val	516
QY	39017	GAC	AC	CTC	CA	TAG	CA	CTT	CA	AT	T	TAA	TAT	TA	39076
Db	517	His	Ser	Leu	Thr	Val	Leu	Asn	Met	Ser	His	Asn	Gly	Leu	536
QY	39077	TCA	TCC	CA	AT	TAA	C	AG	CTG	TA	TCC	T	CAG	CA	39136
Db	537	Thr	Phe	Leu	Thr	Gly	Asn	Pro	Leu	His	Ser	Leu	Ala	Gly	556
QY	39137	GAG	CA	CT	TAA	--	GGA	T	ACT	CA	CTG	CA	CA	CTT	39193
Db	557	Met	Ala	Ser	Val	Ser	Glu	Gln	Leu	Gln	Asn	Leu	Pro	Arg	576
QY	39194	ACT	TA	CA	AT	TCT	GTG	CTT	G	TAT	T	GTG	AA	C	39254
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QY	39254	CAG	AA	G	CA	GT	TCT	G	TG	GA	AT	GT	TGA	CA	39313
Db	597	Gln	Arg	Gln	Leu	Leu	Val	Gly	Ala	Gln	Met	Cys	Ala	Gln	616
QY	39314	ACC	T	C	T	T	AG	T	G	GA	T	T	T	T	39373
Db	617	Asp	Met	Pro	Val	Leu	Ser	Phe	Ala	Arg	Ala	Thr	Cys	Gln	636
QY	39374	GTC	TA	G	GT	CA	G	TG	AT	GT	TG	GA	T	T	39433
Db	637	Val	Ser	Val	Val	Thr	Val	Leu	Leu	Val	Ser	Val	Val	Gly	656
QY	39434	TTT	CA	C	CG	TA	CA	T	T	T	T	T	T	T	39493
Db	657	Phe	His	Ser	Met	Cys	Leu	Ala	Gly	Cys	Val	Ser	Thr	Gly	676
QY	39494	GCA	T	T	T	T	G	A	T	CTA	CT	CA	G	A	39553
Db	677	Ala	Phe	Val	Ile	Thr	Ser	Ser	Gln	Asp	Gln	Asp	Thr	Val	696
QY	39554	TTT	AA	GA	GA	GA	G	TG	CCC	CG	T	T	T	T	39613
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QY	39674	GTA	GT	CT	TA	CA	CTT	TAT	T	CA	G	AG	CG	T	39733
Db	737	Val	Val	Ser	Gln	His	Ser	Ala	Gln	Ser	Arg	Thr	Cys	Ile	756
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Db      757  ThrTrpGlnPheLeuSerSerSerArgAlaGlyIleIlePheIleValLeuGlnIlybLeuGln 776
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Db      777  LysSerIleuLeuArgIlnGlnIlnValGlnLeuTyrArgIleuLeuSerArgSerThrTyrLeu 796
QY      39854  GAATGGAGAGCAATCCTCTGGGAGGAGCAGACATCTTTCGAGAAAGACTTAAATAGCCCTTA 39913
Db      797  GluTrpGlnIlybSerPheValIleuGlyArgHlsValPheTrpArgArgIleuArgIlybAlaLeu 816
QY      39914  TTGGATGAAAAGCGCTCGAATCCGTAGCAGCAACGAGCAGAGAAACA-----CAAGAA 39964
Db      817  LeuAlaGlyIlybProGlnSerProGlnGlyThrAlaSerAlaGlnThrAsnProGlnIln 836
QY      39965  ACGGCAACTTGACCC 39979
Db      837  AlaThrThrSerThr 841

RESULT 14
ID      TLR4_HORSE  STANDARD;  PRT;  843  AA.
AC      09MYW3:
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      05-JUN-2004 (Rel. 44, Last annotation update)
DR      Toll-like receptor 4 precursor.
GN      Name=TLR4;
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Butheria; Perissodactyla; Equidae; Equus.
OK      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Vandenplas M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT      "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).";
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ database.
CC      - FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      - SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, LY96 and TLR4.
CC      Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
CC      their respective TIR domains (By similarity).
CC      - SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      - SIMILARITY: Belongs to the Toll-like receptor family.
CC      - SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC      - SIMILARITY: Contains 1 TIR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
Cc      EMBL; AY005808; AAP1076.1; -.
DR      HSBP; A105399; 1PTV.
DR      GO; GO:0046656; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappa-B inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:mast cell activation; ISS.
DR      GO; GO:0045362; P:negative regulation of osteoclast different. . ; ISS.
DR      GO; GO:0045362; P:negative regulation of interleukin-1 biosyn. . ; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . ; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-13 biosyn. . ; ISS.
DR      GO; GO:0045438; P:positive regulation of interleukin-6 biosyn. . ; ISS.
DR      GO; GO:0005510; P:positive regulation of interleukin-6 biosyn. . ; ISS.

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DR	GO: 0042088; P-1-helper 1 type immune response; ISS.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR000483; LRR.Cterm.	
DR	InterPro; IPR003591; LRR.tyr.	
DR	InterPro; IPR001571; TIR.	
DR	Pfam; PF00560; LRR; 13.	
DR	Pfam; PF01582; TIR; 1.	
DR	PRINTS; PR00019; LEURCHAPT.	
DR	SMART; SM00369; LRR.tyr; 1.	
DR	SMART; SM00082; LRRCT; 1.	
DR	SMART; SM00255; TIR; 1.	
DR	PROSITE; PSS0104; TIR; 1.	
KW	Glycoprotein; Immune response; Inflammatory response; Lysine-rich repeat; Receptor; Signal; Transmembrane.	
KM	Leucine-rich repeat; Receptor; Receptor; Signal; Transmembrane.	
FT	SIGNAL	1
FT	CHAIN	24
FT	DOMAIN	24
FT	TRANSMEM	634
FT	DOMAIN	655
FT	REPEAT	53
FT	REPEAT	77
FT	REPEAT	101
FT	REPEAT	128
FT	REPEAT	150
FT	REPEAT	174
FT	REPEAT	203
FT	REPEAT	277
FT	REPEAT	311
FT	REPEAT	351
FT	REPEAT	374
FT	REPEAT	401
FT	REPEAT	423
FT	REPEAT	447
FT	REPEAT	471
FT	REPEAT	496
FT	REPEAT	521
FT	REPEAT	545
FT	REPEAT	569
FT	DOMAIN	674
FT	CARBOHYD	35
FT	CARBOHYD	189
FT	CARBOHYD	205
FT	CARBOHYD	282
FT	CARBOHYD	295
FT	CARBOHYD	498
FT	CARBOHYD	527
FT	CARBOHYD	576
FT	CARBOHYD	626
FT	SEQUENCE	843 AA; 96495 MW; B5976898AD6F7A69 CR64;

Alignment Scores:	
Pred. No.:	2,17e-179
Score:	843
Percent Similarity:	51.9%
Best local Similarity:	72.32%
Query Match:	59.86%
DB:	2.35%
	1
US-09-396-985B-48 (1-50000) x TLR4_HORSE (1-843)	
	Length: 843
	Matches: 519
	Conservative: 108
	Mismatches: 182
	Indels: 58
	Gaps: 9

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US-09-396-985B-48 (1-50000) x TLR4_HORSE (1-843)
QY      37400 TGGAAAAATGCATMAATTATCTGAACACTACATCATCACTGCTTTAATGTACCACA 37459
           |||         |||:::
Db      26   TPSPAPROCYTAAAGlnAlvalProAsnThrThrTyrlcn----- 39
QY      37460 GTTATGATCTTGAAATTGATTTTTCTTAAGTATTTGCTGCGTCGACATAGTGATGATT 37519
           |||         |||:::
Db      40   CysMetCaspLeuasnLeuTrpLysIlePrgGluAsnIlePro----- 53
QY      37520 ATCATCATCTGAGACAGGTGGAATAATGACAATACTGCAGAGTTCCTCTCGTCACACC 37579
           |||         |||:::
Db      54   -----ThrSerThrLysGluLeuAspLeu---SerHisasnProLeuLysGlu 68
QY      37580 ATCATCACTGTGTTTGCTCTGTGACAGTTTTCTCTTACCAATTAACATGATATCATATCT 37639

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D6	69	Leu	-----	glyserhisserphe	-----	74
QY	37640	GTATTGATCATAGTATGATGGAGCACTGTAATGTCATTAGAAAAGGTTTTTTTTCAGCAA				37699
D6	75	-----	-----	-----	-----	79
QY	37700	AAATCACTAATTTGGTATCTTTTGGCCCATAGGTGTGAAATTGAAACATTTGAAGCAAG				37755
D6	80	LeuGlnValLeuAspLeuSer	-----	ArgCysGlnIleGlnMetIleGlnAsp	-----	96
QY	37760	GCATGGCATGGCTTATACACCAACCTTCGAACCTTGATCTGACAGAAACCTTATCCAGAGT				37819
D6	97	AlaTyrGlnIleuLeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleArgSer				116
QY	37820	TTTTCCCAAGAAAGTTTCTCTGGACATCAAGATTTAGAAATCTGGTGGCTGGAGACA				37879
D6	117	LeuAlaLeuGlyAlaPheSerGlyLeuLeuSerSerLeuGlnThrLeuValAlaValGlnThr				136
QY	37880	AAATGGCCCTCTGTAAAGACCTTCCTATTTGACACAGCTTATACCTTAAAGAACTCAAT				37939
D6	137	LysLeuSerSerLeuGlnLysPheProIleGlnIleLeuLysThrLeuLysGlnLeuAsn				156
QY	37940	GTGGCTCAACAATTTTATACATCTCCCTATAGTATCCGCATTTTTCATCCATGGACAGAC				37999
D6	157	ValAlaIleAsnLeuIleHisSerPheLysLeuProGlnLysTyrPheSerLysMetProAsn				176
QY	38000	CTAGTACATCGGATCTTTCTTATATCTATATTCGAACATTTATCTGCACAGCTTACAG				38059
D6	177	LeuGlnHisLeuAspLeuSerLeuAsnAsnLysIleGlnAsnIleSerHisGlnAspLeuArg				196
QY	38060	TTTTCTACGTAAATTCACACAGTCAATCTCTCTTATGACATGTCTTTGAACCCCAATTGAC				38119
D6	197	ValLeuHisGlnMetProLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuGln				216
QY	38120	TTGATTTCAACCAACGCTTTTCAGGGAATTAAGCTCCATGAACCTGCTATAGAGGTAT				38179
D6	217	PheIleGlnProAspIlePheLysGlnIleLysLeuHisLysLeuThrLeuLysSerAsn				236
QY	38180	TTTTAATGCTCAATTAATTAATGAACCTTGCCCTCAAAACCTGGAGCTGTTTACACGTCAT				38239
D6	237	PheAspSerIleAspIleMetLysSerCysIleGlnGlyLeuAlaGlyLeuLysValAsn				256
QY	38240	CGGTTGATCTTGGAGAAATTTAAAGATGAAGAGATCTGGAAATTTTGAACCTCTATC				38299
D6	257	ArgLeuValLeuGlyGlnPheLysAsnGlnLysGlyLeuGlnLysArgPheAspThrSerAla				276
QY	38300	ATGGAAGACATATGATGATGACCATATGATGAGTTTACGTTAACAATGATTTT				38359
D6	277	LeuArgGlyLeuHisAsnLeuThrIleGlnGlnPheArgLeuAlaTyrIleAspAsnTyr				296
QY	38360	TCA-----GATGATATTTGTTAAGTTCACATGGCTTGGAGCAATGTTTCTGCATATGCTCG				38413
D6	297	SerSerLysAspSerIleLeuPheLeuAsnAsnCysLeuAlaAspIleSerLysIleSerLeu				316
QY	38414	GCAGGTGATCTTAAATAATATCTAGAAGATGTTCTCTAAACATTTCAATGGCAATCTTAA				38473
D6	317	ValSerLeuAspLeuGlyAsnLeuLysAspPheProLysGlyPheLysTyrGlnAspPhe				336
QY	38474	TCAATCATTTAGATGCACTTAAAGCAATTTCCAACTCTGGATCTACCTTTCTTAAAGT				38533
D6	337	GlnLeuValAsnGlySerGlnIleGlnGlyPheProThrLeuGlnLeuThrSerLeuLysArg				356
QY	38534	TTGACTTTTACCTTGAAGAAAGGCTCTACAGTTTAAAAAAAGTGGCCCTACCAAGTTC				38593
D6	357	LeuValAlaPheThrSerAsnLysAspMetLysSerPheAsnGlnValLysLeuProSerLeu				376
QY	38594	AGCTATCTAGATCTTAGTGAAGATGACATGCAAGCTTTAGTGTGCTCTTATTTCTAT				38653
D6	377	GlnPheLeuAspLeuSerThrArgAsnLysGlnLeuSerPheLysSerCysGlySerGlnAlaAsp				396
QY	38654	TTGGAGCAAAACGCTGAGACCTTGAACCTTACAGTTTCAATGTTGCTCATCTTATTAAGT				38713

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Db      397 LeuylsThrThrArgLeuLysHisLeuAspLeuSerPheAsnAspValIleSerMetSer 416
Qy      38714 GCGAATTCATGGGTAGAGAGAGCTGACAGCTGGATTTCAGCACTGCTACTTAA 38773
Db      417 SerAsnMetGlyLeuGlnLeuGlnHisLeuMetPheGlnHisSerThrLeuLys 436
Qy      38774 AGGGTCACAGAAATTCGAGCGTTTCATCCCTTGAAAAAGTACTTTTACCTTGACATCTCT 38833
Db      437 GlnAspSerAspPheProValPheLeuSerLeuLysAsnLeuArgTrpLeuAspIleSer 456
Qy      38834 TATCTACACCAAAATTCAGTTCGATGATATTTCTGGCTTGACAGCTTCACACA 38893
Db      457 TyrThrAsnThrArgValPheHisGlyTrpPheAspGlyLeuValSerLeuGlnVal 476
Qy      38894 TTTAAATGGCTGGCAATTCCTTCAAGAACAACCCCTTCAAATGCTTCGAAACA 38953
Db      477 LeuLysMetCysGlyAsnSerPheLysAspAsnPheLeuProAsnIlePheAspGluMet 496
Qy      38954 ACAAACTGCACATTCCTGCATCTTTCTAAATGTCATTTGCAAAATATCTGGGGGTA 39013
Db      497 ThrAsnLeuThrThrLeuAspLeuSerLysCysAsnLeuGlnValSerGlnGlnVal 516
Qy      39014 TTGACACCTTCATGACATTCATTAATAATGATGCAACAATCTTATGTTTGG 39073
Db      517 PheCysLeuLeuProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuLeuPheLeu 536
Qy      39074 GATTCATCCCATTTAAACAGCTGATTCCTCGACACTCTGATTCGAGTTCAATGCG 39133
Db      537 AspMetLeuProLysTrpLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArg 556
Qy      39134 ATAGACATCTAA---GGAAATCTGCACATTTTCCAAGAGCTTCAGCTTCAT 39190
Db      557 IleValAlaPheLysTrpGlnGlnLeuGlnHisPheProSerSerLeuAlaSerLeuAsn 576
Qy      39191 CTTATCTAACATTTCTGTTGCTTGTATATGTAACATCAAAATTCCTGCAGCTGGCTAG 39250
Db      577 LeuThrGlnAsnAspPheAlaCysValCysGlnLysTrpGlnSerPheLeuGlnTrpValLys 596
Qy      39251 GAAACAGAGAGCTTCCTGTAATGTTGAACAATGATGATGCAACCTGTCAGAGTG 39310
Db      597 AspGlnAspGlnLeuLeuValGlnValGlnHisLeuValCysValAlaIleProLeuGlnMet 616
Qy      39311 AATACCTCTAGTGGTGGATTTTAAATATCTACTGTTATATGTAACAAGCATCATC 39370
Db      617 ArgGlyMetProValLeuGlnPheAsnAsnAlaThrCysGlnIleSerLysThrIleVal 636
Qy      39371 AGTGTGACAGTGGTCAGTGTATGTTGATTCACCTGTAGCATTTTCATACCACTTC 39430
Db      637 GlyLysSerValPheSerIleLeuMetValSerValIleAlaValLeuValTyrLysPhe 656
Qy      39431 TATTTACCTGATCTTATTTGCTGGCTGTAAGATACACAGAGAGAGATCAT 39490
Db      657 TyrPheHisLeuMetLeuLeuAlaGlyCysLeuLysTrpGlyAspGlyLysSerIleLys 676
Qy      39491 GATCATTTTGTGATCTACTCGAGTCAGATGAGAGCTGGTGAAGAAATGAGCTGTAAAG 39550
Db      677 AspAlaPheValIleLysSerSerCysAspIleAspIleAspTrpValAlaGlnGlnLeuValLys 696
Qy      39551 AATTTAAGAAGAAGATGCCCCGCTTCACCTGCTTCCTCACTACAGAGACTTATTCCT 39610
Db      697 AsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTrpYArgAspPheIlePro 716
Qy      39611 GGTGTAGCATTTGCTGGCAATCATCATCAGAGAGCTTCACAGAGCCGGAAGTATT 39670
Db      717 GlyValAlaIleAlaAlaAsnIleIleGlnGlnGlyPheHisLysSerAspGlyValIle 736
Qy      39671 GTGTAGTGTCTGACACTTATTCAGAGCGCTGGTGTATCTTCTGATATGAGATTGCT 39730
Db      737 ValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAla 756
Qy      39731 CAACATGAGCATTTCTGAGAGCGCGCTTCGACATCATTTCTGATTCCTTGAAGAGTT 39790
Db      757 GlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuHisLysLeu 776

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Qy      39791 GAGAGTCCCTGTCGAGAGAGAGCTGGAATTGTATGCTTCTAGCAAAACCTTAC 39850
Db      777 GlnLysSerLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgAsnTrpTyr 796
Qy      39851 CTGGAATGGAGAGCAATCTCTGGGAGGACACTTTCTGGAGAGACTTAAAAATGCC 39910
Db      797 LeuGlnTrpGlnAspSerValLeuGlnGlyArgHisIlePheTrpArgArgLeuArgLysAla 816
Qy      39911 CTTATGGATGGAAACCTCGAATCTCGAGCAAAACGCA-----GAG 39952
Db      817 LeuLeuAspGlyLysProTrpSerProAlaGlyThrAlaAspAlaIleGlnSerArgGln 836
Qy      39953 GAAGAAACAAGAAACGCAACT 39973
Db      837 HisAspAlaGlnThrSerThr 843

RESULT 15
ID      TLR4_FELCA STANDARD; PRT; 833 AA.
AC      P58727;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Toll-like receptor 4 precursor.
GN      Name=TLR4;
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yoshiooka N., Kano R.;
RT      "Felis catus Toll like receptor 4";
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Cooperates with Lys6 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, Lys6 and TLR4.
CC      Binds Lys6 via the extracellular domain. Binds MYD88 and TIRAP via
CC      their respective TIR domains (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC      -1- SIMILARITY: Contains 1 TIR domain.
CC      -----
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB060687; BAB3947.1; -.
DR      HSSP; O60603; LPTX.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004688; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macrophage activation; ISS.
DR      GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.

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DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01582; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 DR Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 833 TIR-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 833 Cytoplasmic (Potential).
 FT REPEAT 76 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.
 FT REPEAT 310 334 LRR 9.
 FT REPEAT 350 372 LRR 10.
 FT REPEAT 373 398 LRR 11.
 FT REPEAT 399 421 LRR 12.
 FT REPEAT 442 465 LRR 13.
 FT REPEAT 447 469 LRR 14.
 FT REPEAT 470 494 LRR 15.
 FT REPEAT 495 518 LRR 16.
 FT REPEAT 520 542 LRR 17.
 FT REPEAT 544 566 LRR 18.
 FT REPEAT 568 592 LRR 19.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 570 570 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 833 AA; 95592 MW; 3B3A84F2BEBB55EA CRC64;

Alignment Scores:

Pred. No.: 4.08e-176 Length: 833
 Score: 2522.50 Matches: 490
 Percent Similarity: 78.76% Conservative: 107
 Best Local Similarity: 64.64% Mismatches: 156
 Query Match: 2.90% Indels: 5
 DB: 1 Gaps: 3

US-09-396-985B-48 (1-50000) x TIR4_FELICA (1-833)

QY 37691 TTTCAGCAAAATCATATATGTTATCTTTGGCCCATAGGTGGAATTAACAATT 37750
 DB 77 PheProGluLeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnIleIle 93
 QY 37751 GAAAGCAAGGATGGATGGCTTACACCACTTCAAACTTGATATGACGAAACCTT 37810
 DB 94 GluAspAspAlaTyrGlnGlyLeuAsnHisLeuSerIleLeuIleThrGlyAsnPro 113
 QY 37811 ATCCAGAGTTTTCCTCCAGAGTTCTCTGACATACAAATTTAGAGAACTGTGGCT 37870
 DB 114 IleGlnIleArgLeuPheProGlyAlaPheSerIleGlyLeuSerIleGlnIleValAla 133
 QY 37871 GTGAGACAAATATGGCTCTCTCTAGAAAAGCTTCCCTAATTGACAGCTTAACCTTAAG 37930

DB 134 ValGluThrAsnIleLeuSerLeuGluAspPheProIleGlyHisLeuIleThrLeuLys 153
 QY 37931 AAATCAATATGGGCTGACAAATTTATATATCTCTGTAAGTTACCTGCAATTTTCCAT 37990
 DB 154 GluLeuAsnValAlaHisAsnLeuIleHisSerPheLysLeuProGluTyrPheSerAsn 173
 QY 37991 CTGACGAACCAATGACATGATGATCTTTATATATATATGTAAGCTATATACGTCAAC 38050
 DB 174 MetSerAsnLeuGluTyrLeuAspLeuSerAsnAsnLysIleGlnAsnIleTyrHisLys 193
 QY 38051 GACTTACAGTTTTCACGTGGAATAATCCAAAGTCAATCTCTTTAGACATGCTTTGAA 38110
 DB 194 AspLeuGlnValLeuHisGlnLysProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsn 213
 QY 38111 CCATTTGATCTTCAAGACCAAGCTTTCAGGGAATTAAGCTTCAATGAACTGCTA 38170
 DB 214 ProLeuAspPheIleGlnProGlyAlaPheLysGlnValLysLeuArgGluLeuThrLeu 233
 QY 38171 AGAGTAATTTTATAGCTCAAAATATATGAAACTTGCCTTCAAACTGCGTGTTA 38230
 DB 234 ArgSerAsnPheAsnSerThrAspValMetLysAlaSerIleGlnGlyLeuAlaGlyLeu 253
 QY 38231 CACGTCCATCGTGTATCTTGGAGAAATTTAAGATGAAGAAATCTGAAATTTTGA 38290
 DB 254 GlnIleHisGlnLeuValLeuGlyGluPheLysAsnGlnArgAsnLeuGlyArgPheAsp 273
 QY 38291 CCCTCTATCATGGAAGCATATGATGATGACCATTTGATGATGATGATGATGATGAT 38350
 DB 274 LysSerIleLeuGlnGlyLeuCysAsnLeuIleIleGlnLysPheArgIleAlaTyrPhe 293
 QY 38351 AATGATTTTCAATGATATTTGT---AAGTTCATGCTTGGGAATGTTTCGAATG 38407
 DB 294 AspLysPheSerGlnAspAlaIleAspSerPheAsnCysLeuAlaAsnValSerThrIle 313
 QY 38408 TCTTCGACAGAT 38467
 DB 314 SerLeuValHisLeuTyrPheLysGlyLeuLysGlnLeuProLysAsnLeuGlyTyrGln 333
 QY 38468 TCCTTATCAATCATTAATGATGATCACTTAAGCATTTTCAACTGATCTTCTTCTT 38527
 DB 334 ArgLeuValLeuValAlaCysGlnPheGlnPheProThrTyrLysAspProLeu 353
 QY 38528 AAAAGTTGACCTTAATATATGAAAGGAGCTATGCTTTTAAAGGCGCTTACA 38587
 DB 354 LysGluLeuValPheSerAlaAsnGluValArgAsnAlaPheThrGlnValLysLeuGlu 373
 QY 38588 AGTTCAGCTATATGATCTTATGATGAAATGCACTGAGCTTATGCTGTTCTTAT 38647
 DB 374 SerLeuGluPheLeuAspLeuSerArgAsnAspPheSerLeuLysSerCysCysSerGlu 393
 QY 38648 TCTGATTTGGAAACAAACAGCTGACACTTACAGCTTCAATGATGCTTCAAT 38707
 DB 394 ArgAspLeuGlyThrThrArgLeuLysHisLeuAspLeuSerPheAsnAlaIleIleThr 413
 QY 38708 ATGAGTGCATTTCAAGGCTTACGAAAGCTGACAGCTTATGCTGCTGCTTACT 38767
 DB 414 IleSerSerAsnPheLeuGlyLeuGlnLeuGlnLysLeuAspPheGlnHisSerSer 433
 QY 38768 TTAAGAGGCTCAAGAAATCTGACGCTTATCCCTTAAAGCACTTATGCTTAC 38827
 DB 434 LeuLysGlnValSerAspPheSerValPheLeuProLeuLysAsnLeuAlaGlyTyrLeuAsp 453
 QY 38828 ATCTCTTATATCAACCAAAATGATGATGATGATGATGATGATGATGATGATGAT 38887
 DB 454 IleSerLysThrHisThrGlnValAlaPheHisGlyLysPheAsnGlnLysLeuSerLeu 473
 QY 38888 AACACATTAATAATGCTGCAATCTTCTTCAAGACCAACCTTCAATATGCTTGA 38947
 DB 474 GlnIleLeuLysMetAlaGlyAsnSerPheGlnAspAsnLeuProAsnIlePheMet 493
 QY 38948 AACACAAACAAATGACATTCCTGATCTTCTTCAATATGCAATGCAATATCTTGG 39007

Db 494 GlutenthreonineleucineasparagineleucinevalineSerGln 513
QY 39008 GGGGTAATTTGACACCCCTCCATAGCTTCAATTATAATATGATGACACACATCTATTG 39067
Db 514 ValAlaPheAsnSerLeuProlyseuGlnleuLeuAsnMetSerHisAsnHisleuLeu 533
QY 39068 TTTTGGATTATCCCATTTAATACCGAGCTGATTCCTCCAGCACTCTTGATTCAGATTTC 39127
Db 534 SerleuAspThrleuProTyrGluProleuHisSerleuGlnThrleuAspCysSerPhe 553
QY 39128 AATGCATAGACACTTAA--GGAATCTGCACATTTTCCAAAGACTTACCTTC 39184
Db 554 AsnArgIleValAlaSerIyGluGlnleuArgHisPheProSerAsnleuSerSer 573
QY 39185 TTCAATCTTAACTATTCCTGTTGCTTGTATATGTAACATCGAAATTCCTCCAGTGG 39244
Db 574 LeuAsnleuThrArgAsnAspPheAlaCysValCysGlnHisGlnSerPheleuGlnTyr 593
QY 39245 GTCAGGACACAGACAGATTCCTGATGATGTTGAACAAATGATGTCACACCTGTA 39304
Db 594 ValIysAspGlnArgleuLeuValGluValGluGlnMetValCysAlaIysProleu 613
QY 39305 GAGATGAATACCTCTTAGTGGTGAATTTAATAATCTTACCTGTATATGTAACAACA 39364
Db 614 AspmetGlnIyMetProMetleuAsnPheArgAsnAlaThrCysGlnValArgIySerThr 633
QY 39365 ATCATCAGTGTGTCAGTGTGATGTGATGTGATTCACCTAGCATTTCTGATATAC 39424
Db 634 IleIleThrGlySerValPheThrValleuValPheleuValValleuValTyr 653
QY 39425 CACTTCATTTTTCACCTGATCTTAATGCTGGCTGTAAAAAGTACAGCAGAGAGAAAAGC 39484
Db 654 LysPheTyrPheHisbleuMetleuLeuHisGlyCysIysIysTyrSerArgGlyGlnSer 673
QY 39485 ATCTATGATGCATTTGTGATCTACTCGATGAGAATGAGACTGGTGAATGAGCTG 39544
Db 674 ThrTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyrValArgAsnGlnleu 693
QY 39545 GTAAAGAAATTTAGAAAGAGAGTGGCCGCTTTCACCTTGCTTCCTACACAGACTTT 39604
Db 694 ValIysAsnleuGluGluValProProPheGlnleuCysleuHisTyrArgAspPhe 713
QY 39605 ATTCCTGGTGTAGCCATGTGTCGCAACATCATCCAGAAAGCTTCCACAAAGCCGGAAG 39664
Db 714 IleProGlyValAlaIleAlaIleAsnIleIleGlnGluGlyPheHisIysSerArgIys 733
QY 39665 GTTATGTGTAGTGTCTAGACACTTATTCAGAGCCGTTGGTGTATCTTTGAATGAG 39724
Db 734 ValIleValValIseSerGlnHisPheIleGlnSerArgTyrCysIlePheGluTyrGly 753
QY 39725 ATTGCTCAACATGGCATTTCTGAGCAGCGCTCTGCGCATCATCTTGTCTCTGAG 39784
Db 754 IleAlaGlnThrTyrGlnPheleuSerSerArgAlaGlyIleIlePheIleValleuGln 773
QY 39785 AAGGTTGAGAGTCCCTGCTGAGCAGCAGGATGTAATGTATCGCTTCTTAGAGAAAC 39844
Db 774 LysleuGlnIySerSerleuArgGlnIleValGlnleuTyrArgleuLeuAsnArgAsn 793
QY 39845 ACCTACTGGAATGGAGAGACATCTCTGGAGAGGCATCTTCTGAGAAAGACTTAA 39904
Db 794 ThrTyrleuGlnTyrGlnIyAspSerValleuGlyArgHisIlePheTyrArgArgleuArg 813
QY 39905 AATGCCCTATTGGATGGAAAAAGCCTCGAATCTGAGCAAAACAGCAGAGAAAGAA 39958
Db 814 LysAlaIleuLeuAspGlyLysProArgCysProGlnIyMetAlaAspAlaGln 831

2000


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Db      521 SerLeuGlnValIleuAsnMetSerHisAsnAsnPhpeSerLeuAspThrPheProTyr 540
Qy      1874 AAACAGCTGTAACCTCCAGGACTCTGATGACGTTTCATTCGATTCAGACATCC-- 1930
Db      541 LysCysLeuAsnSerLeuGlnValIleuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy      1931 AAAGAAATACCTCAACATTTTCCAAAGAGTACCGCTTCCTCAATCTGACTAATATTCCT 1990
Db      561 LysGlnGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
Qy      1991 GTTGCTGTATATGTAATATCATCAAGATTTCTTGCAAGTGGTCAAGAGACCAAGAAATGTC 2050
Db      581 PheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 600
Qy      2051 TTGGTGAATGTGAAACAAATGAATGTGACATCCATTAAGACATGAAGCCCTCCCTGGTG 2110
Db      601 LeuValGlnValGlnValGlnMetGlnCysAlaThrProSerAspLysGlnGlnMetProVal 620
Qy      2111 TTGGATTTTACGAATTCACCTGTTATATATACAAAGATCATCATCAGTATCGGTGGTC 2170
Db      621 LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 639
Qy      2171 AGTGTCTGTGTGGTACCTGTAAGCATTTCTGATATACCATTTCTATTTTACCTGATA 2230
Db      640 SerValIleuValIleSerValIleValIleValIleValIleValIleValIleValIle 659
Qy      2231 CTTATTTGCTGGCTGTAAATAATACAGACGAGAGAAAGCATCTTATGATGATTTGTATC 2290
Db      660 LeuLeuAlaGlyCysIleLysTyrGlyArgGlnAsnIleTyrAspAlaPheAlaIle 679
Qy      2291 TACTCGAGCCAGATGAGAGACTGGGTGAGAAACAGCTGTAAAGAAATTTAGAAAGAGA 2350
Db      680 TyrSerSerGlnAspGlnAspTrpValAlaArgAsnGlnLeuValLysAsnLeuGlnGln 699
Qy      2351 GTGCCCGCTTTCAGCTTGTGCTTCATTAACAGGACCTTATTTCTGTGAGCCATGCT 2410
Db      700 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 719
Qy      2411 GCCAATCATTCAGGAAGCTTCCACAGAGCCGGAAGTATTTGGTGGTGGTCTAGA 2470
Db      720 AlaAsnIleIleHisGlnGlyPheHisIleLysSerArgLysValIleValValIleValIle 739
Qy      2471 CACTTTATCCAGAGCCGTTGGTGTATCTTGAATATGATGATGCTCAGACATGCGAGTTT 2530
Db      740 HisPheIleGlnSerArgTrpCysIlePheGlnIleValIleAlaGlnThrProGlnPhe 759
Qy      2531 CTGAGTACCGCTCTGGCATCATCTTCATTTGCTTGAAGAAAGTGAGAGACCTCTGCTG 2590
Db      760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeu 779
Qy      2591 AGGACAGAGCTGCATTTGTATTCGCTTTTTCAGCAAAACACCTACCTGAGTGGAGAGAC 2650
Db      780 ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAsp 799
Qy      2651 AATCTCTGGGAGAGACATCTTCTGAGAGAGACTCAAAAAGCCCTTGGATGAGAAA 2710
Db      800 SerValLeuGlnGlyArgHisIlePheThrArgArgLeuAlaGlyAlaLeuLeuAspGlyLys 819
Qy      2711 GCCTTGAATCCAGAT-----GAAACATCAAGAGAGAAACAAAGAACCAACTTGG 2761
Db      820 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839

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RESULT 2
ABU04774
ID      ABU04774 standard; protein; 839 AA.
XX      AC      ABU04774;
XX      DT      29-JAN-2003 (first entry)
XX      DE      Human expressed protein tag (EPT) #1440.
XX      KW      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

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KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KW      receptor; transcription factor; cancer; MHC;
KW      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS      Homo sapiens.
PN      WO200278524-A2.
PD      10-OCT-2002.
PP      28-MAR-2002; 2002WO-US009671.
PR      28-MAR-2001; 2001US-0279495P.
PR      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
PA      (ZYCO-) ZYCO INC.
PI      Chicx RM, Tomlinson AJ, Urban RG;
PI      WPI; 2003-040607/03.
PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukaemia.
PS      Example 2; SEQ ID NO 1440; 134p; English.
XX      CC      The invention describes a purified polypeptide, which comprises a
XX      CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      CC      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      CC      polypeptide is useful as an immunogenic composition for eliciting in a
XX      CC      mammal an immunogenic response directed against any of the purified
XX      CC      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      CC      polypeptide, is useful for treating cancer. The polypeptide is also
XX      CC      useful for identifying compounds that bind to a naturally processed
XX      CC      class I or class II MHC-binding polypeptide. The polypeptides and
XX      CC      polynucleotides are particularly useful for treating or preventing
XX      CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      CC      lymphoma or leukaemia. These are also useful for screening agents for
XX      CC      treating the above mentioned diseases. This sequence represents an
XX      CC      expressed protein tag (EPT) isolated from human tissue for translational
XX      CC      profiling. Note: This sequence does not appear in the printed
XX      CC      specification but was obtained in electronic format directly from WIPO at
XX      CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 839 AA;

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Alignment Scores:
Qy      260 ATGATGCTCTCTTGCACTGCGTGGAGCTCTGATCATGCGATG---TTCCTTTCTCTGC 316
Db      1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
Qy      317 CTGAGACCAAGAGAGCTGAATCCCTGCATGAGAGTACTTCTCATATATTACTACCAATGC 376
Db      21 ValArgProGlnSerTrpGlnProCysValGlnValAlaProAsnIleThrTyrGlnCys 40
Qy      377 ATGATGAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACCTGAT 436

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Dh 41 MetGluLeuAsnPhenylrlyslleProAspAsnLeuProPheSerThrlyAsnLeuAsp 60
Qy 437 CTGAGCTTCAACCCCTGAGATCTTAAAGATATAGCTTACCAATTTCTCAAACTT 496
Dh 61 LeuSerPheAsnProLeuArgHileuGlySerTyxerPhePheSerPheProGluLeu 80
Qy 497 CAGGCGCTGATTTATCCAGGTGGAATTTGACAAATTGAGCAAGCAAGCATGGC 556
Dh 81 GluValLeuAsnLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyxGlnSer 100
Qy 557 TTAACACAGCTCTCAACCTTGTACTGACAGAAACCCCTATCAAGATTTTCCCAAGA 616
Dh 101 LeuSerIleLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
Qy 617 AGTTTCTGACCTACAAATTTAGAAATGGTGGCTGGGAGACAAAATGACCTCT 676
Dh 121 AlahSerGlyLeuSerSerLeuGlnlyLeuValAlaValGluThrAsnLeuAlaSer 140
Qy 677 CTAGAGGCTTCCATATGACAGCTTATATCTTAAAGAACTAAATGGCTCATAT 736
Dh 141 LeuGluAsnProIleGlyHileuLystrLeuLystrGluLeuAsnValAlaHisAsn 160
Qy 737 CTATATACATTCCTTAAAGTTCCTGAATATTTTCTATCTGACAAACCTAGAACATGTG 796
Dh 161 LeuIleGlnSerPheLystrLeuProGluTyxPheSerAsnLeuThrAsnLeuGlnHileu 180
Qy 797 GATCTTTCTTATATCTATATTCATTAACCTTTCTGCAAGCTTACAGTTTCTACGTA 856
Dh 181 AspLeuSerSerAsnLystrIleGlnSerIleTyxCysThrAsnLeuArgValLeuHileGln 200
Qy 857 AATCCCAAGCATATCTCTTTAGACCTGTCTTAAACCCATGACCTGACCAAGC 916
Dh 201 MetProLeuLeuAsnLeuSerLeuAsnProLeuSerLeuAsnProMetAsnProIleGlnPro 220
Qy 917 CAACCTTTCAGGAAATTAGGCTCCATGAATTGACTTAAAGAAATTTTAAATAGCTCA 976
Dh 221 GlyAlaPheLystrGluIleArgLeuHileLystrLeuThrLeuArgAsnAsnPheAspSerLeu 240
Qy 977 AATGATCGAAATGTGCTTCAAAACATGACTGTGTTTACATGTCCATCGGTGATCTTG 1036
Dh 241 AsnAlaMetLystrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspGlyLeuValLeu 260
Qy 1037 GGAGAAATTTAAATAAGAAAGATCTGGAAGTTTTCGCTTGCATGAGAAAGATA 1096
Dh 261 GlyIleuPheArgAsnGluGlyAsnLeuGluLystrPheAspLystrSerAlaLeuGlnGlyLeu 280
Qy 1097 TGCATGTGACATTTGATGAGTTCAGGTTAACATATATTAATCATTTTTCAGATGATTT 1156
Dh 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyxLeuAspTyxTyxLeuAspAspIle 300
Qy 1157 TATATCTC--AATTCCTTGGCAAAATTTTCTGCAATGTCTTTCACAGGTGTACATTA 1213
Dh 301 IleAsnLeuPheAsnCysLeuThrAsnValSerSerPheSerPheSerValThrIle 320
Qy 1214 AAACACATGAGAGATGTTCTCAGGATTTCAAAATGCAATCCTTATCATCATTAAGATTT 1273
Dh 321 GluArgValLystrAspPheSerTyxAsnPheGlyTrpGlnHileuGluLeuValAsnCys 340
Qy 1274 CATCTTAAGCCTTTTCCAAAGCTGAGTCTTACCTTTTAAAGTTGAGCTTAACTACC 1333
Dh 341 LysPheGlyGlnPheProThrLeuLystrLeuLystrSerLeuLystrArgLeuThrPheThrSer 360
Qy 1334 AACGAGAGGATACGCTTTGGTCAAGTTGGCTGCGCAAGTCTCAAGATATCTAGATTTT 1393
Dh 361 AsnLystrGlyAsnAlaPheSerGluValAsnLeuProSerLeuGluPheLeuAspLeu 380
Qy 1394 AGTGAATATGCATTTTGAAGGTGCTGTTCTTATTTCTGATTTTGAACAAACAC 1453
Dh 381 SerArgAsnGlyLeuSerPheLystrCysSerGlnSerAsnAspPheGlyThrThrSer 400
Qy 1454 CTGAAGTACTTGAACCTCAGCTTCAATGTGTCTCATCTGATGAGTCCCAACTTCAAGGT 1513
Dh 401 LeuLystrTyxLeuAsnLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420

Qy 1514 CTGAAGAGCTGGAAATACCTGGACTTTCAGCACTTCCACTTTAAAGGTCACAGAAATTC 1573
Dh 421 LeuGlnIleuLeuIleHileuAsnPheGlnHileSerAsnLeuLystrMetSerGluPhe 440
Qy 1574 TCAGTGTCTTATCTCTTGAAGAACTTTTACCTTACATCTCTTACACTTAATACAA 1633
Dh 441 SerValPheLeuSerLeuAsnArgAsnLeuIleTyxLeuAspIleSerHileThrHileArg 460
Qy 1634 ATTGACTTTGATGGCATTTTCTTGGCTTGATGATGCTCAACACTTTAAATAATGGCTGGC 1693
Dh 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLystrMetAlaGly 480
Qy 1694 AATCTTTGAAGACAAACCCCTTCAATGTCTTAAATGCTTAAACAAACAACTTACACTTC 1753
Dh 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
Qy 1754 CTGATCTTTTAAATGCCCAACTGGAACAGATATCTTAGGGGGGTATTTGACACACTTAC 1813
Dh 501 LeuAsnLeuSerGlnCysGlnLeuGlnIleuSerProThrAlaPheAsnSerLeuSer 520
Qy 1814 AGACTCCAGTTATTAACATGAGTCAACACACTTACTGTTTGGATCCATCCATTAAT 1873
Dh 521 SerLeuGlnValLeuAsnMetSerHileAsnAsnPhePheSerLeuAspThrPheProTyx 540
Qy 1874 AACACGCTGATCCCTCCAGCACTTGTGATGAGTTTCAATGCAATGACATPAGAGATCC-- 1930
Dh 541 LysCysLeuAsnSerLeuGlnValLeuAspTyxSerLeuAsnHileMetThrSerLystr 560
Qy 1931 AAAGAAATCTGCAACATTTTCCAAAGCTTACCCGCTTCAATCTGACTTAATTAATCTT 1990
Dh 561 LysGlnGluLeuGlnHilePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
Qy 1991 GTTGTCTGTATATGTGAATATCAGAATTTTTCAGAGTGGCTCAAGCAAGAAATGCTTC 2050
Dh 581 PheAlaCysThrCysGlnHileGlnSerPheLeuGlnIleTyxLystrAspGlnArgGlnLeu 600
Qy 2051 TTGGTGAATTTGACAAATGAATGCAATGCGATCACTATAGACATGAAGCCCTCCGCTGT 2110
Dh 601 LeuValGluValGluArgMetGluCysAlaThrProSerAspLystrGlnLystrMetProVal 620
Qy 2111 TTGGATTTTACGAATTTCCACCTGTATATATACAGAATCATCATCATGATGATGCGTGC 2170
Dh 621 LeuSerLeu--AsnIleThrCysGlnMetAsnLystrHileIleGlyValSerValLeu 639
Qy 2171 AGTGTCTTGTGGTACCTGTAGCATTTTCTGATATCAACTTCTTATTTTCACTGATA 2230
Dh 640 SerValLeuValSerValAlaValAlaValLeuValTyxPheTyxPheHileMet 659
Qy 2231 CTATATGCTGCTGTAATAAGTACAGACAGAGAAAGCATCTATGATGATGATTTGTGATC 2290
Dh 660 LeuLeuAlaGlyCysHileLystrGlyArgGlyGluAsnHileTyxAsnAlaPheValIle 679
Qy 2291 TACTCGAGCCGATGAGAGCTGAGTGAAGAAAGAGCTGTGTAAGATTTTGAAGAAAGA 2350
Dh 680 TyxSerSerGlnAspGluAspTrpValArgAsnGluLeuValLystrAsnLeuGluGly 699
Qy 2351 GTGCGCGCTTTCAGCTTTGCTTCATTTACAGGACCTTATTTCTGCTGTGAGCATTTGCT 2410
Dh 700 ValProProPheGlnLeuCysLeuHileTyxArgAspPheIleProGlyValAlaIleAla 719
Qy 2411 GCCAACATATCCAGAAAGGCTTCCAAAGCCGAGAAAGCTTATTTGCTGCTGTCTAGA 2470
Dh 720 AlaAsnIleHileHileGluGlyPheHileLystrArgLystrValIleValValSerGln 739
Qy 2471 CACTTTATCCAGAGCCCTTGTGTATCTTTGAATATGAGATTTGCTGACATGGCAGTTT 2530
Dh 740 HilePheIleGlnSerArgTrpCysIlePheGluTyxGluIleAlaGlnThrTrpGlnPhe 759
Qy 2531 CTGAAGAGCGCTTGCATCATCTTCTTATTTCTTGAAGAAAGTGAAGAACTCTTCTG 2590
Dh 760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLystrValGluTyxThrLeuLeu 779

QY 1157 TATATCTC--AATTCCTGGCAAAATATTTCTGCAATGTCCTTTACAGAGTGATACATATA 1213
 Db 301 ILeasrpeuhencyEleuThrAsnValSerSerSerLeuValSerValThrIle 320
 QY 1214 AAACACATCAGCAATGTTCTCAGGCAATTCGAATCGCAATCCTTATCATCATTAAGTGT 1273
 Db 321 GluArgValIlyAspPheSerTyRAsnPhedIyTrpIlnhSleuGluLeuValAsnCys 340
 QY 1274 CATCTTAAGCCTTTCCAAAGCTGAGTCTACCTTTCTTAAAGTGGCACTTAACTACC 1333
 Db 341 LyePheGlylnPheProThrLeuIlySerLeuIlySerLeuIlySerLeuIlySerLeuIlySer 360
 QY 1334 AACAGAGAGATATCAGCTTGTGTCAGTGGCTGTCGCAATCTCAGATATCTAGATCTT 1393
 Db 361 AsnIlyGlyIlyAsnAlaPheSerGluValAspLeuProSerLeuGluIupheLeuAspLeu 380
 QY 1394 AGTGAATGCGCATGAGCTTTAGAGTTCCTGCTTATTTCTGATTTTGGACAAACAC 1453
 Db 381 SerArgAsnGlyLeuSerPheIlyGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGACTTACAGCTCAGCTTCAATGGTGTGTCATCCGATGAGTGGCACTTATGAGGT 1513
 Db 401 LeuIlyTyRLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhelGly 420
 QY 1514 CTGAAGAGCTGAATACCTGACTTTCAGCACTCACTTAAAGTGGTCAAGAAATTC 1573
 Db 421 LeuGlnGlnLeuGlnIlySleAspPheGlnIlnhSerAsnLeuIlySglMetSerGluPhe 440
 QY 1574 TCAGTGTTCTTATCTTTGAAAACTTCTTATCCTTGCATCTTTCACATTAATACCAA 1633
 Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyRLeuAspIleSerIlnhStrIlnhArg 460
 QY 1634 ATTGACTTGGGATATTTCTTGGCTGATCTGATCTGCAACACTTAAAGTGGTGGC 1693
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValIleIlySmeAlaGly 480
 QY 1694 AATTCCTTCAAGCAACACCTTCAATGCTTTCATCAACACAACTTAACATTC 1753
 Db 481 AsnSerPheGlnGlnIlyAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1754 CTGATCTTTTAAATGCGCACTGGAACAGATATCTAGGGGGGATTTGGACACCTTAC 1813
 Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1814 AGACTCCAGTATTAACATGAGTCACAACTAGCTGTTCTGATCCATCCATTAAT 1873
 Db 521 SerLeuGlnValIleuAsnMetSerIlnhAsnPhelPheSerLeuAspThrPheProTyR 540
 QY 1874 AAACAGCTGACTCCCTCAGACTCTGATTCAGTTTCATCCATAGACATCC-- 1930
 Db 541 LysCysLeuAsnSerLeuGlnValIleuAspTyRSerLeuAsnIleIleMetThrSerLys 560
 QY 1931 AAAGGAATCTGCAACATTTTCCAAAGAGTGTAGCCGCTTTCATCTGACATTAATCTT 1990
 Db 561 LysGlnGlnLeuGlnIlnhPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
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 Db 581 PheAlaCysThrCysGlnIlnhSerPheLeuGlnTrpIleIlyAspGlnArgGlnLeu 600
 QY 2051 TTGGTGAATGTGAACAATGAATGTGCATCAGTTATAGCAAGAGGCTCCCTGGTGT 2110
 Db 601 LeuValGlnValIlyGlnArgMetGluCysAlaIleThrProSerAspIlySglIlyMetProVal 620
 QY 2111 TTGCAATTTACGAATTCCTGTTATATATACAAAGATATCATCAGTGTATCGGTGTC 2170
 Db 621 LeuSerLeu--AsnIleThrCysGlnMetAsnIlyStrIleIleGlyValSerValLeu 639
 QY 2171 AGTGGCTGTGTTGAGCACTGTAGCACTTCTGATATCAGCTTCTATTTTCACTGATA 2230
 Db 640 SerValIleuValIleSerValIleValAlaIleuValIlyTyRLeuTyRPhelIleuMet 659
 QY 2231 CTTATTCGTGCTGTAAAGTACAGACAGAGAAAGCATCTATGATGATTTGTGATC 2290

Db 660 LeuLeuAlaGlyCysIleLeuTyRgIlyArgGlyGluAsnIleTyRAspAlaPheValIle 679
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 QY 2351 GTGCCCCGCTTTCAGCTTGTGCTTTCATTAACAGGACTTATTCCTGGTGTAGCCATTC 2410
 Db 700 ValProPheGlnLeuIlyCysLeuIlnhTyRArgAspPheIleProGlyValAlaIleAla 719
 QY 2411 GCCAATCATTCAGGAAGGCTTCCAAAGAGCCGGAAGTTATTTGTGGTGTCTAGA 2470
 Db 720 AlaAsnIleIleIleGlnGlyPheIlnhIlySerArgIlyValIleValValIleSerGln 739
 QY 2471 CACTTTATCCAGAGCCGTTGGTGTATCTTGAATATGAGATTCGACATGGCAGTTT 2530
 Db 740 HisPheIleGlnSerArgTrpCysIlePheGlnIlyGlnIleAlaGlnIlnhTrpGlnPhe 759
 QY 2531 CTGAGTAGCCGCTCTGGCATCATCTTCATTTGCTTTCAGAAAGTGAAGAGTCTGCTG 2590
 Db 760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIlyValGlnIlySerLeu 779
 QY 2591 AGCAGAGAGTGCATTTGATTCGCTTCTTTCAGAAACACCTTACCTCGAGTGGAGAGAC 2650
 Db 780 ArgGlnGlnValGlnIlyLeuTyRArgLeuLeuSerArgAsnThrTyRLeuGlnTrpGluAsp 799
 QY 2651 AATGCTCTGGGGAGGACATCTTCTGAGAGACCTGAAAGCCCTGTTGATGGAGAAA 2710
 Db 800 SerValLeuIlyArgIlnhIlePheThrPArgLeuArgIlyValIleuLeuAspGlyLys 819
 QY 2711 GCCTGTGATCCAGAT-----GAAACATCAGAGAAAGMACAGAGCAACATTTG 2761
 Db 820 SerTrpAsnProGlnGlnIlyThrValGlnIlyThrGlyCysAsnTrpGlnIlyIlnhTrSerIle 839

RESULT 4
 ADC78785
 ID ADC78785 standard; protein; 839 AA.
 AC ADC78785;
 XX 01-JAN-2004 (first entry)
 DT XX
 DE Human PRO protein #7.
 DE human, PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.
 OS Homo sapiens.
 PN W02003034984-A2.
 XX 01-MAY-2003.
 PD 15-OCT-2002; 2002W0-US033070.
 PF 15-OCT-2001; 2001US-0340083P.
 PR 19-OCT-2001; 2001US-0340083P.
 XX (GETH) GENENTECH INC.
 PA Goddard A, Gurney AL;
 PI WPI; 2003-461990/45.
 DR N-PSDB; ADC78784.
 XX New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 PS Claim 12; SEQ ID NO 14; 327bp; English.
 XX The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

SO Sequence 839 AA:

Alignment Scores:

Pred. No.:	2,67e-280	Length:	839
Score:	2860.50	Matches:	559
Percent Similarity:	80.24%	Conservative:	115
Best Local Similarity:	66.55%	Mismatches:	159
Query Match:	48.13%	Indels:	7
		Gaps:	5

US-09-396-985B-5 (1-3395) x ADCT8785 (1-839)

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QY 260 ATGATGCTCTCTTGATCTGGCTGGAGCTGTGATCATGCAATG--TTCTTTCTCTGC 316
Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 317 CTGAGACGAGGAGGATGATCCCTGACATAGAGGACTCTTATATATTACCTACCAATGC 376
Db 21 ValArgProGluSerThrPgluProCysValGluValAlaProAsnIleThrTyGlnCys 40
QY 377 ATGATCAGAACTCTCAGCAAAATCCCTCATGACATCCCTTATTAACCAAGACCTAGAT 436
Db 41 MetGluLeuAsnPheTyLeuIleProAsnLeuProPheSerThrTyLeuAsnLeuAsp 60
QY 437 CTGAGCTTCAACCCCTGAAAGATCTTAAGAGCTTACCTTACCAATTTCTCAACTT 496
Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGluLeu 80
QY 497 CAGTGGCTGATTTATCCAGGTGTAATGAGCAATTAAGACAAAGGACATGAGTGC 556
Db 81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyGlnSer 100
QY 557 TTAACACGCTCTCAACCTTGATCTGACAGAAACCTTACAGAGTTTTCCTCCAGGA 616
Db 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaGlnGly 120
QY 617 AGTTTCTGACATCAAAATTTAGAGATCTGGTGGCTGTGAGACAAAAATGACCTCT 676
Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValAlaGluThrAsnLeuAlaSer 140
QY 677 CTAGAGGGTCTTCATTTGACAGCTTATATCTTTAAAGAACTTAATGGCTCATAT 736
Db 141 LeuGluAsnPheProIleGlyHisLeuAspThrLeuAspGluValAlaHisAsn 160
QY 737 CTATACATTCCTTAAGTGCCTGAATATTTTCTATCTGACAAACCTGAAACATGTG 796
Db 161 LeuIleGlnSerPheLeuLeuProGluIlePheSerAsnLeuThrAsnLeuGlnHisLeu 180
QY 797 GATCTTTCTTAATCTATATCAAACTATTTCTGCAAAAGCTTACAGTTTCTACGTGA 856
Db 181 AspLeuSerSerAsnIleGlnSerIleTyCysThrAspLeuAspValLeuHisGln 200
QY 857 AATCCCAAGCATCTCTCTTGAAGCTGTCTTAAACCAATTCATCCATCAAGCC 916
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 917 CAAGCCTTTCAGGAAATTAGCTCCATGATTAATGACTTAAGAGTAATTTTAATAGCTCA 976
Db 221 GlyAlaPheLeuGluIleArgLeuHisIleLeuThrIleuArgAsnAsnPheAspSerLeu 240
QY 977 AATGTACTGAAATGCTCTTCAAAACATGACTGCTTATCACTGTCATGGTGTATCTTG 1036
Db 241 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisIleArgLeuValLeu 260
QY 1037 GAGAGATTTAAATGAAGAAATCTGGAAGATTTCAGCTGTGTCAGTGAAGAGCTA 1096
Db 261 GlyIleuPheArgAsnGlnGlyAsnLeuGluIleuAspLeuSerAlaGlnGlyLeu 280
QY 1097 TGAATGTGACATTTGATGAGTTACGTTAAACATATTAATCATTTTTCAGATGATATT 1156

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Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyThrLeuAspTyTyTyLeuAspAspIle 300
QY 1157 TATAATCTC--AATTCCTGGCAAAATATTTCCGATGCTTTCACAGGTGCATATA 1213
Db 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerSerLeuValSerValThrIle 320
QY 1214 AATCAGATAGAGATGTTCTTACGATTTCAATGCAATTCCTTATCAATCATTAAGATGT 1273
Db 321 GlnArgValIleAspPheSerTyThrAsnPheGlyTyProIleHisLeuGluLeuValAsnCys 340
QY 1274 CATCTTAAGCCTTTCCAAAGCTGAGTCTACCTTTTCTTAAAGTTGAGCTTAATAC 1333
Db 341 LysPheGlyGlnPheProThrLeuTyLeuTySerLeuTySerLeuTyArgLeuThrPheThrSer 360
QY 1334 AACAGAGAGATATACACTTTGTGCACTTGCTGTGCAAGTCTCAATATCTGATCTT 1393
Db 361 AsnIleGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1394 AGTGAATATGCATGACCTTACGAGTGTGCTGTTCTTATCTGATTTTGAACAAACAC 1453
Db 381 SerArgAsnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1454 CTGAAGTACTTGAACCTTCAATGATGTGCAATCCTGATGAGTGCACCACTTATGAGGT 1513
Db 401 LeuTyThrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1514 CTGAAGAGCTGGAATACCTGAGCTTTCAGCACTCCCACTTAAAAAAGTCACAGAAATTC 1573
Db 421 LeuGlnGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuTyGlnMetSerGluPhe 440
QY 1574 TCAAGTCTTATCTCTTGAAGAACTCTTACCTTACATCTCTTACATCAATATACAAA 1633
Db 441 SerValPheLeuSerLeuAspGlnLeuIleTyThrLeuAspIleSerHisThrHisArg 460
QY 1634 ATGACTTTGATGAGCATATTTCTTGCTGATGATGATCAACCTTAAATAGGTGCTGC 1693
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuTyMetAlaGly 480
QY 1694 AATCTTTCAAAAGACACACCTTTCAAATGCTCTTTCACAAACACAAACTTCAACTTC 1753
Db 481 AsnSerPheGlnGlnLeuAsnPheLeuProAspIlePheThrGluLeuAspAsnLeuThrPhe 500
QY 1754 CTGATCTTTCTAATGSCCAATGAGACAGATATCTAGGGGGGATTTGACACACTATC 1813
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1814 AGACTCCAGTTATTAACATGAGTCAACAACCTACTGTGTTCTGATTCATCCCATAT 1873
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProTyx 540
QY 1874 AAACAGCTGATCTCCCTCAGAGCTCTTGATTCAGATTCATGACATAGACATCC-- 1930
Db 541 LysCysLeuAsnSerLeuGlnValLeuAspTySerLeuAsnHisIleMetThrSerLys 560
QY 1931 AAAGAAATATCGAATTTTCCAAAGAGCTAGGCGCTTTCATGCTGACATTAATTTCT 1990
Db 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1991 GTTGCTTGATATGATGATACAAATTTCTGACAGTGGTCAAGACAGAAATGTTTC 2050
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleTyIleuAspGlnAlaGlnLeu 600
QY 2051 TTGGTGAATTTGAACAAATGAATGTCATCCTTATGACATGAAGGCTCCCTGCTG 2110
Db 601 LeuValGlnValGluArgMetGluCysAlaThrProSerAspLysGlnLysMetProVal 620
QY 2111 TTGATTTTACGAATTCACCTGTTATATTAACAAGCTATCACTACAGTATGATGAGTGT 2170
Db 621 LeuSerLeu--AsnIleThrCysGlnMetAsnIleThrIleIleGlyValSerValLeu 639
QY 2171 AGTGTGCTGTGTAGCCACTGTGACATTTCTGATATACCACTTATTTTTCAGCTGATA 2230

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Dh	640	Se rValleLeValValSe rValValAlaValLeuValTrgluS rPheTy rPheHi sVleuMet	655
Qy	2231	CTTATTCGTCGCGCTGTAAAAAGTACACGACGAGGAGAAAGACATCTATGATGACATTTGTGCATC	2230
Dh	660	LeuLeuAlaGluCy sValLeTy sTy rGly rArgGlyGluA nniLeTy rAspAla rPheValIle	679
Qy	2291	TACTGACGCGAATAGAGACGTCGGGTGGAAACGAGCTGTAAAGAAATTTTGAAGAAGCA	2350
Dh	680	Ty rSe rSe rGlna rPheGlna rPheTrVala rArga nGlnLeuVala rAsnLeuGlnGluGly	699
Qy	2351	GTGCCCCGCTTTCAGCTTTGCTGCTTCATTACACGGGACCTTATTCCTGTGTAGCCATTGCT	2410
Dh	700	Val rPro rPheGlnLeuCy sVleuHi sTy rAla rAsp rPheIle rProGlyValAlaIleAla	719
Qy	2411	GCCAAACATCATCCGGAAGGCTCTCCAGAAAGCCGGAAGCAATTAATTCGTGTGTCATGA	2470
Dh	720	AlaAsnIleIle nLeuGlnGly rPheHi sTy sSe rArgIy sValIleValaValaSe rGln	739
Qy	2471	CACCTTATTCACAGAGCCGTGTGTGTATCTTTGAAATAGATTTGCTCAGACATGGCAGTTT	2530
Dh	740	His rPheIleGlnSe rArgTrpCy sIle rPheGlnTrglu nIleAlaGlnInTr rTrpGlnPhe	759
Qy	2531	CTGAGTACGCGCTCTGGGACATCTTCATCTTCATTTGCTTGGAAAGTGGAGAACTCCTTGCTG	2590
Dh	760	LeuSe rSe rArgAlaGlyIleIle rPheIleValLeuGlnIy sValGlnIy sTrhIleuLeu	779
Qy	2591	AGGCGACAGTGCMAATTTGTATTCGCTCTTTCAGCAGAAACACCTACCTCGAGTGGGAGGAC	2650
Dh	780	ArgGlnGlnValaGlnLeuTy rArgLeuLeuSe rArga nGlnTrTy rLeuGlnTr rPheI nAsp	799
Qy	2651	AATGCTCTGGGAGGCGACACATCTTCTGAGAAAGACTCAAAAAAGCCCTGTGTGATGGAAAA	2710
Dh	800	Se rValLeuGlnGly rArgHi sIle rPheTr rArgIleu rGly sAlaLeuLeuAspGly yAs	819
Qy	2711	GCGTTTGATCCAGAT-----GAAACATTCAGAGGAAGAAACAAGAACAACTTGTG	2760
Dh	820	Se rTr rPasn rProGlnIy rTh rValGly rTh rGlyCy sAsnTr rPheGlnI nAla rTrhSe rIle	839
RESULT 5			
ADD48826	ADD48826	standard; protein; 839 AA.	
AC	ADD48826;		
XX	02-DEC-2004 (revised)		
DT	29-JAN-2004 (first entry)		
XX			
DE	Human Protein AAF05316, SEQ ID NO 14536.		
XX			
KM	Human; pain; neuronal tissue; gene therapy;		
KM	spinal segmental nerve injury; chronic constriction injury; CCI;		
KM	spared nerve injury; SNI; Chung.		
XX			
OS	Homo sapiens.		
OS	Unidentified.		
XX			
PN	MO2003016475-A2.		
XX			
XX	27-FEB-2003.		
XX			
PF	14-AUG-2002; 2002MO-US025765.		
XX			
PR	14-AUG-2001; 2001US-0312147P.		
PR	01-NOV-2001; 2001US-0346382P.		
PR	26-NOV-2001; 2001US-0333347P.		
XX			
PA	(GEHO) GEN HOSPITAL CORP.		
PA	(PARB) BAYER AG.		
XX			
PI	Woolf C, D'urso D, Befort K, Costigan M,		
XX			
DR	WPI; 2003-268312/26.		
DR	GENBANK; AAF05316.		

[illegible]

QY 677 CTAGAGGGTTTCCATATTGGACAGCTTATCTTAAAGAACTAAATGGCTCATAT 736
 Db 141 LeuGluAsnProIleGlyHisLeuYsThrLeuYsGluLeuAsnValAlaHisAsn 160
 QY 737 CTTATACATCTCTTAAAGTTGGCTGAATTTTCTAATCTGACAAACCTAGACATGTG 796
 Db 161 LeuIleGlnSerPheIysLeuProGluYrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 797 GATCTTCTTATACATATTCATCAACTATTTCTGCAAGAACTTACAGTTCTAGCTAA 856
 Db 161 AsnLeuSerSerAsnLysIleGlnSerIleYrCysThrAspLeuArgValIleHisGln 200
 QY 857 AATCCCAAGTCATCTCTTAAAGCTGTCTTAAACCCAAATGACCTCCATCAAGCC 916
 Db 201 MetProLeuLeuAsnLeuSerLeuAsnSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 917 CAAAGCTTCAAGGAATTAAGCTCCATGAATTAAGCTTAAGAAATTAATTAAGCTCA 976
 Db 221 GlyAlaPheIysGluIleArgLeuHisIlysLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 977 AATGACGAAATGCTGCTTCAAAACATGACTGGTTTACATGTCATCGGTGATCTTG 1036
 Db 241 AsnValMetLysThrCysIleGlnIleGluAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 1037 GGAGAAATTTAAATGAAGAACTGGAAGATTTTGAACCGTTCTGTCAAGGAAGACTA 1096
 Db 261 GlyIlePheArgAsnGluGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnLysLeu 280
 QY 1097 TGCATGTGACATTAATGAGTCAAGTTCAATATATATATATATATATATATATATAT 1156
 Db 281 CysAsnLeuThrIleGluGluPheArgLeuAlaYrLeuAspYrYrLeuAspPheIle 300
 QY 1157 TATATATCTC--AATGCTTGGCAAAATATTTCTGAAGTCTTTCACAGGTGATCATTA 1213
 Db 301 IleAspLeuPheAsnCysLeuHisThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1214 AAACATAGACAGATGTTCTTAGGCAATTTCAATGGCAATCTTATCAATTAAGATGT 1273
 Db 321 GluArgValLysAspPheSerYrAsnPheGlyTrpGlnHisIleGluLeuValAsnCys 340
 QY 1274 CATCTTAAGCTTTCCAAAGCTGAAGTCTTACCTTTTAAAGTTGAGCTTAAGTACC 1333
 Db 341 LysPheGlyGlnIlePheProThrLeuLysLeuYsSerLeuLysArgLeuThrPheThrSer 360
 QY 1334 AACAGAGAGATATGACTTGTGACAGTGGCTGCGCAATCTCAGATATCTAGATTT 1393
 Db 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1394 AGTAGAAATGCCATGAGCTTAAAGTTGCTGTTCTTATTTCTGAATTTGAAACAACAC 1453
 Db 381 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGTATCTTAAGCTCAGCTTCAATGAGTCAATCTGATGAGTGCACATTCATGGGT 1513
 Db 401 LeuYrYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnAsnPheLeuGly 420
 QY 1514 CTAAGAAGCTGGAATACCTGAGCTTTAGACATCTCCATTTAAAGAAACAGAAATTC 1573
 Db 421 LeuIleGlnLeuGlnHisIleAsnAspPheGlnHisSerAsnLeuYsGlnMetSerGlnPhe 440
 QY 1574 TCAGTGTCTTATCTCTTGAAGAACTCTTAAACCTTGAACATCTTCAACATTAACAAA 1633
 Db 441 SerAlaPheLeuSerLeuArgAsnLeuIleYrLeuAspIleSerHisIleThrArg 460
 QY 1634 ATTGACTTTGATGACATATTTCTTGCTTGAATCAAGTCAACACTTAAATTAAGCTGCG 1693
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuYsMetAlaGly 480
 QY 1694 AATTCTTTAAAGACACACCTTTCAAAATGCTTTTACAAACACAAACCTTAACATTC 1753
 Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500

QY 1754 CTGATCTTTTAAATGSCAACTGAAACAGATATCTAGGGGGGTATTGACACACTTAC 1813
 Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLysLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1814 AGACTCCAGTTATTAACATGAGTCAACAACACTTACTTTCTGATTCATCCCATATAT 1873
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProYr 540
 QY 1874 AAACAGGCTATCCCTCAGACCTTGAATTCGATTCGATTCGATTCGATTCGATTC 1930
 Db 541 LysCysLeuAsnSerLeuGlnValLeuAspYrYrSerLeuAsnHisIleMetThrSerLys 560
 QY 1931 AAAGAAATCTGCAACATTTTCCAAAGCTTACCGCTTCTTCAATCTGATTAATTAATTC 1990
 Db 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1991 GTTCTGTATATGTAATATCAAGATTTCTTGAGTGGGTCAAGAACCAAGAAATGTC 2050
 Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrIleYsAspGlnArgGlnLeu 600
 QY 2051 TTGGTAAATGTTGAACAAATGAATGCAATCACTTACATCAAGTGAAGGCTCCCTGTG 2110
 Db 601 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 620
 QY 2111 TTGATTTTGAATTCACCTGTTATATATACAAAGCTATCATCAAGTATCGGTGCTG 2170
 Db 621 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 639
 QY 2171 AGTGTGCTTGTGAGCACTGTAGCAATTTCTGATATACCACTTCAATTTTCACTGATA 2230
 Db 640 SerValLeuValValSerValValAlaValLeuValYrLysPheYrPheHisLeuMet 659
 QY 2231 CTTATGCTGCTGTAAAGATGACAGAGAGAGAAAGCATCTATGATGATTTGATTC 2290
 Db 660 LeuLeuAlaGlyCysIleLysYrGlyArgGlyGluAsnIleYrAspAlaPheValIle 679
 QY 2291 TACTCAGACAGATGAGACTGGGGTGAAGAAAGAGCTGTGAAGATTTAGAAAGAGGA 2350
 Db 680 TyrSerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGlnGly 699
 QY 2351 GTGCGCGCTTGAAGCTTTGCTTCAATTAAGGAGCTTATATCTGAGTGAAGCATTTGCT 2410
 Db 700 ValProProPheGlnLeuCysLeuHisYrArgAspPheIleProGlyValAlaIleAla 719
 QY 2411 GCCAACAATCAAGAAAGCTTCCACAGAGCCGGAAGAAATTTATGCGGTGCTTGA 2470
 Db 720 AlaAsnIleIleHisGluGlyPheHisLysSerArgLysValIleValValIleSerGln 739
 QY 2471 CACTTATCCAGAGCCGTGTGATCTTGAATTAAGATGATGCTCAGATGAGCATTT 2530
 Db 740 HisPheIleGlnSerHisGlyTrpCysIlePheGlnYrGluIleAlaGlnHisTrpGlnPhe 759
 QY 2531 CTGAGTAGCGCTGTGACATCATCTTATGCTTGAAGAAAGTGAAGAGTCTTGTGCTG 2590
 Db 760 LeuSerSerArgLysGlyIleIlePheIleValLeuGlnLysValGluYsThrLeuLeu 779
 QY 2591 AGGCAAGAGTCAATTTGATGCTTCTTGAAGAAACCTTACAGTGGAGAGAC 2650
 Db 780 ArgGlnGlnValGluLeuYrArgLeuLeuSerArgAsnThrYrLeuGlnIleTrpGluAsp 799
 QY 2651 AATGCTCTGGAGGAGCAACCTTCTGAGAGAACTCAAAAAGCCGTGTGATGAGGAAA 2710
 Db 800 SerValLeuGlnYrGlnHisIlePheThrArgLysLeuArgLysAlaLeuLeuAspGlyLys 819
 QY 2711 GCCTGAATTCAGAT-----GAAACATCAAGAGAAAGAACAGAGCAACACTTGT 2761
 Db 820 SerTrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839

RESULT 6

AAW86361 standard; protein; 837 AA.

AC AAW86361;


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Db      420  GluInLeuGluHLeuAspPheGlnHsSerLeuLeuYgLIuMetSerGluPheSer 439
Qy      1577  GTGTTCTATCTCTGAAAACTTCTTACCTTGACATCTCTTACACATTAATCAAAAT 1636
Db      440  ValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrIleThrArgVal 459
Qy      1637  GACTTTGATGCGATATTTCTTGAGTCAGTCCACACTTAAATGAGCTGGCAAT 1696
Db      460  AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuYgMetAlaGlyAsn 479
Qy      1697  TCTTTCAAGACACACACCTTTCAATGTCTTTACAAACACAAACAACTTAACTTCGT 1756
Db      480  SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeu 499
Qy      1757  GATCTTTTAAATGCAACTGGAACAGATATCTAGGGGGATTTTGAACACTCTACAGA 1816
Db      500  AspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
Qy      1817  CTCCAGTATTAATACATGATGATCAACAACCTACTGTTCTTGATCCATCCATTATAA 1876
Db      520  LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
Qy      1877  CAGCTGTAACCTCCAGACCTTTGATTCAGTTTCAATCCGATAGACATCC--AAA 1933
Db      540  CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysLys 559
Qy      1934  GGAATACCTGCAACATTTTCCAAAGCTAGCCGCTTCATCTGACATTAATCTCTTT 1993
Db      560  GlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
Qy      1994  GCTTGATATGATGATATCAAGATTTCTTGACAGTGGTCAAGAACAGAAATGTTCTTG 2053
Db      580  AlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleYgAspGlnArgGlnLeuLeu 599
Qy      2054  GTGAATGTTGAACAATGAATGTGCATCACCATTATGACATGAAAGCCTCCCTGGTGTG 2113
Db      600  ValGluValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu 619
Qy      2114  GATTTTACGATTCACCTGTATATATACAAAGATATCATCAGTATCGGTGTCAGT 2173
Db      620  SerLeu--AsnIleThrCysGlnMetAsnIleThrIleGlyValSerValLeuSer 638
Qy      2174  GTGCTTGAGTAGACATGTGATTCGATTCGATTCACACTCTATTTTCACTGATACTT 2233
Db      639  ValLeuValIleSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 658
Qy      2234  ATTGCTGCTGTAAAGATACAGACAGAGAGAAAGCATCTATGATGATTTGTGATCTAC 2293
Db      659  LeuAlaGlyCysIleTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyr 678
Qy      2294  TCGAGCCGAATGAGGACTGGGTGAGAAACAGCTGTGAAGATTTTGAAGAAAGAGTG 2353
Db      679  SerSerGlnAspGluAspTyrValArgAsnGlnLeuValYgAsnLeuGlnGlyVal 698
Qy      2354  CCCCCTTGCTGCTTGCTTCATATACAGAGGCTTATCTCGGCTGAGCATTTGCTGCC 2413
Db      699  ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 718
Qy      2414  AACATCATCAGAAAGCTTCCACAAGAGCCGGAAGATTATGTGCTGCTGCTAGACAC 2473
Db      719  AsnIleIleHisGlnGlyPheHisIleYgSerArgLysValIleValIleValSerGlnHis 738
Qy      2474  TTTATTCAGAGCCGTGGTGTATCTTGAATATGAGATGTCTCAGACATGCGAGTTTCTG 2533
Db      739  PheIleGlnSerArgTyrCysIlePheHisTyrGlnIleAlaGlnThrThrGlnPheLeu 758
Qy      2534  AGTAGCCCTCTGCGCATCTTCATTTCTCTTGAGAAAGTGAGAAAGTCTTGCTGAGG 2593
Db      759  SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 778
Qy      2594  CAGCAGGTGGAATTGTATGCGCTTTTGAAGAAACACCTTCTGAGTGGAGAGACAT 2653

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Db      779  GlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluTyrGluAspSer 798
Qy      2654  GCTCTGGGGAGAGCATCTTCTGAGAGACTCAAAAAAGCCGTGGATGAGAAAGCC 2713
Db      799  ValLeuGlyArgHisIlePheTyrArgLeuArgLysAlaLeuLeuAspGlyLysSer 818
Qy      2714  TTGATCCAGAT-----GAAACATCAGAGAGAACAAAGAAAGCAACACTTGG 2761
Db      819  TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTyrGlnIleAlaThrSerIle 837

RESULT 7
AAE16102
ID   AAE16102 standard; protein; 837 AA.
AC   AAE16102;
DT   26-MAR-2002 (first entry)
DX
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM   Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
OS   Homo sapiens.
OX
PM   WO2001.90151-A2.
PD   29-NOV-2001.
PE   23-MAY-2001; 2001WO-US016766.
PR   25-MAY-2000; 2000US-0207558P.
RA   (SCHE ) SCHERING CORP.
XX
XX   Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y,
XX   WPI; 2002-083085/11.
XX   N-PSDB; AAD26292.
XX
XX   New DNAX Toll like receptor (DTLR) proteins, useful for treating
XX   conditions exhibiting abnormal expression of the receptors of their
XX   ligands, particularly abnormalities manifested by immunological
XX   disorders.
XX
XX   Claim 3; Page 41; 297dp; English.
XX
XX   The invention relates to mammalian receptor proteins, e.g., primate,
XX   human DNAX Toll like receptor (DTLR) protein and their corresponding
XX   nucleic acids. The DTLR is useful for treating conditions exhibiting
XX   abnormal expression of the receptors of their ligands. Such abnormality
XX   is manifested by immunological disorders. In particular, the DTLR is
XX   useful for treating various disease or disorders associated with abnormal
XX   expression or abnormal triggering of response to a ligand. The DTLR is
XX   also useful as an immunogen for the production of antisera or antibodies
XX   specific, e.g. capable of distinguishing between other interleukin (IL)-1
XX   receptor family members, for the DTLR or its various fragments. The
XX   purified DTLR can be used to screen monoclonal antibodies or antigen-
XX   binding fragments. The antibodies are useful for screening expression
XX   libraries for particular expression products. These are useful for
XX   detecting or diagnosing various immunological conditions related to
XX   expression of DTLR or cells that express it. The present sequence is
XX   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
XX   Note: The present sequence SEQ ID NO 26 is stated to be similar to the
XX   sequence shown in page 240-243 (AAE16116). However these sequences differ
XX   at several locations
XX
XX   Sequence 837 AA:
XX
XX   Alignment Scores:
XX   Pred. No.: 1,26e-278 Length: 837
XX   Score: 2844.00 Matches: 558
XX   Percent Similarity: 80.10% Conservative: 114

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Best Local Similarity: 66.51%

Mismatches: 159

159

159

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Query Match: 47.85%
DB: 5
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Indels: 8
Gaps: 6
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US-09-396-985B-5 (1-3395) x AAE16102 (1-837)

Oy	263	TTGGCTCTTGGACTGGCTGGGACTCGAATCAGGCAATGG---TTGCTTTCCTGGCGG	313
Db	1	MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal	20
Oy	320	AGACGAGAGAAGTTGAATCCCTCGCATAGAGTACTTCCTAAATATTACTCCATCAAGATGCAAG	379
Db	21	ArgProGluSerThrGluProCysValGluVal---ProAsnIleThrTyrGlnCysMet	39
Oy	380	GATCAGAAATCTCAGCAAAAATCCCTCATGACATCCCTTATTCAACCAAGAACTGATCTTG	439
Db	40	GluLeuAsnPheTyrLeuIleProAspAsnLeuProPheSerThrTyrAsnLeuAspLeu	59
Oy	440	AGCTTCACCCCTCGAAGATCTTAAAGACCTATAGCTTACCAAAATTTCTCAACCTTGA	499
Db	60	SerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerThrProGluLeuGln	79
Oy	500	TGGCTGATTTATCCAGGTGTGAATTTGACAATTTGAAGACAGCATGAGCATGGCTTAA	559
Db	80	ValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeu	99
Oy	560	AACCAAGCTCTCAACCTTGGTACTGACAGGAAACCTATCAAGAGTTTTCCTCCAGGAAGT	619
Db	100	SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaGluGlyAla	119
Oy	620	TTTTTGGACTCAACAAATTTGAAGATCTGGGGGCTGGAGAGCAAAAATGACCTGTCA	679
Db	120	PheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGluThrAsnLeuAlaSerLeu	139
Oy	680	GAGGGTTTCCATATTGGAACAGCTTATATCTTAAAGAACTAAATGGCTCATATCTT	739
Db	140	GluAsnPheProIleGlyHisLeuYsrThrLeuLysGluLeuAsnValAlaHisAsnLeu	159
Oy	740	ATACATTCCTTTAAAGTTGGCTGAATATTTTCTTAATCTGACAAACCTAAGACATGTGGAT	799
Db	160	IleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAsp	179
Oy	800	CTTTCTTAACTAATTAATCAAACTATTTCTGTCAAAGACTTACAGTTTCTACGCGAAAT	859
Db	180	LeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet	199
Oy	860	CCCCAAGTCATCTCTCTTAAAGCTGTCTTTAAACCCAAATTGACTCCATTCAGGCCAA	919
Db	200	ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGly	219
Oy	920	GCCTTTCAGGGAAATTAAGGCTCCATGAATGACTCTTAAGAAGTAAATTTAAATGCTCAAT	979
Db	220	AlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeuAsn	239
Oy	980	GTACTGAAAAATGGCTTCMAAACATGACTGGTTTACATGTCCTCATCGTGTGATCTTGGGA	103
Db	240	ValMetLysThrCysIleGlnIleGluLeuAlaGlyLeuGluValHisArgLeuValLeuGly	259
Oy	1040	GAATTTAAAAATGAAGAAGATCTGAAAGTTTGAACGTTCTGTCTCATGGAAGACTATGC	109
Db	260	GluPheArgAsnGluGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeuGly	279
Oy	1100	AATGAGAGATGATGAGTTCAGGTTCAATATATATATAATCATTTTCAGATGATATTAT	115
Db	280	AsnLeuThrIleGlnIleGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspPheIleIle	299
Oy	1160	AATCTC---AATTGGCTTGGCAATATTTTCGCAATGCTTTTCAACAGTGTATACATAAA	121
Db	300	AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu	319
Oy	1217	CACATAGCAGATGTTCTTAGGCATTTCAATGGCAATCCTTATCAATCATAGATGTCAAT	127
Db	320	ArgValIlyAspAspPheSerTyrAsnPheGlyTyrPrgIinhIleGlnIleuValIleuValCysValS	339

QY	1277	CTTAAGCCTTTTCCAAAGCTAGTCTACCTTTTCTTAAAGTTGGACTTAACTACCAAC	1336
Db	340	PheGlyInlPheProThrLeuIlybLeuIySerLeuIyValGlyLeuThrPheHisSer	359
QY	1337	AGAGAGATATCAGCTTTGTCAGTGGCTCTGCCAAGCTCAGATATCTAGATCTTAAT	1396
Db	360	LysGlyGlyAlaMetAlaPheSerGluValAlaPheProSerLeuGluPheLeuAspLeuSer	379
QY	1337	AGAAATGCCATGAGCTTTAGAGCTTGCTGTCTTATCTGATTTTGGAAACAACAACCTG	1456
Db	380	ArgAsnGlyLeuSerPheIyGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu	399
QY	1457	AAGTACTAAGCCTCAGCTCAATAGGTGTCACTCGATAGAGGCCAACTTGAGGCTTA	1516
Db	400	LysTyrLeuAspLeuSerPheAsnGlyAlaIleHmetSerSerAsnPheLeuGlyLeu	419
QY	1517	GAAGAGCTGAATACCTGCACTTTCAGCACTCCACTTTAAAAAGTCCACAGATTTCTCA	1576
Db	420	GluGlnLeuGlnIleLeuAspPheGlnHisSerAsnLeuIyGlyIleMetSerGluPheSer	439
QY	1577	GTGTTCTTATCTCTTGGAAAACTTTCTTAACCTTGACATCTCTTACACTAATACCAAAAT	1636
Db	440	ValPheLeuSerLeuArgAsnLeuIleYrLeuAspIleSerHisThrHisIleThrArgVal	459
QY	1637	GACTTTATGAGCATTTTCTTGAGCTGTGATCAGTCTCAACACTTTAAAAATGCTGGCAAT	1696
Db	460	AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuIyMetAlaGlyAsn	479
QY	1697	TCTTTCAAGAACAACCCCTTCAAAATGCTTTACAAACAACAACCTTAAACATTCCTG	1756
Db	480	SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeu	499
QY	1757	GATCTTTTAAATGCACTGGAACAGATATCTAGGGGGATTGACACACTGTACAGA	1816
Db	500	AspLeuSerGlnCysGlnLeuGluIleLeuSerProThrAlaPheAsnSerLeuSerSer	519
QY	1817	CTCCAGTTTAAACATGAGTACACAACAACCTACTGTTCTGATTCATCCCATTTAA	1876
Db	520	LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspPheProTyrIys	539
QY	1877	CAGCTGTACTCCCTCAGAGACTTTGATGCACTTCAATGCGATAGACATCC---AAA	1933
Db	540	CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleLeuThrSerIyIys	559
QY	1934	GGAATACTGCAACATTTTCCAAAGAGCTAGCCGCTTCAATCTGACTAATATTTGTT	1993
Db	560	GlnGluLeuGlnIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnIleAsnAspPhe	579
QY	1994	GCTTGATATGTGAATTCAGAAATTTCTTGCACTGGGCTCAAGACCAAAAAATGTTCTTG	2053
Db	580	AlaCysThrCysGlnHisGlnSerPheLeuGlnTrrIleYrAspGlnArgGlnLeuLeu	599
QY	2054	GTGAATGTTTGAACAATAAATGTCATCACTATAGACATGAAAGGCTCCCGTGCTTG	2113
Db	600	ValGluValGluAspMetGluCysAlaIleHrProSerAspIyGlnIyMetProValLeu	619
QY	2114	GATTTTACGAATTCACCTGTATTATATACAGACTATCATCATGTGTATCGGTGCTAGT	2173
Db	620	SerLeu---AsnIleThrCysGlnIleMetAsnIySerThrIleIleGlyValSerValLeuSer	638
QY	2174	GTGCTTGTGGTAAAGCCACTGTAGCACTTTGTGAATACACTTCTTATTTTCACTGTAATCT	2233
Db	639	ValLeuValValSerValValAlaValLeuValTyrIyIyPheTyrPheHisIleuMetLeu	658
QY	2234	ATTTGCTGCTGTAAAAATACAGCAGAGAGAAACAACATCTATGATGATGCACTTTGTGATCTAC	2293
Db	659	LeuAlaGlyCysIleIySerIyGlyArgGlyGluAsnIleIyAspAlaPheValIleIyIy	678
QY	2294	TCGAGCCAGAAATGAGACTGGGTGTGAACAAGACTGTGTAAAGAAATTTAGAGAGAGCTG	2353
Db	679	SerSerGlnAspGlnAspTrrValArgAsnGluLeuValValAsnLeuGluGlyGlyVal	698

```
QY 2354 CCCCCTTTGAGCTTGGCTTCATTACAGGAGCTTATTCCTGGTGTAGCCATGCTGCC 2413
    |||
Db 699 ProProheglnleuCysleuHieTyrlarGspheileProglYValAlailela 718
QY 2414 AACATCATCCAGGAAGGCTTCCACAGAGCCGGAAGTTATTTGGTGTCTTACAGAC 2473
    |||
Db 719 AsnleileHsGluGlyPheHsIlySerIarGlyValIleValIValSerGlnHs 738
QY 2474 TTTATCCAGAGCCGCTGGTGTATCTTTGATATGATGATGCTCGACAGATGGCTTCTG 2533
    |||
Db 739 PheileGlnSerIarGlyPheHsIlyPheHsIlyGlnIleAlaGlnIlePheHs 758
QY 2534 AGTACCGCTCTGGCATCATCTTCATTCCTTGAAGAAGTGAAGAAGCTCTGGTGAAG 2593
    |||
Db 759 SerSerIarGlnIleIlePheileValleuGlnIlyValGlnIlyThreleuHs 778
QY 2594 CAGCAGGCTCGAATGTATGCTGCTTTTGACAGAAACACTTACCTGAGTGGAGAGCAT 2653
    |||
Db 779 GlnGlnIleValGlnIleuTyrlarGlnleuSerIarGlnIleuTyrlarGlnIleu 798
QY 2654 GCTCTGGGAGAGCATCTCTGAGAGAGCTCAAAAAGCCCTGGTGAAGAAAGCC 2713
    |||
Db 799 ValleuGlnIleuTyrlarGlnleuTyrlarGlnleuTyrlarGlnleuTyrlar 818
QY 2714 TTGATCCAGAT-----GAAACATCAGAGGAAGAACAGCAACACTTGG 2761
    |||
Db 819 TrypanProgluGlyThreValGlyThreGlyCysAsnIlePheGlnIleThreSer 837

RESULT 8
ABU04776
ID ABU04776 standard; protein; 837 AA.
XX
AC ABU04776;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1442.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN W0200278524-A2.
XX
PD 10-OCT-2002.
XX
PE 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukaemia.
XX
PS Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
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CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_sequences
XX
SQ Sequence 837 AA;
XX
Alignment Scores:
Pred. No.: 1,266-278 Length: 837
Score: 2844.00 Matches: 558
Percent Similarity: 80.10% Conservative: 114
Best Local Similarity: 66.51% Mismatches: 159
Query Match: 47.85% Indels: 8
DB: 6 Gaps: 6
US-09-396-985B-5 (1-3395) x ABU04776 (1-837)
QY 263 ATGCTCTCTTGATCTGCTGGAGCTGTGATCATGAGCATG--TTCTCTTCTGCTG 319
    |||
Db 1 MetSerIaserArgleuAlaGlyThreleuIleProIleAlaPheleuSerCysVal 20
QY 320 AGACGAGGAAGCTTGAATCCCTGCATAGAGGACTTCTTATTTACCTACCAATGCATG 379
    |||
Db 21 ArgProGlnSerIlePheGlnProCysValGlnVal--ProAsnIleIleTyrlarGlnCysMet 39
QY 380 GATCAGAACTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTGATCTG 439
    |||
Db 40 GlnleuAsnIleTyrlarGlnleuPheAsnleuProIleSerIleTyrlarGlnleuAsnleu 59
QY 440 AGCTTCAACCCCTGAGATCTTGAAGGATATAGCTTCAACATTTCTGACAACTTCAG 499
    |||
Db 60 SerPheAsnProleuArgHsIleuGlySerTySerPheSerPheProGlnleuGln 79
QY 500 TGCGTGAATTTATCAGGTGTGAATTTAGACAAATTGAAGCAAGCATGCGCTTA 559
    |||
Db 80 ValleuAsnleuSerIarGlnIleGlnIleThreIleGlnIlePheGlnIleTyrlarGlnSerleu 99
QY 560 AACAGCTCAACCTTGTGATGACAGAAACCTTCAAGATTTTCCCGAGAGT 619
    |||
Db 100 SerHsIleuSerIleuIleleuThreGlyAsnProIleGlnSerleuAlaIleuGlyAla 119
QY 620 TTTTCTGATTAACAATTTTGAAGATCTGTGCTGTGAGACAAATAATGACCTCTCTA 679
    |||
Db 120 PheSerIlyleuSerSerleuGlnIleValAlaIleValGlnIleThreAsnleuAlaSerleu 139
QY 680 GAGGTTTCATATTTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCATATCTT 739
    |||
Db 140 GlnAsnIleProIleGlnIleTyrlarGlnleuTyrlarGlnleuValAlaIleAsnleu 159
QY 740 ATACATTCCTTTAAGTGGCTGAAATATTTTCTTAAATGACAAACCTGAGATGAT 799
    |||
Db 160 IleGlnSerPheIleuProGlnIlyPheSerIarGlnIleuTyrlarGlnIleAsnleu 179
QY 800 CTTTCTTATATCATATTTCAAACTATTTCTGTGACAAAGCTTACAGTTTCAACGAAAT 859
    |||
Db 180 LeuSerSerIarGlnIleGlnIleTyrlarGlnIleTyrlarGlnIleTyrlarGlnIle 199
QY 860 CCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCAATGATGCATTCAGGCCAA 919
    |||
Db 200 ProleuAsnleuSerleuAsnleuSerleuAsnleuProIleGlnIlePheIleGlnProGly 219
```


XX		29-NOV-2001.
XX		
PF		23-MAY-2001; 2001MO-US016766.
XX		
PR		25-MAY-2000; 2000US-0207558P.
XX		
PA	(SCHE) SCHERING CORP.	
XX		
PI	Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y,	
XX	WPI; 2002-063085/11.	
DR	N-PSDB; AAD26306.	
XX		
PT	New DNAX Toll like receptor (DTR) proteins, useful for treating	
PT	conditions exhibiting abnormal expression of the receptors of their	
PT	ligands, particularly abnormalities manifested by immunological	
PT	disorders.	
XX		
PS	Claim 3; Page 240-243; 297pp; English.	
XX		
CC	The invention relates to mammalian receptor proteins, e.g., primate,	
CC	human DNAX Toll like receptor (DTR) protein and their corresponding	
CC	nucleic acids. The DTR is useful for treating conditions exhibiting	
CC	abnormal expression of the receptors of their ligands. Such abnormality	
CC	is manifested by immunological disorders. In particular, the DTR is	
CC	useful for treating various disease or disorders associated with abnormal	
CC	expression or abnormal triggering of response to a ligand. The DTR is	
CC	also useful as an immunogen for the production of antisera or antibodies	
CC	specific, e.g. capable of distinguishing between other interleukin (IL)-1-	
CC	receptor family members, for the DTR or its various fragments. The	
CC	purified DTR can be used to screen monoclonal antibodies or antigen-	
CC	binding fragments. The antibodies are useful for screening expression	
CC	libraries for particular expression products. These are useful for	
CC	detecting or diagnosing various immunological conditions related to	
CC	expression of DTR or cells that express it. The present sequence is	
CC	human DTR4 protein, alternative version. The DTR4 gene is located on	
CC	chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to	
CC	be similar to the sequence shown in page 41 (AAB16102). However these	
CC	sequences differ at several locations	
XX		
XX	Sequence 837 AA:	
SO		
Alignment Scores:		
Pred. No.:	6,47e-278	Length: 837
Score:	2837.00	Matches: 557
Percent Similarity:	79.98%	Conservative: 114
Best local Similarity:	66.39%	Mismatches: 160
Query Match:	47.74%	Indels: 8
DB:	5	Gaps: 6
US-09-396-985B-5 (1-3395) x AAB16116 (1-837)		
OY	263 ATGCGTCCTTGATCATGTGGCTGGAGCTGCATCATGAGATG--TTCCTTTCTGCGCTG 319	
Dd		
Dd	1 WeSeRlaseRargLeuaIagIyHrleuIIeProAlameRaIaPeLeSeCysVal 20	
OY	320 AGACGAGAAGCTTGATCCCTGCATAGAGTACTCTAAATAATTACTTACCATGATGATG 379	
Dd		
Dd	21 ArgProGlusertIrpeIubProCySvalGIuVal---ProAnIIetHrTygInCysMet 39	
OY	380 GATCAGAAATCTGCAGAAAATCCCTCATGCATCCCTTAATCAACCAAGAACCTAGATCTG 439	
Dd	::::	
Dd	40 GlLueAsnPhetyrLyIsIlleProLaepAntleuPropheSerThrLyAsnLeuAspLeu 59	
OY	440 AGCTCAACCCCTGAAGATCTTAAAGAGCTTACTTACCATCACCAATTTCTCAACTGAG 499	
Dd		
Dd	60 SerPheAsnProLeuArghIsleuGlYserTYSerPhePheSerPheProGlnLeuGln 79	
OY	500 TGCGTAGATTATTCAGGTGTGAAATTGACAATGGAACAAGGACGATGAGCTTA 559	
Dd		
Dd	80 ValLeuAspLeuSerArgCysgluIleGlnThrIleGluAspGlyAlaTyrgInSerLeu 99	
OY	560 AACCAAGCTTCAAACCTTGATGCAGAGAAACCTTCAAGAGATTTTTCCCAGGAAT 619	

Db	100	Serial	leuSerThrIleuIleuLeuThiGlyAsnProIleGlnSerLeuAlaLeuGlyAla	119
Qy	620	TTTTCTGAC	TAAACAATTTAGAAATCTGTGGCTGTGAGACAAATAATGACCTCTGA	679
Db	120	PheSerGly	leuSerSerSerLeuGlnIleLeuValAlaValGluThrAsnLeuAlaSerLeu	139
Qy	680	GAGGCTT	CCATATTTGACACAGCTTATATCCTTAAAGAACTAAATGTGGCTATATCTT	739
Db	140	GluAsn	PheProIleGlyAlaSerLeuThySerLeuGlySerLeuAsnValAlaHisAsnLeu	159
Qy	740	ATACATTC	CCCTTAAGTGGCCGAATATTTTTCTATCTGACAAACCTTGAAACATGTGGAT	799
Db	160	IleGlnSer	PheIlyleuProGluThyPheSerAsnLeuThrAsnLeuGlnHisLeuAsp	179
Qy	800	CTTTCTTA	TAACTATATTAATCAAACTATTTCTGTCAAAAGCTTACAGTTCTTACGTGAAT	859
Db	180	LeuSerSer	AsnIlySileGlnSerIleIyrcyThrAspLeuAlaGlyValLeuHisSerIlnet	199
Qy	860	CCCCAAG	CAATCTCTCTTTAGACCTGTCTTTAAACCCATGACCTACATTCACGCCCA	919
Db	200	ProLeu	AsnLeuSerLeuAspSerLeu**PrometAsnPheIleGlnProGly	219
Qy	920	GCTTTT	CAGGAATTAAGCTCCCAAGAAATGACCTTAAGAACTATATTTTAATAGCTCAAT	979
Db	220	AlaPhe	lySGluIleArgLeuHisIleSylleuThrLeuArgAsnAsnPheAspSerLeuAsn	239
Qy	980	GTACTGA	AAATATGTGCTTCAAAATGACACTGTTTACATGACCCATCCGCTTATCTTGGA	1039
Db	240	ValMet	lyStrIySileGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly	259
Qy	1040	GAATTTA	AAAAATGAAGCAATCTGAAAGATTGTAACGCTTGTCATGAAAGCACTATGC	1099
Db	260	GluPhe	ArgGlnGlyAsnLeuGlnIlyAspPheAspSerAlaLeuGlnGlyLeuGlycys	279
Qy	1100	AATGTG	AGCATTTGATGAGTTACAGGTTTAAACATATATATCATTTTTCAGATGATTTAT	1159
Db	280	AsnLeu	ThrIleGlnGluPheArgLeuAlaIyIyLeuAspIyIyIyLeuAspAspIleIle	299
Qy	1160	AATCTC	---AATGCTTGGCAAAATATTTTCTTGCAAGTGTACATATTA	1210
Db	300	AspLeu	PheAsnCySylleuThrAsnAlaSerSerPheSerLeuValSerValThrIleGlu	319
Qy	1217	CACATG	ACAGATGTCTCGAGCATTTGCAATGCAATCCTTATCAATCATTAGATGTGAT	1276
Db	320	ArgVal	IlyAspPheSerTyArgAsnPheGlyTrpGlnHisLeuGluValAsnGlySyls	339
Qy	1277	CTTAAG	CTTTCCAAAGCTGAGTCTACCTTTCTTAAAGTGGACTTTAACTAACAC	1333
Db	340	PheGly	IlnPheProThrLeuIlyleuHisSerLeuIySylArgLeuThrPheThrSerAsn	359
Qy	1337	AGAAAG	ATATACCTTGGTCAGTATGGCTGTGGCAAGTCTCAGATTTCTAGATCTTATGT	1396
Db	360	LysGly	IlyAsnAlaPheSerGluValAspLeuProSerIleuGlnPheLeuAspLeuSer	379
Qy	1397	AGAAAT	GCATGACCTTTAGAGTGTGTCTTATCTGATTTTGGAAACAACACCTG	1456
Db	380	ArgAsn	GlyleuSerPheIlySylCyCysSerGlnSerAspPheGlyThrThrSerIleu	399
Qy	1457	AAGTACT	TAGACTCAGCTCAATGAGTGTCACTCTGATGAGTGCACATTCATGAGTCTTA	1516
Db	400	LysTy	LeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyIy	419
Qy	1517	GAAGA	GTGAATCTGGAATCTGGAATTCAGACATTCACATTTAAAAAAGGTACAGGAATTC	1576
Db	420	GluGln	IleuGlnHisLeuAspPheGlnHisSerAsnLeuIlySylMetSerGlnPheSer	439
Qy	1577	GTGTTC	TATCTCTTGAAAACTTTTACCTTGACATCTCTTACACATATACAAAAAT	1636
Db	440	ValPhe	leuSerLeuAlaGlyAsnLeuIleTyIleuAspIleSerHisIyThrHisArgVal	459
Qy	1637	GACTTT	GATGAGCATATTTCTTGCTGTATCAGTCTCAACATTTAAAAATGGCTGGCAAT	1696

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Db      460 AlaheannglyllepheannglyleuserSerleuGlValleuylsMetAlaGlyAsn 479
Qy      1697 TCCTTCAAAAGACACACCCCTTCAAAATGCTTTCAAAACACAACTTAACCTTCTG 1756
Db      480 SerheglnngluenpheleuProAspIlepheThrGluLeuArganleuThrPheleu 499
Qy      1757 GATCTTCTAAATGCCAACTGGAACAGATATCTAGGGGGGTAATTTGACACACTCTACAGA 1816
Db      500 AspleuserGlnCySgInleuGlnleuSerProThrAlaPheAnSerleuSerSer 519
Qy      1817 CTCAGTATTATTAACATGAGTCACAAACACTACTGTTCTGGATCCATCCATTATPAA 1876
Db      520 LeuGlnValleuAnMetSerHlaAsnAnpHeSerleuAnpThrPheProTyls 539
Qy      1877 CAGGTGATCCCTCAGAGCTCTGATTCGATTCATGTCATAGAGACATCC--AAA 1933
Db      540 CysleuAnSerleuGlnValleuAnpTyrSerleuAnHlaSileMetThrSerLys 559
Qy      1934 GGAATACCTCAACATTTTCCAAAGACTAGCCGCTTTCATCTGACTATATATCTGTT 1993
Db      560 GlnGluLeuGlnHlaPheProSerSerleuAlaPheleuAnleuThrGlnAnpPhe 579
Qy      1994 GCTTGATATGTGAATATCAGAAATTTCTTGCAGTGGGTCAAGAACCAAAAATCTTCTG 2053
Db      580 AlaCysThrCySgInHlaSerPheleuGlnTrpIleTylsAspGlnArgGlnleu 599
Qy      2054 GTGAATGTTGAACAAATGAATGTGCATCAGCTTAAGACATGAAGGCTCCCTGCTGTG 2113
Db      600 ValGluValGluArgMetGluCySalThrProSerAspLysGlnGlyMetProValleu 619
Qy      2114 GATTTTGAATTCACCTGTTATATATACAAAGACTATCACTGATCGGTGTCAGT 2173
Db      620 Serleu---AnlelThrCySgInMetAnlyThrIleleGlyValSerValleuSer 638
Qy      2174 GTGCTTGAGTACGCACTGATGACATTTCTGATATACACTTCTATTTTCACTGATCTT 2233
Db      639 ValleuValValSerValValAlaValleuValTylsLysPheTyrPheHlaLeuMetleu 658
Qy      2234 ATTCGTGCTGTAAATAAGTACAGCAGAGAAAGCACTGATGATGTCATTTGATGATCTAC 2293
Db      659 LeuAlaGlyCysIleLysTylArgGlyGluAnlelTylsAspAlaPheValIleTyr 678
Qy      2294 TCGAGCCAGATGAGCACTGGGTGAGAAACAGCTGTAAAGAAATTTAGAAAGAGATG 2353
Db      679 SerSerGlnAnpGluAspTrpValAlaArgAnGluLeuValValAnleuGlnGlyVal 698
Qy      2354 CCCGCTTTCAGCTTGTGCTTCATTAACGGAATTATCTCTGCTGATCCATGCTGCC 2413
Db      699 ProProPheGlnLeuCyLeuHlaTylsArgAspPheIleProGlyValAlaIleAlaAla 718
Qy      2414 AACATCAATCCAGAAAGCTTCCACAAAGCCGGAAGTATTTGGGTGGTCTACAGAC 2473
Db      719 AsnIleIleHlaSgInGlyPheHlaIlySerArgLysValIleValValSerGlnHla 738
Qy      2474 TTATCCAGAGCCGCTGCTGATCTTTGAATATGATGCTCAGACATGCAAGTTCTG 2533
Db      739 PheIleGlnSerArgTrpCysIlePheGluTyrGluIleAlaGlnThrTrpGlnPheleu 758
Qy      2534 AGTAGCCGCTGTGCATCATCTTCATTTCTTGAAGAAAGTGAGAGAGCTCTGCTGAGG 2593
Db      759 SerSerArgAlaGlyIleIlePheIleValleuGlnLysValGluTyrThrLeuLeuArg 778
Qy      2594 CAGCAGGTGCAATGTATCGCTTCTTACGAGAAACACTTACCTCGAATGGAGAGCAAT 2653
Db      779 GlnGlnValGluLeuTyrArgLeuLeuSerArgAnThrTylsLeuGlnTrpGluAspSer 798
Qy      2654 GCTCTGGGAGGACATCTTCTGAGAGAGACTCAAAAAGCCCTTGATGAGAAAGCC 2713
Db      799 ValleuGlnArgHlaIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 818
Qy      2714 TTGAATCCAGAT-----GAAACATCAGAGAGAAACAAGAGCAACTTTG 2761
Db      819 TrpAnpProGlnGlyThrValGlyThrGlyCysAnpTrpGlnGluAlaThrSerIle 837

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RESULT 10
AD057797
ID AD057797 standard; protein; 801 AA.
XX
XX
AC AD057797;
XX
DT 12-AUG-2004 (first entry)
XX
DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS Saimiri sciureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /label= Leu, Phe
XX
XX W02004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI; 2004-400726/37.
XX
XX DR N-PSDB; AD057795, AD057796.
XX
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents squirrel monkey TLR4.
XX
XX
SQ Sequence 801 AA;
XX
XX
Alignment Scores:
Pred. No.: 8.16e-274 Length: 801
Score: 2796.50 Matches: 539
Percent Similarity: 80.90% Conservative: 105
Best Local Similarity: 67.71% Mismatches: 149
Query Match: 47.06% Indels: 3
DB: Gaps: 3
XX
US-09-396-985b-5 (1-3395) x AD057797 (1-801)
Qy      350 GTACTTCTAATATTAATTAATCAATGATGATGATCTCAGAAATCCCTCATGAC 409
Db      1 ValValProAnValThrTyrGlnCyMetGluLeuAn***TyrLysIleProAspAn 20
Qy      410 ATCCCTTATTCACCAAGAACTTGAATCTGAGCTTCAACCCCTGAAAGATCTTAAGAAG 469
Db      21 IleProPheSerThrLysAnleuAnpLeuSerPheAnpProleuAnArgHlaSleuGlySer 40

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470 TATAGCTTCAACAAATTTCTCAACATTCAGTGGCTGATTTATCCAGGTGGAATTAG 529
 41 HiserPhePheAsnPheProGluLeuGlnValLeuAspLeuSerArgCysAspIleGln 60
 530 ACAATTGAAGACAAAGCATGGCATGGCTTAAACAGCTCTCAACCTTGGTATGACAGA 589
 61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisIleSerThrLeuIleLeuThrGly 80
 590 AACCTATCAAGAGTTTTCCTCCAGGAGTTTTCCTGACATCAACAAATTTGACAAATG 649
 81 AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
 650 GTGGCTGGGAGACAAAATGACCTCTAGAGGGTTTCCATATTGACACAGCTTATATCC 709
 101 ValAlaValGluThrHisLeuLeuSerLeuGlnAsnProIleGlyHisLeuLysThr 120
 710 TTAAGAACTAAATGTGGCTCATATCTTATACATTCCTTAAAGTTGCTGAATATTTT 769
 121 LeuLysAspLeuAsnValAlaHisIleAsnLeuIleGlnSerPheLysLeuProGluTyrPhe 140
 770 TCTATCTGACAAACCTGACATGTGATCTTTCTTATCTATATTCAAACTATTTCT 829
 141 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnAsnIleGlnAsnIleTyr 160
 830 GTCAAGACTTACAGTTTCTACGTGAATAATCCCAAGCTCATCTCTTATGACCTGTCT 889
 161 CysLysAspLeuGlnValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
 890 TTAACCCCAATGTGATCCATTCACAGCCCAAGCCTTTCAGGGAATTAGGCTCCATGAATTG 949
 181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisIleLysLeu 200
 950 ACTGTAAGAGTAAATTTTATAGCTCAATATGATCGAAATGTGCTTCAAAACATGACT 1009
 201 ThrLeuArgAsnAsnPheAspSerLeuAsnAlaMetLysThrCysIleGlnGlyLeuAla 220
 1010 GATTATGATGTCATCGGTTGATCTTGGGAGAAATTGAAGAAAGGATTCGGAAGT 1069
 221 GlyLeuGlnValHisArgLeuValLeuGlyLysPheAsnGlnAlaArgAsnIleGlnLys 240
 1070 TTGACCGTCTGTGATGGAAGACTATGACATGTGACATGTGATGAGTTCAGGTTACA 1129
 241 PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleAsnGluPheArgLeuAla 260
 1130 TATATAATCATTTTTCAGATGATTTTATATCTC--AATGCTTGGCAAAATTTCT 1186
 261 TyrLeuAspAspPheLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnValSer 280
 1187 GCATGCTTTCACAGGTGATCATATAAACACATAGCAGATGTTCTTCAAGCATTTTCAA 1246
 281 SerPheSerLeuValAsnValHisIleLysArgValGluAspPheSerTyrAsnPheArg 300
 1247 TGGCAATCTTATCATCATATGATGATCTTAAAGCTTTCAAAGCTGATCTTACT 1306
 301 TrpGlnHisLeuGlnLeuValAsnCysValAlaPheGlnGlnPheProPheLysLeuLys 320
 1307 TTTCTTAAAGTTGACCTTAACTACCAACAGAGATATCAGCTTGGTACAGTGGCT 1366
 321 SerLeuLysArgLeuThrPheThrAlaAsnLysGlyArgAsnHisPheSerGlnValAsp 340
 1367 CTGCAAGTCTCAGATATCTAGATCTTAGTAAGATGCAAGAGCTTGAAGTTGCTGCT 1426
 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysArg 360
 1427 TCTTATCTGATTTTGAACAAACCACTGAAAGTACTTGAAGCTCAGGCTCAATGATGTC 1486
 361 SerGlnSerArgPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnAspVal 380
 1487 ATCTGATGATGCCAATTCATGGGCTTGAAGAGCTGGAATACCTGACCTTCACAGAC 1546
 381 IleThrMetGlySerAsnPheLeuGlyLeuGlnGlnLeuGlnHisIleLeuAspPheGlnHis 400

1547 TCCACTTAAAGATGACAGAAATCTCAGTGTCTTATCTCTTGAAGAACTTCTTAC 1606
 401 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyr 420
 1607 CTGACATCTCTTACACTAATACCAAAATGACTTTGATGGCATATTTCTTGGCTGATC 1666
 421 LeuAspIleSerHisThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuPhe 440
 1667 AGCTCAACACTTAAAAAAGGCTGGCAATCTTTCGAAGCAACACCTTCAAAATGTC 1726
 441 SerLeuLysValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuGlnAspIle 460
 1727 TTAACAAACCAACAACTTAACTTACATTCCTGATCTTTCTAATGCCAATGGAACAGATA 1786
 461 PheThrAspLeuAsnLeuIlePheLeuAspLeuSerGlyCysGlnLeuGlnLeu 480
 1787 TCTAGGGGGGATTTGACACACTGACAGCTCCAGTTATTTAAACATGAGTCACAAACAC 1846
 481 SerProThrAlaPheAspSerLeuProArgLeuArgIleLeuAsnMetSerHisAsnAsn 500
 1847 CTATGTTTCTGATCCATCCCAATTATAAACAGTGTACCTCCAGAGCTCTGATGTC 1906
 501 PhePheAlaLeuAspThrPheProTyrLysHisLeuTyrSerLeuGlnValLeuAspTyr 520
 1907 AGTTCAATGCAATGAGACATCCAAAGCA--ATACCTGACAACTTTTCCAAAGAGCTTA 1963
 521 SerLeuAsnHisIleGlyThrSerLysAsnGlnGlnLeuGlnHisPheProSerSerLeu 540
 1964 GCCGCTTCAATCTGACTTAATATTTCTGTTGCTTGATGATGAAATATCAGAAATTTCTTG 2023
 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
 2024 CAGTGGGTCAAGACCAAGAAATGTTGTTGTAATTTGAACAAATGAATGTCATCA 2083
 561 GlnTrpLysAspGlnArgLeuValGlnValGlnGlnMetGlyCysAlaThr 580
 2084 CCTATGACATGAAGGCTCCCTGCTGTGATTTTGAATTCACCTGTATATATATAC 2143
 581 ProLeuAsnArgLysGlyIleProValLeuSerLeu--AsnIleThrCysGlnMetSer 599
 2144 AAGACTATCATGATGATGATGCTGCTGATGCTGCTTGTGATGACCTGATGACATTTCTG 2203
 600 LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaValAlaLeu 619
 2204 ATATACACTCTATTTTACCTGATCATCTTATGCTGCTGCTGTAAGAAAGTACAGAGAGA 2263
 620 ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 639
 2264 GAAAGCATATGATGATGATTTGATCTACTCGACCAAGATGAGACTGGGTGAGAAAC 2323
 640 GlnAsnThrTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsn 659
 2324 GAGCTGTAAGAAATTTGAAGAGAGAGTCCCGCTTCAAGCTTGGCTTCAATTACAG 2383
 660 GlnLeuValLysAsnLeuGlnGlnGlyValIleProProPheGlnLeuCysLeuHisTyrArg 679
 2384 GACTTATCTGCTGATGACCATTTGCTGCGCAATCATCAAGAGAGCTTCCAAAGAGC 2443
 680 AspPheIleProGlyValAlaIleAlaAlaAsnIleHisGlnGlyPheHisLysSer 699
 2444 CGAAAGTATTTGAGGTGGTGTGACACTTATCCAGAGCGGTGATGATCTTGAAG 2503
 700 ArgLysValIleValAlaValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 719
 2504 TATGAGATCTCAGACATGGCAGTTTCTGATGAGCGCTCTGGCATCATCTTCAATTGTC 2563
 720 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgIleIleIlePheIleVal 739
 2564 CTGAGAGAAATGAGAGAGTCTTGTGAGAGAGAGTCCAAATGTATGCTTGCCTTGAAGC 2623
 740 LeuGlnLysValGlnLysSerLeuLysArgGlnGlnValGlnLeuTyrArgLeuLeuSer 759
 2624 AGAAACCTTACCTCGATGGGAGAGCAATGCTCTGGGAGGACATCTTCTGAGAGAGA 2683


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Db      361 SerGlnSerAspPheGlyThrThrSerLeuYsTyrLeuAspLeuSerPheAsnAspVal 380
Qy      1487 ATCTGATGAGGCGCAACTTCATGGGCTGAGAAAGCTGGAATACCTTGCACTTTCAGCAGC 1546
Db      381 IleThrMetSerSerAsnPhenLeuGlyLeuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 400
Qy      1547 TCCACTTTAAAAAGGTGACAGAAATTCAGTGTCTTATCTCTTGAAGAAATTCCTTTCATC 1606
Db      401 SerAsnLeuYsGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyr 420
Qy      1607 CTGACATCTCTTACATTAATCCAAATATGACTTGTAGGATATTTCTTGAGCTTGATC 1666
Db      421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAspIlyLeuLeu 440
Qy      1667 AGTCTCAACACTTTAAAAATGCGTGGCAATCTTCTCAAGAACACACCTTTCATCAATGTC 1726
Db      441 SerLeuYsValLeuYsMetAlaGlyAsnSerPheGlnGlnAsnPhenLeuProAspIle 460
Qy      1727 TTTACAAACACAAACCTTAACATTCCTGATCTTCTTAATGCGCAACTGGACAGATA 1786
Db      461 PheThrAspLeuYsAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIleu 480
Qy      1787 TCTAGGGGGGATTTGACACACTCTACAGACTCCGATTATTAACATGATGACACACAC 1846
Db      481 SerProThrAlaPheAspThrLeuAsnYsLeuGlnValLeuAsnMetSerHisAsnAsn 500
Qy      1847 CTACTGTTCTGATCCATCCATATTAACAGCTGTCTCCCTGACGACCTTGATGTC 1906
Db      501 PhePheSerLeuAspThrPheProTyrIleCysLeuProSerLeuGlnValLeuAspTyr 520
Qy      1907 AGTTTCAATGCGCATAGACATCCAAAGAA--ATACTGCAACATTTTCCAAAGATCTA 1963
Db      521 SerLeuAsnHisIleMetThrSerAsnAsnGlnIleuGlnHisPheProSerSerLeu 540
Qy      1964 GCCGCTTCATCTGACTTAATTAATCTGTGCTGTATATGTAATATACAAATTTCTTG 2023
Db      541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
Qy      2024 CAGTGGGTCAAGSACAGAAATGTTCTGGTGAATGTTGAACAAATGAAATGTCACACA 2083
Db      561 GlnTrrIleYsAspGlnArgGlnLeuLeuValGlnAlaGlnArgMetGlnCysAlaThr 580
Qy      2084 CCTATAGACATGAAGGCTCCCTGTGTGTGAATTTACGAATTCACCTGTTATATATAC 2143
Db      581 ProSerAspYsGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsn 599
Qy      2144 AAGACTATCATCAGTGTATCGGTGCTCAGTGTGCTTGTTGGTACCATGACATTTCTG 2203
Db      600 LysThrIleIleGlyValIleSerValPheSerValLeuValIleSerValAlaValLeu 619
Qy      2204 ATATACCACTTCTATTTTACCTGATCTTATTTGCTGCTGCTGAATAAATACAGACAGAGA 2263
Db      620 ValTrrYsPheTyrPheHisIleuMetLeuLeuAlaGlyCysIle**TyrGlyArgGly 639
Qy      2264 GAAAGCATCTATGATGATTTGTGTATCTTACTCGAGCCAGAAATGAGACTGGGTGGAAC 2323
Db      640 GlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAsnAspIleAspTrrValArgAsn 659
Qy      2324 GAGCTGTGAAGAAATTTGAAGAGAGAGTCCCGCTTCAGCTTTCGCTTCATATACAG 2383
Db      660 GluLeuValYsAsnLeuGlnGlnGlyValProProPheGlnLeuYsLeuHisTyrArg 679
Qy      2384 GACTTATCTCTGCTGTAGCATTTGCTGCAACATTCATCCAGSAGAGGCTTCACAGAGC 2443
Db      680 AspheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisIleYsSer 699
Qy      2444 CGAAAGTATTTGCTGTGTGTCTAGACATTTATCCAGACCGTGTGTATCTTTGAA 2503
Db      700 ArgYsValIleValIleValIleSerGlnHisPheIleGlnSerArgTrrCysIlePheIleu 719
Qy      2504 TATGAGATTTGCTCAGACATGGCAGTTTCTGAGTACCGCTTCGCAATATCTTCAATGTC 2563
Db      720 TyrGlnIleAlaGlnIleThrTrrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739

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Qy      2564 CTGAGAAAGTGAAGAGTCCCTGCTGAGCAGACAGGTGCAATTGTATCGCTTCTTAC 2623
Db      740 LeuGlnYsValGlnYsThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 759
Qy      2624 AGAAACACTTACCTTGAGTGGAGACAAATCTCTGGAGGACATCTTGTGAGAAAGA 2683
Db      760 ArgAsnThrTyrLeuGlnTrrGlnAspSerValLeuGlyGlnHisIlePheTrrArgArg 779
Qy      2684 CTCAAAAAGCCCTTGATGATGAGAAAGCCCTTGAATCCAGATGAA 2728
Db      780 LeuArgYsAlaLeuLeuAspGlyArgSerTrrAsnProGlnGln 794

RESULT 12
AD057800
ID AD057800 standard; protein. 795 AA.
XX
AC AD057800;
XX
DT 12-AUG-2004 (first entry)
XX
DE Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS Papio hamadryas.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PE 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
XX
DR N-PSDB; AD057798, AD057799.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 21; 111bp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents hamadryas baboon TLR4.
XX
SQ Sequence 795 AA:
Alignment Scores:
Pred. No.: 2,71e-272 Length: 795
Score: 2781.50 Matches: 538
Percent Similarity: 81.01% Conservative: 106
Best Local Similarity: 67.67% Mismatches: 148
Query Match: 46.80% Indels: 3
DB: 8 Gaps: 3
US-09-396-985B-5 (1-3395) x AD057800 (1-795)

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QY 350 GTACTCTTATATATTACCTACCAATGATGATGATCTCAGAGAAATCCCTCATGAC 409
Db 1 ValValProMetIleThrTyGlnCysMetGluLeuAsnPheTyLysIleProAspAsn 20
QY 410 ATCCCTATTTCACCAAGAACCTTAGATCTGAGCTTCAACCCCTGAGAGATCTTAAAGAC 469
Db 21 IleProPheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHisIleGluGlySer 40
QY 470 TATAGCTTACCAATTTTCTCAAACTTCAGTGGCTGATTTATTCAGAGTGTGAATGAG 529
Db 41 TyzSerPheLeuArgPheProGluLeuGlnValIleuAspLeuSerArgCysGluIleGln 60
QY 530 ACAATTGGAAGACAGACATGAGCTTAAACGAGCTTCAACCTTGTGTGACAGAGA 589
Db 61 ThrIleGluAspGlyAlaTyGlnSerLeuSerHisIleuSerThrLeuIleLeuThrGly 80
QY 590 AACCTTATCAAGAGTTTTCCTCCAGAGAGTTTTCGAGCTTACAAATTTAGAGATCTG 649
Db 81 AsnProIleGlnSerLeuAlaIleuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
QY 650 GTGGCTGTGAGACAAAATGACCTCTTAGAGGCTTCCATATTGACAGCTTATATCC 709
Db 101 ValAlaValGluThrAsnLeuAlaSerLeuGluAsnPheProIleGlyHisIleuLysThr 120
QY 710 TTTAAGAACTAAATGTGGCTCATPATCTTTATACATCTCTTAAAGTTGGCTGAATTTT 769
Db 121 LeuLysGluLeuAsnValAlaHisIleAsnLeuIleGlnSerPheLysIleuProGluIleTyPhe 140
QY 770 TCTATCTGACAAACCTTAGAACATGTGGATCTTTCTTAACTATATTCAACTATTTCT 829
Db 141 SerAsnLeuThrAsnLeuGluHisIleuAspLeuSerSerAsnLysIleGlnAsnIleTyx 160
QY 830 GTCAAAAGCTTACAGTTTCTACGTGAATAATCCCAAGTCATCTCTTTAGACCTGTCT 889
Db 161 CysLysAspLeuGlnValIleuHisIleGlnMetCProLeuProAsnLeuSerLeuAspLeuSer 180
QY 890 TTTAACCCTTATGATCTCATCAAGCCCAAGGCTTTTCAAGATTAAGGCTCCAGAAATG 949
Db 181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleAspLeuHisIleLysLeu 200
QY 950 ACTCTAAGAGTAATTTTATAGCTCAATATGACTGAATAATGTGCTTCAAAATGACT 1009
Db 201 ThrLeuArgSerAsnPheAspAspLeuAsnValMetLysThrCysIleGlnGlyLeuAla 220
QY 1010 GGTTTACATGTCCATCGGTGATCTTGGAGAAATTTAAATAATGAAGAAATCTGGAAAGT 1069
Db 221 GlyLeuGluValHisArgLeuValLeuGlyLysPheArgAsnGluHisArgAsnLeuGluLys 240
QY 1070 TTTGACGCTGTGTCATGGAAGAGACTATGCAATGTGAGCATTTGATGAGTTAACA 1129
Db 241 PheAspLysSerAlaLeuGluGlyLeuCysAsnLeuMetIleGluGluPheArgLeuThr 260
QY 1130 TATATAATCATTTTTCAGATGATATTTATATCTC--AATGTGTGGCAATATTTCT 1186
Db 261 TyzLeuAspTyTyTyLeuAspAsnIleIleAspLeuPheAsnCysIleuAlaAsnAlaSer 280
QY 1187 GCATGTCTTTCACAGGTGTACATATTAACAACAGATGTTCCTTAGGCAATTTCAA 1246
Db 281 SerPheSerLeuValSerValAsnIleLysArgValGluAspPheSerTyzAsnPheArg 300
QY 1247 TGGCACTCTTATCATCATTAGATGATGATCTTAAAGCTTTTCAAGAGCTAGCTACT 1306
Db 301 TrpGlnHisIleuGluLeuValAsnCysLysPheGluGlnPheProThrLeuGlnLeuGlu 320
QY 1307 TTTCTTAAAGTTGAGCTTTTAACTACCAACAGAGAGATATCAGCTTTGTCAATGTGCT 1366
Db 321 SerLeuLysArgLeuThrPheThrAlaAsnLysGlyLysAsnAlaPheSerGluValAsp 340
QY 1367 CTGCCAAGTCTCAGATATCTAGATCTTTGAGAAATGCCATGAGCTTTGAGGTTGCTGT 1426
Db 341 LeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysCys 360

QY 1427 TCTTATTTCTGATTTTGGAAACAACAACCTGAGTACTTAGACTTACCTCAGCTTCAATGCTGTC 1486
Db 361 SerGlnSerAspPheGlyThrThrSerLeuLysTyzLeuAspLeuSerPheAsnAspVal 380
QY 1487 ATCCCTAGATGTCCAACTTCATGGCTCTTGAAGAGCTGGAAATACCTGCACTTTCAGCAC 1546
Db 381 IleThrMetGlySerAsnPheLeuGlyLeuGluGlnLeuGluHisIleuAspPheGlnHis 400
QY 1547 TCCACTTTAAAGGACAGAAATTCAGTGTCTTATCTCTTGAAGAAACTTCTTTAC 1606
Db 401 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnIleTyx 420
QY 1607 CTTGACATCTCTTACATATACCAAAATTGACTTGAATGAGCATATTTCTTGCTGATC 1666
Db 421 LeuAspIleSerHisIleThrHisIleThrValAlaPheAsnGlyIlePheAspGlyLeuLeu 440
QY 1667 AGTCTCAACATTTTAAAAATGCTGGCAATCTTTTCAAGACAAACCCCTTCAATGTC 1726
Db 441 SerLeuLysValIleuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAspIle 460
QY 1727 TTTTCAAAACAACAACAACTTAATTCCTGATCTTTCTTAAATGCCAATGGAACAGATA 1786
Db 461 PheThrAspLeuLysAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGluGlnLeu 480
QY 1787 TCTAGGGGGGTATTTGACACACTCTACAGACTCCAGTTATTAACATGAGTCAACAAC 1846
Db 481 SerProThrAlaPheAspThrIleuAsnLysLeuGlnValLeuAsnMetSerHisAsnAsn 500
QY 1847 CTACTGTTTGTGATTCATCCATTTATTAACAGCTGTACTCTCAGAGCTTGTATTGC 1906
Db 501 PhePheSerLeuAspValPheProTyTyLysCysLeuProSerLeuGlnValLeuAspTyx 520
QY 1907 AGTTTCAATGCGATPAGAGATCAACAAGCA--ATPACTGCAACATTTTCAAGAGCTTA 1963
Db 521 SerLeuAsnHisIleMetCThrSerLysAsnGlnGluProGlnHisPheProSerSerLeu 540
QY 1964 GCCGCTTTCATCTGACTAATTAATCTGTGTCTGTATATGTAATATCAAAATTTCTTG 2023
Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
QY 2024 CAGTGGTCAAGACCAAGAAATGTTCTTGCTGAATGTTGAACAATGAATGTCATCA 2083
Db 561 GlnTrpIleLysAspGlnArgGlnLeuLeuValGluAlaGlnArgMetGluCysAlaThr 580
QY 2084 CCTATGACATGAAGGCTCCCTGGTGTGATTTTACGAATTCACCTGTATATATAC 2143
Db 581 ProSerAspLysGlnGlyMetProValLeuSer--ValAsnIleThrCysGlnMetAsn 599
QY 2144 AAGACTATCATAGTGTATGCTGTCAGTGTGCTGTGTGATGACACTGTAGCAATTTCTG 2203
Db 600 LysThrIleIleGlyValSerValPheSerValLeuValValSerValValAlaValLeu 619
QY 2204 ATATACACTTATTTTCACTGATATCTTATTTGCTGTGGCTGTAAGAAATGTCACAGAGGA 2263
Db 620 ValTyzLysPheTyzPheHisIleMetLeuLeuAlaGlyLysLeuTyzGlyArgGly 639
QY 2264 GAAGCACTATGATGATTTGTGATCTACTCGAGGCAAGAAATGAGCACTGGGTGAGAAAC 2323
Db 640 GlnAsnIleTyzAspAlaPheValIleTyzSerSerIleAspGlnAspTrpValArgAsn 659
QY 2324 GAGCTGTGAAGAAATTTAGAGAAAGAGTCCCGGCTTTCAGCTTTCCTTCAATACAG 2383
Db 660 GlnLeuValLysAsnLeuGluGluGlyValProProPheHisIleuCysLysHisIleTyArg 679
QY 2384 GACTTATTCCTGTGTGAGCAATGTGCTGCAACATCAATCAAGAGGCTTTCACAGAGC 2443
Db 680 AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGluGlyPheHisIleTyx 699
QY 2444 CGAAGATTTATTTGTGGTGTGCTAGACACTTTATTCAGAGCGGTTGGTATTTTGA 2503
Db 700 ArgLysValIleValValIleSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 719
QY 2504 TATGAGATGCTCAGACATGCGAGTTTCTGAGTAGCGGCTGCGATCATCTTCAATGTC 2563


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Db      341 LeuProSerLeuGluPheLeuAspLeuSerArgSnglYleuSerPheYsgLYCysCys 360
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Db      361 SerInSerAapPheGlyThrThrSerLeuYstyLeuAapLeuSerPheAsnGlyVal 380
Qy      1487 ATCCGATAGTGCACACTTCATGGGCTGAGAGAGCTGGAATCTGCACTTCACAC 1546
Db      381 IleThrSerSerAenPheLeuGlyLeuGluGlnLeuGluGlnIleAapPheGlnHis 400
Qy      1547 TCACCTTAAAAAGTCAAGAAATTCAGTGTCTTATCTTTGAAAACTTCTTAC 1606
Db      401 SerAsnLeuYsgImeSerGluPheSerValPheLeuSerLeuAArgAsnIleYx 420
Qy      1607 CTGACATCTCTGACCTAATACCAAAATGACCTTGAGCATATTCTTGCGTTCATC 1666
Db      421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
Qy      1667 AGTCTCAACACTTTAAAAATGGCTGGCAATCTTTCAAAGACAACACCCTTCAATGTC 1726
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Qy      1727 TTTACAAACACACAACAACTTAACATTCCTGATCTTTTAAATGCCAATGGAACAGATA 1786
Db      461 PheThrGluLeuAArgAsnLeuThrPheLeuAapLeuSerGlnCysGlnLeuGlnIleu 480
Qy      1787 TCTAGGGGGGATTTTGGACACACTCTACAGACTCCAGATTATTAACATGAGTACACAC 1846
Db      481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMeSerHisAsn 500
Qy      1847 CTACTGTTTCTGATTCACATCCATTAATTAACAGCTGTAATCCCTCAGACACTTGTATGC 1906
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Qy      1907 AGTTTCAATGCCATAGACATCC--AAAGAAATCTGCACACTTTTCCAAAGAGTCTA 1963
Db      521 SerLeuAsnHisIleMetThrSerIysGlnGlnIuGlnHisPheProSerSerLeu 540
Qy      1964 GCGCTCTTCACTGACCTAATTAATTCGTGCTGTAATGTAATGTAATTAATTCCTG 2023
Db      541 AlaPheLeuAapLeuThrGlnAsnAapPheAlaCysThrCysGlnHisGlnSerPheLeu 560
Qy      2024 CAGTGGCTCAAGACACAGAAATGTTTGGTGAATGTTGAAACAATGAATGTCATCA 2083
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Qy      2084 CCTAATGACATGAAGGCTCCCTGGTGTGAATTTTGAATTTTCAACCTGTTATATATAC 2143
Db      581 ProSerAapIysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnIleMetAsn 599
Qy      2144 AAGACTATCATCAGTATGAGTGGTGCAGTGGCTGTGGTGAAGCACTGATGCAATTCGTG 2203
Db      600 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 619
Qy      2204 ATATACCACTTCTATTTTCACTGATACTTATTTGCTGGCTGTAATAAAGTACAGAGAGA 2263
Db      620 ValTyrIysPheTyrPheHisIleuMetLeuLeuAlaGlyValIleYstyGlyArgGly 639
Qy      2264 GAAGACATCTATGATGCACTTTGTGATCTATCTGAGCCGAATGAGAACTGGGTGAAGAAC 2323
Db      640 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAapTrpValAlaArgAsn 659
Qy      2324 GAGCGGTAAGAAATTTAGAAGAGAGTGGCCGCTTCAAGCTTGGCTTCATTAACAG 2383
Db      660 GluLeuValIysAsnLeuGlnGlnGlyValAlaProProPheGlnLeuCysLeuHisTyrArg 679
Qy      2384 GACTTTATCTCGTGTAGCACTTGTCTGCAACATCATCCAGAGAGCTTCCAGAAAGC 2443
Db      680 AspPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGlyPheHisIlySer 699
Qy      2444 CGAAAAGTTATTTGGTGGTGTCTAGACACTTATCCAGACCGTGGTGTATCTTTGAA 2503
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Qy      2504 TATGAGATTGCTCAGACATGGCAGTTTCTGAGTAGCCGCTCGACATCATTTCAATGTC 2563
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Qy      2564 CTTGAGAAAGTGAAGAAGTCTTGTGAGGACAGAGTGAATGTATGTCCTTTTAC 2623
Db      740 LeuGlnYsValGlnYsThrLeuLeuAArgGlnValGlnLeuYtyrArgLeuLeuSer 759
Qy      2624 AGAAACCTTACCTCGAGTGGAGGACAATGCTCTGGGAGAGCAATCTTCTGAGAGA 2683
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Qy      2684 CTCAAAAAGCCCTGTGATGAGAAAAAGCTTGAATCCAGAT-----GAAACATCA 2734
Db      780 LeuArgYsAlaLeuLeuAapGlyYsSerTrpAsnProGluGlnValGlyThrGly 799
Qy      2735 GAGGAAAGACAGAAAGCAACACTTGG 2761
Db      800 CysAsnTrpGlnGlnAlaThrSerIle 808

RESULT 14
AD057782 standard; protein; 808 AA.
ID      AD057782
AC      AD057782;
XX      12-AUG-2004 (first entry)
DT      12-AUG-2004 (first entry)
DE      Chimpazee toll-1-like receptor 4 SEQ ID NO:3.
XX      toll-1-like receptor 4; TLR4; old world monkey; antibacterial;
XX      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX      Pan troglodytes.
XX      WO2004042365-A2.
XX      21-MAY-2004.
XX      03-NOV-2003; 2003WO-US036247.
XX      01-NOV-2002; 2002US-0423113P.
XX      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX      Meesler W;
XX      WPI; 2004-400726/37.
XX      N-PSDB; AD057780, AD057781.
XX      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX      sequence of the Old world monkey with that of a human.
XX      Example 1; SEQ ID NO 3; 11pp; English.
XX      The invention relates to a novel method for identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an old world monkey
XX      comprising comparing the TLR4 polynucleotide sequence of the Old world
XX      monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX      method of the invention has antibacterial, immunosuppressive, and
XX      antiasthmatic activity. The method is useful in identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an Old world monkey where the
XX      change may be associated with reduced sensitivity to Gram-negative
XX      bacterial infection. The methods, agents and composition are useful in
XX      treating sepsis, severe sepsis or septic shock and asthma. The present
XX      sequence represents chimpanzee TLR4.
XX      Sequence 808 AA;
XX      Alignment Scores:

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Pred. No.: 1.99e-271 Length: 808
 Score: 2773.00 Matches: 540
 Percent Similarity: 80.59% Conserved: 112
 Best Local Similarity: 66.75% Mismatches: 151
 Query Match: 46.66% Indels: 6
 DB: 8 Gaps: 4
 US-09-396-985b-5 (1-3395) x AD057782 (1-808)

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 1 ValValProbenHleThrTyrGlnGlyMetGluLeuAsnPheTyrLysIleProAspAsn 20
 410 ATCCCTTATTCACCAAGACCTAGATCTGAGCTTCAACCCCTGAAGATCTTAAGAAG 469
 21 LeuProPheSerThrLysAsnLeuAsnProPheAsnProLeuArgHisLeuGlySer 40
 470 TATAGCTTACCAATTTCTCACAACCTTCAGTGGCTGATTTATCCAGGTGTGAATTGAG 529
 41 TyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIleGln 60
 530 ACAATTGAAGACAGACATGAGTGGCTTAACACAGCTCTCAACCTTGGTACTGACAGA 589
 61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
 590 AACCTTACAGAGATTTTCCCGAGAAATTTCTGAGCTACCAAAATTTAGAGAACTCG 649
 81 AsnProIleGlnSerLeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
 650 GTGGCTGTGAGACAAAAATGACCTCTAGAGGGTTTCATATTTGACAGCTTATATCC 709
 101 ValAlaValGluThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuLysThr 120
 710 TTAAGAACAATTAATGTGGCTCATATCTTATATCTCTTAACTTAACTTAACTTAACTT 769
 121 LeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluLysPhe 140
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 221 GlyLeuGlnValHisArgLeuValLeuGlnGluPheArgAsnGlnGlyAsnLeuGlnLys 240
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 241 PheAspLysSerAlaLeuGlnGluLysCysAsnLeuThrIleGlnGluPheArgLeuAla 260
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 1367 CTGCCAAGCTTCAGATATCTTGATCTTATGTAAGAAATGCCATGAGCTTTAGAGCTTCTGT 1426
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 1787 TCTAGGGGGGATTTTGACACACTTACAGACTCCAGATTTATTAACATGACACAAACAC 1846
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 521 SerLeuAsnHisIleMetThrSerLysLeuGlnLysLeuGlnHisPheProSerSerLeu 540
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 2204 ATATACCACTCTTATTTTACCTGATCTTATGCTGCTGTGCTTAAAGTATCAGCAGAGA 2263
 620 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 639
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 Db 600 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 619
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Search completed: March 29, 2005, 17:02:25
 Job time : 215.403 secs

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D	578	eLeuAsnLeuThrGlnPheAspPheAlaCysThrCysGlnHisIleSerPheLeuGlnTr	598
Q	2029	GGTCAAGACACAGAAAATGTTCTTGGTGAATGTTGAACAAATGAATATGTCATCCTAT	2088
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D	618	tAspAspGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsnLeuTrpTh	637
Q	2149	TATCATCAGTATACGGGTGATGTCAGTGTGCTGTGGTGAACCTGTACATCTTCGATATATA	2208
D	637	tIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeuValTrp	657
Q	2209	CCACTTCTATTTTCACTGATACTTATTTGCTGAGCTGTAAAAAGTACAGACAGAGAGAAG	2268
D	657	tTrpPheTrpThrHisIleuMetLeuLeuAlaGlyCysIleTrpGlyArgGlyGlnAs	677
Q	2269	CATCTATATATGCAATTTTGATCTACTGAGGCAGAAATGAAGACCTGGGTGAGAAACAGACT	2328
D	677	nIleTrpAspAlaPheValIleTrpSerSerGlnAspGlnAspTrpValAlaArgAsnGlyLe	697
Q	2329	GGTAAAGAAATTTAGAAAGAAGAGTGCCTTCAGTTGCTTCAAGTTCATTCACAGGACCTT	2388
D	697	uValTrpAsnLeuGluGlnGlyAlaProProPheGlnLeuCysLeuHisTrpTrpAspPhe	717
Q	2389	TATTCCTGTGTAGCCATTTGCTGCAACATCATCAGAAAGCTTCCACAAAGCCGGA	2448
D	717	eIleProGlyAlaAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisTrpSerArgGly	737
Q	2449	AGTTATTTGTGTGTCTAGACACTTATTCAGAGCCGTGGTGTATCTTTGAATATGA	2508
D	737	eValIleValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnTrpGly	757

QY 2509 GATTGCTCAGACATGCGAGTTTCTGAGTAGCCGCTGGCATTCATTGTCCTTGA 2568
 Db 757 UtlalaglnhrtrpqlnphleuseSerxhgaladlyllelehelevalleuGl 777
 QY 2569 GAAAGTGAAGATGCTTGTCTGAGGACAGCAGTGAATTTATGCTCTTTAGCAGAA 2628
 Db 777 nlyvalgluylstrleuLeuAArglnGlnIvalgluLeuylrAArgleuLeuSerAArgA 797
 QY 2629 CACTACTCGAGTGGGAGGACATGCTCTGGAGAGACATCTTCTGGAGAGCTCA 2688
 Db 797 nhrthyrluLeuIurpGluaSpSerValleuGlyAArgHsileheprrAArgleuA 817
 QY 2689 AAAAGCCTGTGGATGAGAAAGCCTTGATCCAGAT-----GAAACATCAGAGA 2739
 Db 817 glyhaleuLeuLeuAepgIylSerTrpAsnProgluGlythrValglYthrGlyCyAAs 837
 QY 2740 AGAACAGAGCAACCAACTTGTG 2761
 Db 837 ntrpGlnGluAthrSerile 844

RESULT 2

US-08-514-014-4
 ; Sequence 4, Application US/08514014
 ; Patent No. 5707829
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McKenough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514,014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-4

Alignment Scores:

Pred. No.: 1.4e-53 Length: 661
 Score: 609.00 Matches: 194
 Percent Similarity: 46.51% Conservative: 133
 Best Local Similarity: 27.60% Mismatches: 303
 Query Match: 10.25% Indels: 73
 Db: 1 Gaps: 21

US-09-396-985B-5 (1-3395) x US-08-514-014-4 (1-661)

QY 208 TACAGTTGTCATGCTTT-----CTCACGGCCTCCGCTGGTCAGAAAATGCGAG 258
 Db 3 PheaspValserCysrphelrtrpValValleuPheSerHlaGlyCyAs----- 19
 QY 259 GATGATGCTCTCTTGATCTGGCTGGACTGTGATCAAGCATGTTCTTCTGCTGCT 318
 Db 20 -----ValIlethrSerTrpAspGln-Met----- 27
 QY 319 GAGACAGAAAGCTGAATCCCTGCATAGAGATCTTCAATATTAATCAATGAT 378
 Db 28 -----CysIleGlySerGlnIleAsnlystrHyraenCyseG 40
 QY 379 GGATCAGATCTCAGAAAATCCCTCATGACATCCCTTATTCAGAAAGAACTAGATCT 438
 Db 40 uAsnleuGlyLeuSerGlnIleProAspThrLeuProAsnThrThrGlnPheLeuGluPh 60
 QY 439 GAGCTTCAACCCCTGAAGATCTTAAGACCTATAGCTTCAACAAATTTCTCAACTTCA 498
 Db 60 eSerPheAsnPheLeuProThrIleHsAsnAArgThrPheSerAArgleuMetAenLeuTh 80
 QY 499 GTGGCTGATTTATCCAGGTGTGAATTTAGACATTTGAACAGACATGGCATGGCTT 558
 Db 80 rPheLeuAspLeuThrAArgCysGlnIleAsnTrpIleHsIleuAspThrPheGlnSerH 100
 QY 559 AAACAGCTCTCAACCTTGGTACTGACAGGAAACCTATCAAGAGTTTTCACGAGAG 618
 Db 100 eHsIleuLeuSerThrLeuValleuThrGlyAsnProLeuIlePheHelaIaGluThrSe 120
 QY 619 TTTTCTGACCTAACAAATTTAGAGATCTGGTGGCTGTGGAGACAAAAATGACCTCT 678
 Db 120 rLeuAsnGlyProlyserLeuYshIleuPheLeuIleGlnThrGlyIleSerAenle 140
 QY 679 AGAGGTTTCATTTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCAATCT 738
 Db 140 uGluPheIleProValHsAsnleuGluAsnleuGlySerLeuYrleuGlySerAsnH 160
 QY 739 TATCATCTCTTGAAGTGGCTGAATTTTCTTAATCTGACAAACCTAGAACATGCTGA 798
 Db 160 sIleSerSerIlelyshPheProlysaPhePro---AlaArgAsnleuYsValleuAs 179
 QY 799 TCTTTCTTAATCAATATTTCAAACTATTTCTGTCAAAAGCTTACAGTTTCTACGTGAAA 858
 Db 179 rPheGlnAsnAsnHalaIleHsTrylIleSerAArgGluAspMetAArgSerleuGluGln-- 198
 QY 859 TCCCAAGTCAATCTCTTGTAGACCTGTCTTAAACCAATGACTTCATCAAGCCA 918
 Db 199 ----AlaIleAsnleuSerleuAsnPheAsnGlyAsnAsnValylsglyIleGluLeuG 217
 QY 919 AGCCTTCAGGAATTAGGCTCCATGAAATTGACCTTAAGAAGTAATTTAATACCTAAA 978
 Db 217 yAlaPheAspSerThrValPheGlnSerLeu-----AsnHegIyGlyThrPr 233
 QY 979 TGTACTGAATAATGCTTCAAAAACATGATGCTGTTTACATGCTCAGTCGATCTTGGG 1038
 Db 233 oAsnleuSerValIlePheAsnGlyLeuGlnAsnSerThrThrGlnSerleuTrpLeuG 253
 QY 1039 AGAATTTAAATGAAGAATCTGGAAGTTTACCGTCTGTCAAGAGACATGAT 1098
 Db 253 yThrPheGluAspIleAspAsp--GluAspIleSerSerAlaMetleuYsglyLeuCy 272
 QY 1099 CAATGTGAGATGATGATGCTTACGATCAATATTAATTAATCAATTTCAAGT---GATAT 1155
 Db 272 eGluMetSerValGluSerleuAsnleuGlnGlu--HisArgPheSerAspIleSerSe 291
 QY 1156 TTATATCTCAATGCTTGGCAAAATATTTCTGCAATGCTTTCACAGAGTGTACATATAA 1215
 Db 291 rThrThrPheGlnCysrphethrGlnleuGlnIleuAspLeuThrIathrHsleuY 311
 QY 1216 ACACATAGCAGATGCTTGGGATTTCAAAATGCAATCTTATCAATCATTA----- 1270
 Db 311 s-----GlyLeuProSerGlyMetLys-----GlyLeuAsnleuLeuYslySle 326

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Qy 1271 -----TTCATCTTAAGCCT-----TTCCAAA 1293
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Qy 1294 GCTGAGCTCTACCTTTTCTTAAGAGTTGACCTTAACCAACAGAGATACACTT 1353
Db 346 rLeuThrHisLeuYrHisLeuArgLy-----AsnValIeuYrHisLeuGlyVa 363
Qy 1354 TGGTCAGCTG---GCTGCGCAAGCTCAGATATATGATCTGATGTAAGATGCGTAG 1410
Db 363 lGlyCysLeuGlnIuYrLeuGlnLeuGlnThrLeuHisPheSerHisAsnArgIleG 383
Qy 1411 CTTAGAGCTGCTCTTCTTATCTGATTTTGGAAACAACAACCTGAAGTACTTGA 1470
Db 383 uAlaSerAspCysSerLeuGlnLeuGlnLeuYrAsnLeuSerHisLeuGlnThrLeu 403
Qy 1471 CAGCTTCAATGGTCTATC---CTGATGAGTGCACAACTTCAAGGCTTGAAGAGCTGGA 1527
Db 403 uSerHisAsnGlnIuProLeuGlnLeuGlnSerGlnAlaPheYrGlnCySProGlnLeuG 423
Qy 1528 ATACCTGGACTTTGAGCACTCCACCTTAACAAAAGTCAACAAGATTCAGTCTTATC 1587
Db 423 uLeuLeuAspLeuAlaPheThrArgLeuHisIleAsnAlaProGlnSerProPheGln 443
Qy 1588 TCTTGAACAACTCTTCACTTGAACATCTCTTACACTTAATCAACAAATTGACTTGA 1647
Db 443 nLeuHisPheLeuGlnIuValLeuAsnLeuThrTyCyPheLeuAspThrSerArgInH 463
Qy 1648 CATATTTCTTGGCTTGATCAGTCTCAACACTTTTAAAAAGCTGGCAATTTTCAAGA 1707
Db 463 sLeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLeuYrGlyAsnHisPheGln 483
Qy 1708 CAACACCCCT-----TCAATGCTTTTACAACAACAACAACAAATTCATCTCCGATCT 1761
Db 483 rGlyThrIleThrHisThrAsnLeuLeuGlnThrValGlySerLeuGlnValLeuIle 503
Qy 1762 TTCTAAATGCCAAGTCAACAGATATCTAGGGGGGTATTGTACACACTTACAGACTCA 1821
Db 503 uSerSerGlyLeuLeuSerIleAspGlnGlnAlaPheHisSerLeuGlnGlyMetSe 523
Qy 1822 GTTATTAACTAGTCAACAACACTTACTG-----TTTGTGATCA---TCCCATTA 1872
Db 523 rHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSerLeuSerHis 543
Qy 1873 TAAACAGCTGATCCCTCAGACACTTGTGATGCACTTTCATGCAATGCAAGACATCAA 1932
Db 543 uYrGlyIleTy-----LeuAsnLeuAlaHisAsnSerIleAsnIleIleSe 559
Qy 1933 AGGAATCTGCACATTTTCCAAAGAGTCTAGCCGCTTCACTGATTAATATCTGT 1992
Db 559 rProArgLeuLeuProIleLeuSerGlnGlnSerThrIleHisLeuSerHisAsnPro 579
Qy 1993 TGCCTTGATATGTAATATCAAAATTTCTTGCAGTGGTCAAGACCAAGAAATGTTCT 2052
Db 579 uAspCysThrCysSerAsnIleHisPheLeuThrTyTrpYrGlnAsnLeuHisIle 599
Qy 2053 GGTGAATGTGACAAATGAATGATGACATGACATGACATGAGGCTCCGCGGTT 2112
Db 599 uGlnGlySerGlnGlnThrCysAlaAsnProSerLeuArgIleValIleYrLeuSe 619
Qy 2113 GGATTTTACGAATTC-----ACCTGTATATATATACAAGATCATCATGATGT 2160
Db 619 rAspValIleLeuSerCysGlyIleThrAlaIleGlyIlePhePheLeuIleValPhe 639
Qy 2161 ATCCAGTGTCACTGTCTTGTGTAGCACTGTAGCATTTGTGATATACCACTTCTATT 2220
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US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-Apr-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-Aug-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-5851
; TELEFAX: (617) 498-8224
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-823-4

Alignment Scores:
Pred. No.: 1,4e-53 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conservative: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
DB: 2 Gaps: 21

US-09-396-985b-5 (1-3395) x US-08-833-823-4 (1-661)
Qy 208 TACAGTTCGTCATGCTT-----CTCAGCGCCTCCGCTGTGACAGAAAATGCCAG 258
Db 3 PheAspValSerCysPhePheTrpValValLeuPheSerHisLeuGlyCysIys----- 19
Qy 259 GATGATCCCTCTTGTGATGCTGGAGTCTGTGATCAGATGATGCTTCTTCGCTT 318
Db 20 -----ValIleThrSerTrpAspGln-Met----- 27
Qy 319 GAGACGAGAAAGCTTGAATCCCTGCATAGAGTACTTCTTAATATTTACCAATGCAT 378
Db 28 -----CysIleGlnIuYrGlnAlaAsnIleThrYrAsnCySgl 40
Qy 379 GGATCAGATCTCAGCAAAATCCCTCATGATCATTCCCTTATTCACCAAGACCTAGATCT 438
Db 40 uAsnLeuGlyLeuSerGlnIleProAspThrLeuProAsnThrThrGlnPheLeuGlnIu 60
Qy 439 GAGCTTCAACCCCTGAAAGATCTTAAGAACTTAAGTTACCAATTTCTCACAACCTCA 498

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 Qy 559 AAACAGCTCTCAACCTTGGTACTGACAGAAACCCTTCAAGAGTCTTTCCCAAGAG 618
 Db 100 sHisGlnLeuSerThrLeuValLeuThrGlyAsnProLeuIlePheMetAlaGluThrSe 120
 Qy 619 TTTTTCGACTCAACAAATTGAGAAATCTGTGCTGTGAGAGCAAAAATGACTCTCT 678
 Db 120 rLeuAsnIleProLysSerLeuLysHisLeuPheLeuIleGlnThrGlyIleSerAsnLe 140
 Qy 679 AGAGGTTTCATATGAGACCTTATTCCTTAAAGAACTTAAATGTGGCTCATATCT 738
 Db 140 uGluPheIleProValHisAsnLeuGluAsnLeuGluSerLeuTyLeuGlySerAsnHis 160
 Qy 739 TATACATTCCTTAAAGTGGCTGATATATTTTCAATCTGACAAACCTTGAACATGTGGA 798
 Db 160 sIleSerSerIleLysPheProLysAspPhePro--AlaArgAsnLeuLysValLeuAs 179
 Qy 799 TCTTTCTTATTAATCTATTCAAACTATTTCTGTCAAAAGACTTACAGTTTCACTGAAA 858
 Db 179 pPheGlnAsnAsnAlaIleHisTyIleSerArgGluAspMetArgSerLeuGluGln-- 198
 Qy 859 TCCCAAGTCAATCTCTTAGACCTGTCTTAAACCCATGAGCTCATCAAGCCCA 918
 Db 199 ----AlaIleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValLysGlyIleGluLeuG 217
 Qy 919 AGCCTTTCAGGGAATTGAGCTTCATGATGACTTGAAGATTAATTTAATAGCTCAA 978
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 Qy 979 TGTACTGAATATGTCCTTCAAAACATGACTGTTTACATGCTCAATCGCTGATCTGGG 1038
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 Qy 1039 AGAATTTAAATGAATGAAGATCTGGAATGTTGACCGTCTGTGATGAAAGCATATG 1098
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 Qy 1099 CAATGTGAGCATTTGAGTTCAGGTTCAGATTAATATTAATATTCATTTTCAGAT--GATAT 1155
 Db 272 sGluMetSerValGluSerLeuAsnLeuGlnGlu--HisArgPheSerAspIleSerSe 291
 Qy 1156 TTATTAATCTCAATGCTTGGCAAAATATTTCTGCAATGCTTTCACAGGCTGATATATA 1215
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 Qy 1216 ACACATAGCAGATGTTCTAGGCAATTCGAATGGAATCCCTATCAACATTAAGA---- 1270
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 Qy 1271 -----TGTCATCTTAAGCT-----TTTCCAAA 1293
 Db 326 uValLeuSerValAsnHisPheAspGlnLeuCyGlnIleSerAlaAlaAsnPheProSe 346
 Qy 1294 GCTGAGTCTACCTTTCTTAAAGTTGAGCTTTAATCAACAACAGAGATATCAGCTT 1353
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 Qy 1411 CTTTAGAGGTGCTGTTCTTATTTCTGATTTTGAACAAACACACCTAGATCTTACAGCT 1470
 Db 383 uAlaSerAspCysCysSerLeuGlnLeuLysAsnLeuSerHisLeuGlnThrLeuAsnLe 403
 Qy 1471 CAGCTTCAATGATGATC--CTGATGAGTGGCAACCTTCAATGAGCTTGAAGAGCTGGA 1527
 Db 403 uSerHisAsnGluProLeuGlyLeuGlnSerGlnAlaPheLysGluCysProGlnLeuG 423

Qy 1528 ATACCTGGACTTTTCAGCACTCCATTTAAAAAAGTCAAGAAATTTCAAGTTCCTTATC 1587
 Db 423 uLeuLeuAspLeuAlaThrThrArgLeuHisIleAsnAlaLeuProGlnSerProPheGlnAs 443
 Qy 1588 TCTTGA AAAA CTCTTTCATCTTTCAGTTCATCTCTTACATTAATCAAAAATGACTTGAATG 1647
 Db 443 nLeuHisPheLeuGlnValIleuLeuLeuThrTyCysPheLeuAspThrSerAsnGlnHis 463
 Qy 1648 CATATTTCTTGGCTTGATTCAGTCTCAACACTTTAAATAGGCTGGCAATTTCTTCAAGA 1707
 Db 463 sLeuLeuAlaGlyLeuProValIleuArgHisLeuAsnLeuLysGlyAsnHisPheGlnAs 483
 Qy 1708 CAACAGCTT-----TCAATGCTTTTACAAAACAACAACAACTTCAATTCAGTGGATCT 1761
 Db 483 pGlyThrIleLeuThrArgSerThrAsnLeuLeuGlnThrValGlySerLeuGluValLeuIle 503
 Qy 1762 TTTTAAATGCCACTGGAACAGATATCTAGGGGGGTAATTTGACACACTTACAGACTCCA 1821
 Db 503 uSerSerCysGlyLeuLeuSerIleAspGlnGlnAlaPheHisSerLeuGlyLysMetSe 523
 Qy 1822 GTTATTTAAACATGATGACAAACAACTTACG-----TTTCTGATCA--TCCCAATA 1872
 Db 523 rHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSerLeuSerHisLe 543
 Qy 1873 TAAACAGCTGACTCCCTCAGAGACTCTTGAATGAGCTTTCATGAGCTTACAGACATCCAA 1932
 Db 543 uLysGlyIleTy-----LeuAsnLeuAlaAlaAsnSerIleAsnIleIleSe 559
 Qy 1933 AGGAATCTGCACATTTTCCAAAGAGCTTACCGCTTTCATGCTGATTAATTTCTGT 1992
 Db 559 rProArgLeuLeuProIleLeuSerGlnGlnInserThrIleAsnLeuSerHisAsnProLe 579
 Qy 1993 TGCTTGATATGTAATATGAAATTTCTTGTGACGTGGCTCAGAGCAAGAAATGTTCTT 2052
 Db 579 uAspCysThrCysSerAsnIleHisPheLeuThrTrpTyIleGlySerLeuAsnHisLysLe 599
 Qy 2053 GGTGAATGTTGAACAAATGAATGATGCATCACTATGAGACTTGAAGAGCTCCCTGAGTGT 2112
 Db 599 uGluGlySerGluGluThrThrCysAlaAsnProProSerLeuArgGlyValLysLeuSe 619
 Qy 2113 GGATTTTACGAATTC-----ACCTGTTATATATACAAACTATCATCAGTGT 2160
 Db 619 rAspValLysLeuSerCysGlyIleThrAlaIleGlyIlePhePheLeuIleValPheLe 639
 Qy 2161 ATCGGTGCTCAGTGTCTTGTGTGAGCCACTGTGACATTTGTGATATACCACTTCTATTT 2220
 Db 639 uLeuLeuLeuAlaIleLeuLeuPhePheAlaValLysTyIleuLeuArgTrpLysTyG 659
 Qy 2221 TCACCTG 2227
 Db 659 nHisIle 661

RESULT 4
 US-09-982-308B-23
 : Sequence 23. Application US/09982308B
 : Patent No. 6531290
 : GENERAL INFORMATION:
 : APPLICANT: Daille, Barbara
 : APPLICANT: Fan, Xuedong
 : APPLICANT: Lundell, Daniel
 : APPLICANT: Lunn, Charles A.
 : APPLICANT: Tan, Jimmy C.
 : APPLICANT: Zavodny, Paul J.
 : TITLE OR INVENTION: Mammalian TNF-alpha Convertases
 : FILE REFERENCE: J06010C
 : CURRENT APPLICATION NUMBER: US/09/982,308B
 : PRIORITY FILING DATE: 2001-10-17
 : PRIOR APPLICATION NUMBER: 09/156,163
 : PRIOR FILING DATE: 1998-09-17
 : PRIOR APPLICATION NUMBER: 08/889,909
 : PRIOR FILING DATE: 1997-07-10
 : PRIOR APPLICATION NUMBER: 60/021,710

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; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.:      1.72e-42      Length:      784
Score:          502.00        Matches:      210
Percent Similarity: 41.09%    Conservative: 136
Best Local Similarity: 24.94%  Mismatches:   324
Query Match:     8.45%       Indels:       172
DB:              4           Gaps:          32

US-09-396-985B-5 (1-3395) x US-09-982-308B-23 (1-784)

QY      386  AATCTGAGCAAAATCCCTCATGACATCCCTATTCAACAGAAAGCTAGATCTTGAGCTTC 445
Db      42   SerLeuAsnSerIleProSerGlyLeuThrGluValIlySerLeuAspLeuSerAsn 61
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Db      62   AsnArgIleThrTyrIleSerAsn-----Ser 70
QY      506  GATTATTCAGAGTGTGAATTAATGAGACATTGAAACAAGCATGGCTTAACACAG 565
Db      71   AspLeuGlnArgCysVal-----Asn 77
QY      566  CTCGCAACCTTGAGTACGACAGAAACCCATCAAGAGTTTTCGCCAGAAAGTTTCT 625
Db      78   LeuGlnAlaLeuValIleThrSerAsnGlyIleAsnThrIleGluGluAspSerPheSer 97
QY      626  GAGCTTAACAATTTAGAAATCTGTGGCTGTGAGACAAAAATGACCTCTTAGAGAGT 685
Db      98   SerLeuGlySerLeuGlnIleLeuAspLeuSerTyrAsnTyrIleuSerAsnLeuSerSer 117
QY      686  TTCATATTGACAGCCTTATATCTTAAAGAAACTAAATGTGCTCAATATCTTATACAT 745
Db      118  SerTyrPheIlyProLeuSerSerIleThrPheLeuAsnLeuGlyAsnProTyrIlys 137
QY      746  TCCTTTAAGTTGGCTGAATATTTCTTAATCTGAACAACCTAGAACATGTGATCTT--- 802
Db      138  ThrLeuGlyGlnThrSerLeuPheSerHisIleuThrIlySerGlnIleLeuArgValGly 157
QY      803  -----TCCTTAACCTATATTCAAACTATTTCTGTCAAAAGACTTACAGTTTCTACGT 853
Db      158  AsnMetAspThrPheThrIlyIleGlnArgIlyAspPheAlaGlyLeuThrPheLeuGln 177
QY      854  GAAATATCCCAAGTCAATCTCTTTAGACCTGTCTTAAACCAATGACTCCATTCAA 913
Db      178  Glu-----LeuGlnIleAspAlaSerAspLeuGlnSerTyrGln 190
QY      914  GCCCAAGCCTTTCAGGGAATTAG-----CTCCAT-----GAA 946
Db      191  ProIlySerSerLeuIlySerIleGlnAsnValSerHisIleuIleuHisMetIlyGlnHis 210
QY      947  TTGACTCTAAGAACTAATTTTAATAGCTCAAAATGTACTGAAATGTGCTTCA----- 1000
Db      211  IleLeuLeuLeuGlnIlePheValAspValThrSerSerValGlnCysLeuGlnLeuArg 230
QY      1001  -----AACATGACTGGTTTACATGTCATCGGTGATCTTGGAGAAATTTAAAT--- 1051
Db      231  AspThrAspLeuAspThrPheHisPheSerGlnLeuSerThrIlyGlnThrAsnSerLeu 250
QY      1052  -----GAAAGAACTGGAAGATTGACCGTCTGTGCATGAA----- 1090
Db      251  IleIlySerPheThrPheArgAsnValIlyIleThrAspGlnSerLeuPheGlnValMet 270
QY      1091  -----GACTATGCAATGTGAGCATTTGAGTTGAGTTTACA 1129
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Db      271  IlyLeuLeuAsnGlnIleSerGlyLeuLeuGlnPheAspAspCysThrLeuAsn 290
QY      1130  TATATAATCATTT---TCAGATGATATTTAATCTCAATGCTTGGCAAAATATTTCT 1186
Db      291  GlyValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIlyValGln 310
QY      1187  GCATGCTCTTTCACAGGTGACATATATAACATAGACAGATGTTCTTACGATTTCCAA 1246
Db      311  ThrLeuThrIleArgArgLeuHisIle-----ProArgPheTyrLeu 324
QY      1247  TGGCAATCTTATCATCATTTAGATGTCATCTTAAGCCTTTTCCAAAGCTGATCTACCT 1306
Db      325  PheTyrAspLeuSerThrLeuTyrSerLeuThrGluArgValIlyAsnArgIleThrValGln 344
QY      1307  -----TTCTTAAAGTTGACCTTTACTACCAACAGAGAGATACAGCTTT 1354
Db      345  AsnSerIlyValIleLeuValProCysLeuLeuSerGlnHis----- 358
QY      1355  GGTCAAGTGGCTCTGCCAAGTCTCAATATCTAGATCTTGAATGCAATGACGCTTT 1414
Db      359  -----LeuIlySerLeuGlnTyrLeuAspLeuSerGlnAsnMetVal--- 373
QY      1415  AGAGTTGCTGTTCTTATTCGATTTTGAACAAACCTGAAGTACCTTGAACCTCAGC 1474
Db      374  -----GlnGlnTyrIleuIlyAsnSer 380
QY      1475  TTCAATGTGTATCTCTGATGAGTGCACCTTCATGGGTGTAGAAAGCTGGAATACCTG 1534
Db      381  -----AlaCysGlnAspAlaTyrProSerLeuGlnThrLeuValIleuArg 395
QY      1535  GACTTTCAGACATCCACTTTTAAAAAGTCCACAGAAATCTCAGGTGTTCTTATCTTGA 1594
Db      396  GlnAsnHisIleuAsnIleSerLeuGlnIlyThrGlyGln-----ThrLeuLeuThrLeuIlys 413
QY      1595  AATCTTCTTACCTTGACATCTCTTACACTTAATACAAATTTGACTTGTGATGCAATATT 1654
Db      414  AsnLeuThrAsnIleAspIleSer----- 421
QY      1655  CTTGGCTTGATCAGTGTCAACACTTTAAAAATGGCTGGCAATCTTTCAAAAGCAACACC 1714
Db      422  -----LysAsnSerPhe-----HisSer 427
QY      1715  CTTTCAAAATGCTTTTCAAAACACAACAACTTAACATCTCTGATCTTTTAAATGCCAA 1774
Db      428  MetProGlnThrCysGlnTyrProGlnIlyMetIlyTyrLeuAsnLeuSerSerThrArg 447
QY      1775  CTGAAACAGATATCTAGGGGGGTATTGACACACTTCAAGACTCCAGTTATTAACATG 1834
Db      448  IleHisSerValThrGlyCysIleProIlyThr-----LeuGlnIleLeuAspVal 464
QY      1835  AGTCACACAACACCTA---CTGTTT---CTGGAATCCATCCCATTAATAACAGCTGTAC--- 1885
Db      465  SerAsnAsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIlySerGlnLeuTyrIle 484
QY      1886  -----TCCCTCAGGACTCTT 1900
Db      485  SerArgAsnIlyIleuMetThrLeuProAspAlaSerIleuLeuProMetLeuValLeu 504
QY      1901  GATTGCACTTCAATGCGATAGAGACA---TCCAAAGAAATACTGCAACATTTTCCAAAG 1957
Db      505  IlyIleSerArgAsnAlaIleThrThrPheSerIlySerGlnIleuAspSerPhe---His 523
QY      1958  AGTCTAGCCGCTTTCATCTGACATAATTTCTGTGCTTGTATGATGTAATATCAGAT 2017
Db      524  ThrLeuIlyThrLeuGlnAlaGlyGlyAsnAsnPheIleCysSerCysGlnPheLeuSer 543
QY      2018  TTCTTGACAGGGGTCAAGACACAGAAATGTTCTTGATGATGTGAA-----CAA 2068
Db      544  PheThrGln-----GlnGlnGlnAlaLeuAlaIlyValLeuIleAspTyrProAlaAsn 561
QY      2069  ATGAATGTGCATCACCATTATGACATGAAAGCCTCCTGCTGTGGAT-----TTTACG 2122
Db      562  TyrLeuCysAspSerProSerHisValArgGlyGlnGlnIlyValIleAspValArgLeuSer 581
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Oy	2123	AATTCACCTGTTATATATACAAAGACTATCATCAGTGATCGGTGCTGCTGCTTG	2182
Db	582	ValSerGluCysHisIerGllLeaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu	601
Oy	2183	GTAGCGACAGTGTGACATTTCTGATATACCACTTC-----TATTTCACCTGATA	2230
Db	602	IleLeuLeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpIlyrMetCysMetMet	621
Oy	2231	-----CTTATTGCTGGCTGTAAAAAGTACAGCAGAGAGAAAGC-----ATCTAT	2275
Db	622	TrpAlaTrpLeuGlnAlaLysArgLysProArgGlyAlaProSerItrArgenilleCysTyr	641
Oy	2276	GATGATTTTGATGATCTACTCGAGCCAGGATGAGGATGTGGTGTGAGAAACGAGCTGTAAAG	2335
Db	642	AspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGlnHisMetValGln	661
Oy	2336	AATTAGAGAAGAGAGTGGCCCGCTTCAGCTTTGACCTTCATTACAGAGGACTTAATTCCT	2395
Db	662	GluLeuGluHisPheAsnProProPheLysIleuCysLeuHisLysArgPheIlePro	681
Oy	2396	GGTGTAGCCATTGCTGCCAATCATTCACAGAAAGCTTCCACAGAGCCGAGAAATTATT	2455
Db	682	GlyIstIrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysTrpVal	700
Oy	2456	GTGGTGGGTCTAGACACTTTATTCAGAGCCGCTGTGTGTATCTTGAATATGAGATTGCT	2515
Db	701	PheValLeuSerGluHisPheValLysSerGluTrpCysLysTrpGluLeuAspPheSer	720
Oy	2516	CAGACATGGCAGTTTCTGATGATGAGCCGCTGTGCATCATCTTCATTGCTCTTGAGAAAGTG	2575
Db	721	HisPheArgLeuPheAspGluHisAsnAspAlaAlaIleLeuIleLeuLeuGlnProIle	740
Oy	2576	GAGAAAGTCTTCTCTGAGGAGCAGAG--GTCCGAATTGTATGCGCTTCTTACAGAAACACC	2632
Db	741	GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr	760
Oy	2633	TACCTCGAGTGGAGAGACATGCTGTGGGGAGGACATCTTCTTGAGAGAGACTCAAAA	2692
Db	761	TyrLeuGluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValLeuLeuArgAla	780
Oy	2693	GCCCTG 2698	
Db	781	AlaIle 782	

RESULT 5
US-09-949-016-8799 ; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores: 4,84e-36 Length: 775
Pred. No.: 439.50 Matches: 201
Score:

Percent Similarity:	39.68%	Conservative:	122
Best Local Similarity:	24.69%	Mismatch:	292
Query Match:	7.40%	Indels:	199
DB:	4	Gaps:	32

US-09-396-985B-5 (1-3395) x US-09-949-016-8799 (1-775)

QY	386	AATCTGACGAAATCCCTTCATGACATCCCTTATTCACCAAGAACTTGATCTGAGCTTC	445
		::: ::: ::: ::: :::	
DB	77	SeuLeuAenSerIleProSerGlyLeuThrGluIaValLysSerLeuAspLeuSerAsn	96
QY	446	AAACCCCTGGAAGATCTTAAAGAAAGCATAGCTTCACCAATTTCTCAAACTTCAGGCGTG	505
		::: ::: ::: ::: :::	
DB	97	AsnAlaGlyIleThrTyIleSerAsn-----Ser	105
QY	506	GATTTATCTCAGGTGCGAAATTGAGACAAATGAGCAAGCATGGATGGCTTAAACGAG	565
		::: ::: ::: ::: :::	
DB	106	AspLeuGlnAlaGlyCysVal-----Asn	112
QY	566	CTCTCAACCTTGATCTGACAGCAAAACCTTATCAAGAGTTTTTCCCGAGAGTTTTTCT	625
		::: ::: ::: ::: :::	
DB	113	LeuGlnAlaLeuValLeuThrSerAsnGlyLeuAsnThrIleGluGluAspSerPheSer	132
QY	626	GGACGCTAAAGAAATTTAGAGAACTGTGGTGGCTGTGAGCAAAAATATGACCTCTTAGAGGT	685
		::: ::: ::: ::: :::	
DB	133	SerLeuGlySerLeuGlnIleLeuAspLeuSerTyIleAsnTyIleSerAsnLeuSerSer	152
QY	686	TTCCATATTTGACAGACCTTATGCTTAAAGAAACCTTAATGTGGCTCATAACTTATACAT	745
		::: ::: ::: ::: :::	
DB	153	SerTrpPheLysProLeuSerSerLeuThrPheLeuAsnLeuLeuGlyAsnProTyIlys	172
QY	746	TCCCTTAAAGTGGCTGAATATTTTCTTAAATGTGACCAACCTAGAACATGTGAGATCTT	802
		::: ::: ::: ::: :::	
DB	173	ThrLeuGlyGluThrSerLeuPheSerHisLeuThrLysLeuGlnIleLeuArgAlaGly	192
QY	803	-----TCTTATTAATAATTCAAACTATTCTGTGCAAAAGCTTACATTTCTAGT	853
		::: ::: ::: ::: :::	
DB	193	AsnMetAspThrPheThrLysAlaGlnAlaGlyAspPheAlaGlyLeuThrPheLeuGlu	212
QY	854	GAATAATCCCGAAGTCATCTCTTTAGACCTGCTTTAAACCAATGATGATTCATTCACAA	913
		::: ::: ::: ::: :::	
DB	213	Glu-----LeuGluIleAspAlaSerAspLeuGlnSerTyIcIu	225
QY	914	GCCCAAGCTTTCAGGGAATTAG-----CTCCAT-----GAA	946
		::: ::: ::: ::: :::	
DB	226	ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHisMetLeuGlnHis	245
QY	947	TTGACTCTTAAGAAAGTATTTTAATAGCTCAAAATGACTGAAAATGTGGCTTCAA-----	1000
		::: ::: ::: ::: :::	
DB	246	IleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCysLeuGluIleuArg	265
QY	1001	-----AACATGACGCTGTTACATGCTGCATGCGGTGATCTTGGGAGAAATTAAAAAT--	1051
		::: ::: ::: ::: :::	
DB	266	AspThrAspLeuAspThrPheHisPheSerGlyLeuSerThrArgGlyIuThrAsnSerLeu	285
QY	1052	-----GAAGGAAATCTGAAAGTTTGTGACCTGTCTGTCATGAA-----	1090
		::: ::: ::: ::: :::	
DB	286	IleLysLysPheThrPheThrAsnValLysIleThrAspGlnSerLeuPheGlnValMet	305
QY	1091	-----GAGATGCAATGTGACATGATGACATGATGACATGATGACATGATGATGATGATGAT	1129
		::: ::: ::: ::: :::	
DB	306	LysLeuLeuAsnGlnIleSerGlyLeuLeuGluIleuGluPheAspAspCysThrLeuAsn	325
QY	1130	TATATTAATCAATTTT-----TCAGATGATTTTATATATCTCAATGTGCTTGGCAATATATTTCT	1186
		::: ::: ::: ::: :::	
DB	326	GlyValGlyAsnPheArgAlaSerSerAspAsnAspArgValIleAspProGlyLysValGlu	345
QY	1187	GCAATGTCTTCAAGAGGTACATATAAACACATAGACAGATGTCTTAGGCAATTTCCAA	1246
		::: ::: ::: ::: :::	
DB	346	ThrIleuThrIleAspArgLysHisIle-----ProArgPheTyIleu	359
QY	1247	TGGCAATCTTATCATCATTTAGATGATGTCATCTTAAAGCCTTTCCAAAGCTGATGCTTACT	1306
		::: ::: ::: ::: :::	

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Db      360 PheThraspleuSerThrLeuTySerLeuThrcGluValLysArgIleThrValGlu 379
QY      1307 -----TTTCTTAAAAAGTTGACCTTTAACTTCCAAAGAGATATCAGCTTT 1354
Db      380 AsnSerLysValPheLeuValProCysLeuLeuSerIleHis----- 393
QY      1355 GGTGAGTTGGTCTGCCAAGCTCAGATATCTAGATCTTGTAGTAAGTCATGAGCTTT 1414
Db      394 -----LeuLysSerLeuGluTyLeuAsnLeuSerGluAsnLeuVal--- 408
QY      1415 AGAGTTGCTGTTCTTATTTGATTTTGAACAAACCACTGGAAGTCTTGAAGCTCAGC 1474
Db      409 -----GluLysTyLeuLysAsnSer 415
QY      1475 TTCAATGCTGTCATCTGATGAGTCCAACTTCAATGGGTCTGAAGAGCTGGAATACCTG 1534
Db      416 -----AlaCysGluAspAlaTrpProSerLeuGlnThrLeuIleLeuArg 430
QY      1535 GACTTTCAGACCTCCTTTAAAAAGGTGCAGAAATTTCTGAGTTCCTTATCTTGAA 1594
Db      431 GlnAsnHisLysLeuLysSerLeuGluTyThrGlyLys-----ThrLeuLeuThrLys 448
QY      1595 AAACCTCTTAACTTGAATCTTCACTTCACTAATACCAAAATGACTTGAATGCAATATT 1654
Db      449 AsnLeuThrAsnIleAspIleSer----- 456
QY      1655 CTTCGGCTTGATCACTTCACACACTTTAAAAATGGCTGGCACTTCTTCAAAAGACACACC 1714
Db      457 -----LysAsnSerPhe-----HisSer 462
QY      1715 CTTCCTCAATGCTTTTACAAACACAAACAACTTAACTCCGATCTTCTTAAATGCCAA 1774
Db      463 MetProGluThrCysGlnTrpProGluLysMetLysTyLeuAsnLeuSerThrArg 482
QY      1775 CTGGAACAGATATCTAAGGGGATTTGACACACTCTACAGACTCCAGTATTAACATG 1834
Db      483 IleHisSerValThrGlyCysIleProLysThr-----LeuGlnIleLeuAspVal 499
QY      1835 AGTCACACAAACCTTA---CTGTTT---CTGATTCATCCCTTATTAACAGCTGTAC--- 1885
Db      500 SerAsnAsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyIle 519
QY      1886 -----TCCCTCAGAGACTCTT 1900
Db      520 SerArgAsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeu 539
QY      1901 GATTGCACTTCAATCGCATAGAGACA---TCCAAAGGAATAGTGCACATTTTCCAAAG 1957
Db      540 LysIleSerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---His 558
QY      1958 AGTCTAGCCGCTTCAATCTGACCTAATTAATCTGTGCTTGTATGATGAAATACAGAAAT 2017
Db      559 ThrLeuLysThrLeuGluAlaGlyLysAsnAsnPheIleCysSerCysGluPheLeuSer 578
QY      2018 TTCTTGACGTGGGTCAAGACACAGAAATGTTCTTGAGATGTTGAA-----CAA 2068
Db      579 PheThrGln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn 596
QY      2069 ATGAAATGTCATCCTAATAGACATGAGAGCCCTCCGTGTGGATTTTACAAATTC 2128
Db      597 TyLeuCysAspSerProSerHisValArgLysGlnGlnValGlnAspValArgLeuSer 616
QY      2129 ACCTGTTATATATACAAACATATATCATAGTGTATGGGTGTCAGTGTCTGTGTAGACC 2188
Db      617 ValSerGluCysHisArgThr-----AlaLeuValSerGlyMetCysCysAla 632
QY      2189 ACTGAGCATTTTGTGATATACCACTTTATTTTCACTGATATGATGATGATGATGATGATG 2242
Db      633 -----LeuPheLeuLeuIleLeuLeuThrGlyValLeu 643
QY      2243 TGTAAAAAGTAC----- 2254
Db      644 CysHisArgPheHisGlyLeuThrTrpMetLysMetMetTrpAlaTrpLeuGlnAlaLys 663

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QY      2255 -----AGCAGAGAGAAAGCATCTAATGATGATCTTGTGATCTAC 2293
Db      664 ArgLysProArgLysAlaProSerArg---AsnIleCysTyThrAspAlaPheValSerTy 682
QY      2294 TCGAGCCAGAAATGAGACTGGGTGAGAAAAGACTGGTAAAGATTTAGAAAGAGAGTG 2353
Db      683 SerGlnArgAspAlaTrpTrpValGlnAsnLeuMetValGlnIleLeuGlnAsnPheAsn 702
QY      2354 CCCCCTTTGACGCTTTCCTTCTTCAATTCACAGGACTTATTCCTGTGTAGCCATTGCTGCC 2413
Db      703 ProProPheLysLeuCysLeuHisLysArgAspPheIleProIleTySerTrpIleLeuAsp 722
QY      2414 AACATCATCAGAGAGCTTCCACAGAGCCGGAAGTATTGTGTGTGTGTGTAGACAC 2473
Db      723 AsnIleIle---AspSerIleGluLysSerHisLysThrValPheValLeuSerGluAsn 741
QY      2474 TTATTCAGAGCCGTTGTGTATCTTGAATATGATGATGCTCAGACATGGCAGTTCTTG 2533
Db      742 PheValLysSerGluTrpCysLysTyArgLysLeuAspPheSerHisPheArgLeuPheAsp 761
QY      2534 AGTACCGCTCTGGCATCATCTTCAATTCATGTCCTTGAAGAAAGTG 2575
Db      762 GluAsnAsnAspAlaAlaIleLeuIleLeuGluProIle 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Alignment Scores:
Pred. No.: 8,41e-22 Length: 605
Score: 301.00 Matches: 171
Percent Similarity: 34.99% Conservative: 90
Best Local Similarity: 22.92% Mismatches: 268
Query Match: 5.06% Indels: 217
DB: 3 Gaps: 23

US-09-396-985b-5 (1-3395) x US-09-063-950-5 (1-605)
QY      85 AAGGTTGACCTGCTCACTTCTCTGCTCTGACAGTAACTTGAATTAATATT 144
Db      5 LysGlyGlyLeuAlaLeuAlaLeuLeuLeuLeuSerTrpAlaAlaLeuGlyProArgSer 24
QY      145 ACAAGGGGCAACCGCTGGAGAGAAAGGGCAGAGGCCCAAGGACTCTGCTGCCAC 204
Db      25 LeuGlnGlyLysAlaGluProGlyThrProGlyGluAlaGluLysProAlaCysProAlaThr 44
QY      205 ATTTAACGTTGTCATGCTTTTTCAGAGGCTCCGCTGTGTGCAAGAAATCCAGGAATGAT 264
Db      45 -----CysAlaCysSerTyArgAsp 51
QY      265 GCTCTCTGCAATCTGGCTGGAGACTCTGATCATGCAATGCTTCTTCTCTGCTGAGACC 324
Db      52 GluVal-----AsnGlu-LeuSerValPhe----- 59
QY      325 AGGAAGCTTAATCCCTGCATTAAGAGTACTTCTTAATATTAACCTTACCAATGATGATCA 384
Db      60 -----CysSerSerArg 63

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QY 385 GAATCTCAGAAATCCCTCAGACATCCCTTATTCACCAAGAACTAGATCTGAGCT 444
Db 63 gashleuthrargleuproabpelyleprogllythrinalaleutrpheuaspe 83
QY 445 CAACCCCTGAGATCTTAAAGCTATAGCTTCCACCAATTTCTCAACTTCAGTGGCT 504
Db 83 rshshnleuserSerlIeProProalalapherghshnleuserSerlIeAlaPhele 103
QY 505 GGATTTATCCAGCTGTGAAATTTGAGACAAATGAGACAGGATGCGCTTAAACA 564
Db 103 uashnleuIngllyglInleuInglSerleuInglProglInalaleuIngllyleuIngluas 123
QY 565 GCTCTCAACCTTTGGTACGAGAGAAACCTTACAGATTTTTCACGAGAAAGTTTTC 624
Db 123 nleuCyehlsleuhsleuIngluargshnleuInglserleuInglalavalgllythrPheal 143
QY 625 TGACACTAACAAATTTAGAAATCTGGTGGCTGTGAGACAAAAATGACCTCTTAAAGGG 684
Db 143 atythrProalaleuInglaleuIngllyleuSerashshnleuserSerlIeArgleuIngluas 163
QY 685 TTTCATATTTGAGACGCTTATATCTTAAAGAACTAATGTGGCTCATATCTTATACA 744
Db 163 pgllyleuphegluglyleuInglYashnleuIngltraspheushnleuInglYtrPashnSerleu-- 182
QY 745 TTCCCTTAAGTTGGCTGAA---TATTTTCTAATCTGCAAAACCTAGAAACATGTGGATCT 801
Db 183 ----AlavalaleuProabpalaalapherghlyleuInglYglYleuInglYglYleuValle 201
QY 802 TTCTTATTAAC-----TATATTCAAACTATTTCTGTCAAAGACTTACAGTTTCTACG 852
Db 201 ualaglYashnleuInglYleuInglInProalaleuPheSerghlyleuInglalaglYleuIngl 221
QY 853 TGAATAATCCCAAGTCAATCTCTCTTTGACCTGTCTTAAACCAATGATGCTCATTC 912
Db 221 gglu-----LeuashpLeuserInglYashnleuInglalaleuInglalaleu 234
QY 913 AGCCCAAGCTTTGAGGGAAT---AGGCTCATGATGATGCTGCTGCAAGATTTTAA 969
Db 234 salashnValPhealaglInleuProargleuInglYashnleuInglYleu----- 249
QY 970 TAGCTCAATGTAAGTGAATAATGTGCTTCAAAACATGACTGTTTACATGTCATCGGTT 1029
Db 249 ----- 249
QY 1030 GATCTTGGAGAAATTTAAATAATGAAAGAAATCTGAAAAGTTTACCGTCTGTCATGGA 1089
Db 250 -----Asparghashnleu----- 253
QY 1090 AGGACTATGCAATGTGAGCATTTGATGACTTACGTTAACATATATCAATTTTTCAGA 1149
Db 253 ----- 253
QY 1150 TGATATTTATATCTCAATGCTTGGCAAAATTTCTGCAATGCTTTCACAGGTGTACA 1209
Db 254 -----lealalavalalaleuProglYalaphleuInglYleu-- 265
QY 1210 TATATAACACATGACAGATGTTCTTAGGCAATTTCAATGCAATCTTATCAATCATTTAG 1269
Db 266 -----LysalaleuInglYtrPheushpLeuser----- 274
QY 1270 ATGTCATCTTAAGCTTTTCCAAAGCTGATCTACCTTTTCTTAAAGTTGACCTTTAAC 1329
Db 274 ----- 274
QY 1330 TACCAACAGA-----GAGATATGACGTTTGTGATGCTGCTGCGCAAG 1374
Db 275 -HisashnleuInglYalaglYleuIngluargshnleuInglYleu-----Gl 291
QY 1375 TCTCATATCTTATGATCTTATGAGAAATGCCATGAGCTTTTAAAGGTTGCTGTTTATTC 1434
Db 291 YleuInglYalaleuInglYleuSerInglashnleuInglalaleuInglYleuInglYtrPhegl 311

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QY 1435 TGATTTTGGAAACAACAACCTGAAGTACTTAGACCTGACCTTCAAGTGTGCT---ATCCT 1491
Db 311 uashpLeu-----HisPheleuInglInglInleuInglYhlsashnleuInglleuIngl 329
QY 1492 GATAGTGCACACTTTCATGGCTTTAGAAAGCTGGAATATCTGACCTTACAGACTCCAC 1551
Db 329 ualaglYashnleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 349
QY 1552 TTTAAAGGCTCAGAAATTTCTGAGTGTCTTATCTTCTGAAAACCTTTTACCTTGA 1611
Db 349 nleuInglInglVal--LysValalglYalaphleuInglYleuInglYleuInglYleuInglYleuIngl 368
QY 1612 CATCTCTTACACTAATACCAAAATTTGACTTGTGATGAGCAATATTTCTTGGCTTGAATGCTCT 1671
Db 368 nleuSerghlyashnleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 388
QY 1672 CAACACTTTAAATAATGCTGGCAATCTT----- 1699
Db 388 uHisSerleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 408
QY 1700 -----TTCAAGACACACCTTCAATGTC----- 1726
Db 408 YleuSerghlyleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 428
QY 1727 -----TTTAAACAACAACAACCTTAACTTCTGATCTTCTTAAATGCAACTGGAACA 1782
Db 428 nSerleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 448
QY 1783 GATATCTAAGGGGGTATTTTGCACACTCTTACAGACTGCACTGATTTTAAACAGTACACAA 1842
Db 448 sLeuProhlsleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 468
QY 1843 CAACCTACTGTTTGTGATGATCCATTCATATTAACAGCTGACTCCCTCAGAGACTTTGA 1902
Db 468 nArgleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 488
QY 1903 TTGCAGTTTCAATGCAATGAGACATCCCAAGAAATCTGCAACATTTTCCAAAGAGTCT 1962
Db 488 pValSerHisashnleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 508
QY 1963 AGCCGCTTCAATCTGACTAATAATCTGTGCTTGTATATGTAATATCAGAAATTTCTT 2022
Db 508 uArgYtrleuashnleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 528
QY 2023 GCAG-----TGCGTCAAGACCAAGAAATGTTCTTGTGATGTGAACAAATGAATG 2076
Db 528 ugluInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 540
QY 2077 TGACATCACTTATGAC-----ATGAAGGCTTCCCTGAGTGTGGA 2115
Db 540 sSerCyashnleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 560
QY 2116 TTTTACGAATTCACCTGT-----TATATATACAGAGC 2148
Db 560 gPheValalaglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 580
QY 2149 TATCATCAAGTGTATCG 2164
Db 580 nleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuInglYleuIngl 585

```

RESULT 7
 US-09-353-585-2
 Sequence 2, Application US/09353585
 Patent No. 6287865
 GENERAL INFORMATION:
 APPLICANT: Dixon, Mark S
 Jones, David A
 Jones, Jonathan DG
 TITLE OF INVENTION: Plant pathogen resistance genes and uses
 thereof
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC


```

STREET: 8th Floor, 1100 No. 6287865th Giebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2
Alignment Scores:
Pred. No.: 4,91e-21 Length: 1112
Score: 295.00 Matches: 185
Percent Similarity: 35.43% Conservative: 108
Best Local Similarity: 22.37% Mismatches: 270
Query Match: 4.96% Indels: 264
DB: 3 Gaps: 32
US-09-396-985B-5 (1-3395) x US-09-353-585-2 (1-1112)
QY 326 GGAAGCTTGAATCCCTGATAGAGTACTTCTATATTATACC-----TACCAATGCATG 379
D 397 GlycerileProalaserleuglyAsnleuAsnleuSerAglleuTyrlleuTyAsn 416
QY 380 GATCAAGTCTCAGCAAAATCCCTCATGACATCCCTTAT-----TCACCAAGAACCTTA 433
D 417 AsnGlnleuSerGlySerleleProGlnGlnleuglyTyrlleuSerSerleuThyrlleu 436
QY 434 GATCGAGCTTCAACCCCTGAAGATCTTAGAAGCTATAGCTTCACCAATTTCTCAAA 493
D 437 AspIeuSerAsnAsnSerleleAsnGlyPheleleProalaserPheGlyAsnMetSerAsn 456
QY 494 CTTAGTGGCTGATTATTCAGAGTGTGAAATTGAGACATTTGAAGACAGCATGGCAT 553
D 457 LeuAlaPheleuPheleuTyrlGlnAsnGlnleuAlaserleValProGlnGlnleugly 476
QY 554 GGCCTTAAACGAGCTCTCAACCTTGCTGACTGACAGGAAACCTTATCAGAGATTTTCCCA 613
D 477 TyrlleuArgSerleuAsnValleuAsnleuSerGlnleuAlaIeuAsnGlySerlelePro 496

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QY 614 GGAAGTTTTCTGAGTAAACAATTTAGAGATCTGGTGGCTGGAGCAAAAATGACC 673
D 497 AlaSerPheGlyAsnleuAsnleuSerArgleuAsnleuValAsnAsnGlnleuSer 516
QY 674 TCTCTAGAGGGTTTCCATATTTGACAGCTTATATCTTAAAGAACTTAATGGCTCAT 733
D 517 GlySerleleProGlnGlnleuglyTyrlleuArgSerleuAsnValleuAsnleuSerGln 536
QY 734 AATCTTATACATTCCTTTAAGTGGCTGAATATTTTCTTAATCTGACAAACCTAGAACAT 793
D 537 AsnAlaIeuAsnGly---SerleleProalaserPheGlyAsnleuAsnleuSerArg 555
QY 794 GTGATCTTCTTATATACATATTTCAAACTATTTCTGTCAAGACTTACAGTTTCAAGT 853
D 556 LeuAsnleuValAsnAsnGlnleuSerGlySerleleProGlnGlnleuglyTyrlleuArg 575
QY 854 GAAATCCCAAGTCAATCTCT----- 877
D 576 SerleuAsnAsnleuGlyleuSerGlnleuAsnAlaIeuAsnGlySerleleProAlaserleu 595
QY 877 ----- 877
D 596 GlyAsnleuAsnAsnleuSerMetleuTyrlleuTyrlAsnAsnGlnleuSerGlySerlele 615
QY 878 -----TGAACCTGTCTTTAAACCAATT 901
D 616 ProGlnGlnleuglyTyrlleuSerSerleuThyrlleuSerleuGlyAsnAsnSerleu 635
QY 902 GACTCATTCAGACCCCAAGCTTTGAGGGAATTAG---CTCAGTAATTTGACTTTAAGA 958
D 636 AsnGlyTyrlleuProalaserPheAlaAsnMetArgAsnleuGlnAlaIeuAlaIeuAsn 655
QY 959 AGT-----AATTTTATAGCTCAAAATGTA 982
D 656 AspAsnAsnleuIleuglyGlnleuProSerSerValCysAsnleuThrsSerleuGlnVal 675
QY 983 CTGAAAATG-----TGCTTCAAAACATGACT 1009
D 676 LeuTyrlMetProArgAsnAsnleuGlyGlyValProGlnGlySerleuGlyAsnleuSer 695
QY 1010 GGTTCATGTCATCGGTGATCTTGAGAAATTTAAAAATGAA----- 1054
D 696 AsnleuGlnValleuSerMetSerSerAsnSerPheSerGlyGlnleuProSerSerlele 715
QY 1055 AGGAATCTGGAAGT-----TTTGACCGTCTGTCATGAGAGACTA--- 1096
D 716 SerAsnleuThrsleuGlnleuAsnAsnleuGlyValArgAsnAsnleuGlnGlyAlaIle 735
QY 1097 -----TGC-----AATGAGCAATTTGATGAGTTTAACATATATATCATTTT 1144
D 736 ProGlnCysPheGlyAsnleuSerSerleuGlnValPheAsnMetGlnAsnAsnleuGlyleu 755
QY 1145 TCAGATGATAT-----TATATCTCAATGCTTGCAAAATTTTGTGCAATGCT 1195
D 756 SerGlyThrsleuProThrsAsnPheSerleleGlyCys-----SerleuIleSerleuAsn 773
QY 1196 TTCAAGGTGTACATATATAAACACATAGCAGATGTTCTTAGGCATTTT----- 1243
D 774 LeuHleGlyAsnGlnleuGlnleuAsp-----GlnleleProArgSerleuAsnAsnCysGlyAs 791
QY 1244 AATAGCAATCTTATCATCATTTAGATGTCATCTTAAG---CCTTTCCAAAGCTG--- 1297
D 792 LysleuGlnValleuAsnleuGlyAspAsnGlnleuAsnAsnAsnAsnAsnAsnAsnAsn 811
QY 1298 ---AGTCTACCTTTCTTAAAGTTGACTTTAATCAACCAAGAGAGAT----- 1345
D 812 GlyThrsleuProGlnleuArgValleuArgleuThrsSerAsnGlyAsnGlyProIle 831
QY 1346 ---ATCAGCTTTGGTCAAGTGGCTGCGCAAGCTCAGATATCTAGATCTTAAAGAAAT 1402
D 832 ArgSerSerArgAlaGlnleuIleMetPheProAsnleuArgleleleAsnleuSerArgAsn 851
QY 1403 GCCATGAGCTTTAGAGGTGCTGTTCTTATTCGATTTTGAACAACAACCTGAAGTAC 1462

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[illegible]

```

DB      1104 entYrArgARgArghen 1109

RESULT 8
US-09-353-585-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
            Jones, David A
            Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
                    thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EBO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
                  1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/CB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

Alignment Scores:
Pred. No.:          6,22e-21          Length:    1112
Score:              294.00             Matches:   185
Percent Similarity: 35.43%             Conservative: 108
Best Local Similarity: 22.37%           Mismatches: 270
Query Match:        4.95%               Indels:   264
DB:                  3                 Gaps:     32

US-09-396-985B-5 (1-3395) x US-09-353-585-3 (1-1112)
Oy      326 GGAAGCTTGAATCCCTGATAGAGGTACTTCTTAATATTACC-----TACCAATGCATG 379
Db       ||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
         GlySerIleProAlaSerLeucIysAsnIeuAanIeuSerArgIeuTyrlIeuTyrlAsn 416
Oy      380 GATCGAAATTCGACAAAATCCCTCATGATGACATCCCTTAT-----TCAAACAAGAACCTA 433

```


Oy 2183 GTAGCACTGAGATTCTGATATACACTTCTATTTCACCTGATCTATTGCTGGC 2242
 Db 1065 -----IleSerIleIleTyriIleuIleSerThGlyAsnLeuArgTrpL 1080
 Oy 2243 TGTAAAA-----GTACAGCAGAGAGAAAGCATCTAT 2275
 Db 1080 euAlaArgIleIleGluGluLeuGluHisIleIleMetGlnArgTrpLys----- 1097
 Oy 2276 GATGATTTTGATGATCTACTGAGCCAGATGAGACTGGTGAGAAAGAGCTGGTAAG 2335
 Db 1098 -----LysGlnArgIleGlnArgA 1104
 Oy 2336 AATTGAGAGAGAGAGT 2352
 Db 1104 snTyArgArgArgAsn 1109
 RESULT 9
 US-08-190-802A-50
 ; Sequence 50, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; NUMBER OF INVENTIONS: Thereof
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190, 802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R. 875
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 603 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 ; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 ; US-08-190-802A-50
 Alignment Scores:
 Pred. No.: 1.02e-20 Length: 603
 Score: 290.50 Matches: 156
 Percent Similarity: 37.85% Conservative: 87
 Best Local Similarity: 24.30% Mismatches: 244
 Query Match: 4.89% Indels: 155
 DB: 1 Gaps: 24
 US-09-396-985B-5 (1-3395) x US-08-190-802A-50 (1-603)

Oy 374 TGCATGATCAGATCTCAGCAAAATCCCTGATGACATCCCTTATTTCAACCAAGACCTTA 433
 Db 60 CysSerSerIysAsnLeuThrHisIleuProAspAspIleProValSerThrArgAlaLeu 79
 Oy 434 GATTCGAGCTCAACCCCTGAGATCTTAAGAGCTTAAGCTTACCAATTTCTACAA 493
 Db 80 TrpLeuAspGlyAsnAsnLeuSerSerIleProSerAlaIlePheGlnAsnLeuSerSer 99
 Oy 494 CTTGAGGCTGCGATTTATTCAGGTGGAATTTAGACAAATTTGAGCAATTTGAGCAATGGCAT 553
 Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeu 119
 Oy 554 GAGCTTAACCAAGCTCTGACCTTGTGCTGACAGAAACCTTACAGAGTTTCCCA 613
 Db 120 GlyLeuGlnAsnLeuTyTrpLeuHisIleuGlnArgAsnArgLeuAlaVal 139
 Oy 614 GGAAGTTTCTGAGACTACAAATTTAAGAAATTTGCTGGCTGGAGACAAATGACC 673
 Db 140 GlyLeuPheThrHisThrProSerLeuAlaSerLeuSerLeuSerAsnLeuGly 159
 Oy 674 TCTTGAAGGTTTCCATTTGACAGCTTATATCTTAAGAAACCTTAAGTGGCTCAT 733
 Db 160 ArgLeuGlnGluGlyLeuPheGlnGlyLeuSerHisIleuTrpAspLeuAsnLeuGlyTrp 179
 Oy 734 AATCTATACACTCTTAAAGTTCCTGAA-----TATTTTCTAATCTGACAAACCTGAA 790
 Db 180 AsnSerLeu-----ValValLeuProAspPheValPheGlnGlyLeuGlyAsnLeuHis 197
 Oy 791 CATGTGATCTTCTTAAAC-----TATATTCAACTAATTTCTGCAAGACTTA 841
 Db 198 GluLeuValLeuAlaGlyAsnLeuTyLeuThrTyLeuGlnProAlaLeuPheGlyGlyLeu 217
 Oy 842 CAGTTTCTAGCTGAAATCCCAAGTCAATCTCTTAAACCTCTTAAACCAAT 901
 Db 218 GlyLeuLeuArgGlu-----LeuAspLeuSerArgAsnAlaLeu 230
 Oy 902 GATCCATTCAGGCCCAAGCCTTTCAGGAAT---AGCTCCATGATGACTTAAGA 958
 Db 231 ArgSerValIysAlaAsnValPheValHisIleuProArgLeuGlnIlyLeuAsp 250
 Oy 959 AGTAATTTTAATAGCTCAAAATGTAAGTCAAAATGTCCTTCAAAACATGATGTTTACAT 1018
 Db 251 ArgAsnLeu----- 253
 Oy 1019 GTCCATGCGTTGATCTTGGAGAAATTTAAAGAAATCTGAAAGTTTGACCGT 1078
 Db 254 IleThrAlaValAlaProGlyAlaPheLeuGlyMetIysAlaLeuArgTrpLeuAsp--- 272
 Oy 1079 TCTGTCAVGAAGGACTATGCAATGTGAGCTGATGATGAGTTCAAGTTAAACATATATAAT 1138
 Db 273 -----LeuSer 274
 Oy 1139 CATTTTCAAGATGATTTAATCTCAATTCCTTGGCAATATTTCTGCAATGCTTTTC 1198
 Db 275 His-----AsnArgAlaIleGlyLeuMetGluAspThrPhe 286
 Oy 1199 -----ACAGGTGACATATAAACAATAGCAAT-----GTT 1231
 Db 287 ProGlyLeuLeuGlnHisIleValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArg 306
 Oy 1232 CCTGAGCATTTCAATGAGCAATCTTATCATATTTAGATGATCTTAAGCTTTTCCA 1291
 Db 307 ProArgThrPheLys----- 311
 Oy 1292 AAGCTGAGTCACTTTCTTAAAGTTGAGCTTAACTCAACAGAGAGATATGAGC 1351
 Db 312 -----AspLeuHisPheLeuGlnGluLeuGlnLeuGlyHisAsnArg----- 325
 Oy 1352 TTGGGTGAGTTG-----GCTTGCACAGTCTCAAGATATCTGATCTT 1393
 Db 326 IleArgGlnLeuGlnGlyArgTrpPheGlnGlyLeuGlnIleGlnValLeuThrLeu 345
 Oy 1394 AGTAGAATGCAATGAGCTTATAGAGTTGCTGTTCTTATCTGATTTTGGAAACAACAC 1453

QY	791	CATGGAGATCTTCTTTTAAC-----TATATCAACATATTCTGTCAAGACCTTA	841
Db	198	GlutValLeuAlaGlyAsnIlySerThrTyrLeuGlnProAlaLeuPheCysGlyLeu	217
QY	842	CAGTTTCTACGTGAATAATCCCAAGTCATCTCTTTAGACCTGTCTTAAACCAATT	901
Db	218	GlyIleuLeuArgIle-----LeuAspLeuSerArgAsnAlaLeu	230
QY	902	GACTCCATTCGAAGCCCAAGCCTTTCAGGAATT---AGGCTTCATGAATTGACTTAAGA	958
Db	231	ArgSerValIyValAsnValPheValIhIleuProArgLeuGlnIlyLeuTyrLeuAsp	250
QY	959	AGTATATTTAATAGCTCAATAGTACTGAATAATGTCCCTTCAAAAACATACGTGTTAAT	1018
Db	251	ArgAsnLeu-----	253
QY	1019	GTCCATCCGGTGTGATCTTGAGAAATTTAAAAATGAAGAATCTGGAAGTTTTCACCGT	1078
Db	254	IleThrAlaValAlaProGlyAlaPheLeuGlyMetIyValAlaLeuArgTyrLeuAsp---	272
QY	1079	TCTGTTCATGGAAGACTATGCATGTGACATTTGATGATTCAGTTCAAGTTATATTAAT	1138
Db	273	-----LeuSer	274
QY	1139	CATTTTCAATGATATTTATTAATCTCATATGCTTGGCAAAATTTCTGCATAGCTTTC	1198
Db	275	His-----AsnArgValAlaGlyLeuMetGluAspThrPhe	286
QY	1199	-----ACAGGTGTCATATTAAMAACATACGACAGAT-----GTT	1231
Db	287	ProGlyLeuLeuGlyLeuIhIValLeuArgLeuAlaIhAsnAlaIleAlaSerLeuArg	306
QY	1232	CTTAGGCATTTCAATGGCAATCTTATCAATCATTAAGATGTCAATTTAGCCTTTTCCA	1291
Db	307	ProArgThrPheIys-----	311
QY	1292	AAGGTAGCTTACCTTTCTTAAAGTGGACCTTTAACTTACCAACAGAGAGATATACG	1351
Db	312	-----AspLeuIhIAspPheLeuGlnIleuGlnIlyhIAsnAlaIy-----	325
QY	1352	TTTGGTCAAGTG-----GCTGCGCAAGTCTCAGATCTAGATCTT	1393
Db	326	IleArgGlnLeuGlyGluArgThrPheGlnIleuGlyGlnIleuGlnValLeuThrIleu	345
QY	1394	AGTAGAATGCCATGAGCTTTAGAGGTTGCTGTTTATCTGATTTTGAACAAACAC	1453
Db	346	AsnAspAsnGlnIleThrGlnValAlaArgValGlyAlaPheSer-----GlyLeuPheAsn	363
QY	1454	CTGAAGTACTTAGACCTCAGCTTCAATGTC--ATCTGATGAGTGGCCAACTTCATG	1510
Db	364	ValAlaValMetAsnLeuSerGlyAsnCybLeuArgSerLeuProGluArgValPheGln	383
QY	1511	GATCTAGAAGAGCTGGAAATACCTGGAACCTTGCAGCCTTAAATAAAGTACAGAA	1570
Db	384	GlyLeuSerIyLeuIhIAsnSerLeuIhIleuGlnIhIAsnSerCybLeuGlyhIValAlaArgLeu	403
QY	1571	TTTCAAGTGTCTTATCTCTGAAAAAATCTTTTACCTTGACATCTTCACTAATATAC	1630
Db	404	HisThr-----	405
QY	1631	AAAAATTGACTTGTAGTGCATATTTCTTGCTTGATCAGTCTGCACATTTAAAAATGCT	1690
Db	406	-----PheAlaGlyLeuSerGlyLeuArgArgLeuPheLeu---	417
QY	1691	GGCAATCTTCAAAAGACAAACCTTCAATGTC-----TTTAACAAACCA	1758
Db	418	-----ArgAspAsnSerIleSerSerIleGlyGlnIleuArgLeuAlaGlyLeu	433
QY	1739	ACAAATTAACATTTCTTGATCTTTTAAATGCAACCTGGAACAGATCTTACGGGGGCTA	1798
Db	434	SerGlyLeuLeuGlnIleuAspLeuThrThrAsnArgLeuThrIhIleuProArgGlnIleu	453
QY	1799	TTTGACACACTCTACAGCTCAGTTATTAACATGAGTACAAACAACTTACTGTTTCTG	1858

Db 454 PheGlnGlyLeuGlnGlyHisLeuGlnGlyTyrLeuLeuLeuSerTyrAsnGlnLeuThrThrLeu 473

QY 1859 GATCCATGCCATTTATTAACAAGCTGTACTCCCTCAGACCTTTGATTGCAGTTTCAATGCG 1918

Db 474 SerAlaGlyValLeuGlnGlyProLeuGlnAlaGlyAlaPheThrLeuAspIleSerHisAsnHis 493

QY 1919 ATAAAGACA---TCCAAAGGAATATCGCAACATTTTCCAAAGAGCTTAAGCCGTCTTCAT 1975

Db 494 LeuGlnThrLeuAlaGlnGlyLeuPheSerSerLeuGlnGlyTyr---ValArgTyrLeuSer 512

QY 1976 CTGACTATATATCTGTGTTGCTTGTATATGTGAATATGCAGATTTCTTGACATGGGGTCAAG 2035

Db 513 LeuArgAsnHisSerLeu-----GlnThrPheSerProGlnProGly 526

QY 2036 GACCACGAAGAATGTCTTCTTGCAATATGTTGAACAATATGCAATATGCACTATAGACATG 2095

Db 527 LeuGlnArgLeuThrPleu---AspAlaAsnProThrAspCysSerCysProLeuIlyAla 545

QY 2096 AAGGCTCTCCCTGGTGTGGAT-----TTTACGAATTCACCTGT 2134

Db 546 LeuArgAspPheAlaLeuGlnAsnProGlyValValProArgPheValGlnThrValCys 565

QY 2135 -----TATATATACAGACTATCACAAGTGTATCGGTGTC 2170

Db 566 GlnGlyAspAspCysGlnProValTyrThrTyrAsnAsnIleThrCysAlaGlyProAla 585

QY 2171 AGTGTG 2176

Db 586 AsnVal 587

RESULT 11

US-08-473-089-50
; Sequence 50, Application US/08473089

; patent No. 6342368
; GENERAL INFORMATION:
;

```

; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
;

```

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; thereof
: TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:

CONFERENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
ADDRESS: 3000 Broadway
CITY: New York
STATE: New York
COUNTRY: U.S.A.

STREET: 2000 Pen
CITY: Washington

```

; STATE: DC
; COUNTRY: USA

```

ZIP: 20006-1812
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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CONTROLLER:      IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMMANDS:         DataPath Polaris #10 Version #1.0E

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; SOFTWARE:  palencan release #1.0,
; CURRENT APPLICATION DATA:
;

```

APPLICATION NUMBER: US/08/473, 089
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29.959

REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION.

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

TELEFAX: (202) 887-0765
; INFORMATION FOR SEQ ID NO: 50:
SEQUENCE: 393-393

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids

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TYPE: amino acid
TOPOLOGY: unknown
;

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; MOLECULE TYPE: protein
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; HYPOTHETICAL: NO

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ANTI-SENSE: NO
ORIGINAL SOURCE:

1


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RESULT 12
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theeot
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-487-072A-50
;
Alignment Scores:
Pred. No.: 1,02e-20 Length: 603
Score: 290.50 Matches: 156
Percent Similarity: 37.85% Conservative: 87
Best Local Similarity: 24.30% Mismatches: 244
Query Match: 4.89% Indels: 155
DB: 4 Gaps: 24

US-09-396-985B-5 (1-3395) x US-08-487-072A-50 (1-603)
QY 374 TGCATGAGTGAATCTCAGCAAAATCCCTCATGATCCCTTATTCAACCAAGACTTA 433
D 60 CysSerSerIysAsnIeuThrHsIeuPProAspApIleProValSerThrArgAlaIeu 79
QY 434 GATCTGAAGCTTCAACCCCTGAAAGATCTTAAAGAGCTTATAGCTTACCAATTTCTCAAA 493
D 80 TrpIleuAspOlyAsnAsnIeuSerSerIleProSerAlaIaIleHsGlnAsnIeuSer 99
QY 494 CTTCAAGGAGGTGATTTATTCAGAGTGTGAATTTGAACAATTGAAGAACAGCAATGGCAT 553
D 100 LeuAspPheIeuAsnIeuGlnGlySerTrpIleuArgSerIeuGluPProGlnAlaIeu 119
QY 554 GGCCTTAAACCAAGCTTCAACCTTGGTACTGACAGCAAAACCTTATCAAGAGTTTTCCTCA 613
D 120 GlyIleuGlnAsnIeuTrpIleuHsIeuGlnIuAsnAsnArgIeuAsnIeuAlaVal 139
QY 614 GGAAGTTTTCGAGCTAAACAATTTAGAGAACTGGTGGCTGTGGAGACAAAATGACC 673

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[illegible]

Db 406 -----PheAlaGlyLeuSerGlyLeuArgArgLeuPheLeu--- 417
QY 1691 GGCAATCTTTCAGAACACACCCCTTCAAAATC-----TTTACCAACACA 1738
Db 418 -----ArgAspAsnSerIleSerSerIleGluGlnSerLeuAlaGlyLeu 433
QY 1739 ACAAACTTAACATTCCTGATCTTTCTTAATGCAACATGCAACATATCTAGGGGGTA 1798
Db 434 SerGluLeuLeuGluLeuAspLeuThrThrAsnArgLeuThrIleLeuProArgGlnLeu 453
QY 1799 TTGACACACTCTAGACATCTCCAGTTATTAACATGATGACCAACCACTACTGTTTCTG 1858
Db 454 PheGlnIlyLeuGlyHisLeuGluIyLeuLeuSerIyRasnGlnLeuThrThrLeu 473
QY 1859 GATCCATCCCATTTATAACAGCTGACTCCCTCAGACCTGATTCGATTCGATTCGAATCCG 1918
Db 474 SerAlaGluValLeuGlyProLeuGlnArgAlaPheThrLeuAspIleSerHisAsnHis 493
QY 1919 ATAGAGACA---TCCAAAGCAATACTGCAACATTTTCCAAAGCTGACCGCTTCAAT 1975
Db 494 LeuGluThrLeuAlaGluGlyLeuPheSerSerLeuIyArg---ValArgIyLeuSer 512
QY 1976 CTGACTAATATCTGTGCTTGATATGCAATATGCAATTTCTTGACGTGGGTCAAG 2035
Db 513 LeuArgAsnAsnSerLeu-----GlnThrPheSerProGlnProGly 526
QY 2036 GACCAAGAAATGTTCTTGATGTAATGTAACAAATGGAATGTCATCCTATAGACATG 2095
Db 527 LeuGluArgLeuIyPheLeu---AspAlaAsnProIyPheAspCysPheProLeuAla 545
QY 2096 AAGGCTCCCTGGTGGTGGAT-----TTTGAATTCACCTGT 2134
Db 546 LeuArgAspPheAlaLeuGlnAsnProGlyValValProArgPheValGlnThrValCys 565
QY 2135 -----TATATATACAACTATCATCATGATGATCGGTGTC 2170
Db 566 GluGlyAspAspCysGlnProValIyThrIyRasnAsnIleThrCysAlaGlyProAla 585
QY 2171 AGGTG 2176
Db 586 AsnVal 587

RESULT 13
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE 2 DIABETES, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Alignment Scores:
Pred. No.: 4,87e-20 Length: 623
Score: 284.00 Matches: 169
Percent Similarity: 35.55% Conservative: 88
Best Local Similarity: 23.37% Mismatches: 265
Query Match: 4.78% Indels: 201

DB: 4 Gaps: 24
US-09-396-985b-5 (1-3395) x US-09-949-016-10995 (1-623)
QY 238 GGTGGTTGCAAAAATGCCAGATGATGCTCTTGGATCTGGCTGGGACTTGATCAT 297
Db 12 AlaAlaCysProAlaCys-ArgMet-----AlaLeuArgIyGlyClyLeuAlaLeuAl 29
QY 298 GGCATTTGTCCTTCC-----TGCCTGAGACCAAGAAAGCTTGAAAT----- 337
Db 29 AlaLeuLeuLeuSerIyPheValAlaLeuGlyProArgSerLeuGlnIyAlaAspProGly 49
QY 338 -----CCCTGACATA-----GA 348
Db 49 YThrProGlyGluAlaGluIyProAlaCysProAlaAlaCysValCysSerIyRaspAs 69
QY 349 GGTACTTCTTAATATTAATCTTAACATATGATGATCAAGATCTCAACAAATCCCTATGA 408
Db 69 PAspAlaAspGluLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspGly 89
QY 409 CATCCCTTATTCACCAAGAACTAGATCTGACCTTCAACCCCTGAAGATCTTAAGAG 468
Db 89 ValProGlyGlyIyThrGlnAlaLeuIyPheAspGlyAsnAsnLeuSerValProPr 109
QY 469 CTATACCTTCACCAATTTCTCACAACTTCAGTGGCTGATTTATCCAGTGTGAATGA 528
Db 109 AlaAlaPheGlnAsnLeuSerSerIyPheLeuAsnLeuGlnIyGlyGlnLeuGly 129
QY 529 GACAATGGAAGACAGGATGCGATGCTTAACCAAGCTCTCAACCTTGATCTGACAG 588
Db 129 YSerLeuGluProGlnAlaLeuLeuGlyLeuGluAsnLeuCysHisIleuHisLeuGluIy 149
QY 589 AAACCCATGAAGATTTTCCCAAGAGTTTCCAGATTTTTCGACSTAAACAAATTAAGAAATC 648
Db 149 GaenGlnLeuArgSerIyLeuGlyIyThrPheAlaHisThrProAlaLeuAlaSerIle 169
QY 649 GGTGGCTGTGGAACAAATAATGACCTCTAGAGGGTTTCCATATTTGACAGCTTATATC 708
Db 169 UGlyLeuSerAsnAsnAsnArgLeuSerArgLeuGluAspGlyLeuPheGluIyLeuGlySe 189
QY 709 CTTAAAGAACTTAATGTGGCTCATTAATCTTATATCATCTTTAAGTGGCTGA---TA 765
Db 189 RLeuIyPAspLeuAsnLeuGlyIyTrpAsnSerLeu-----AlaValLeuProAspAlaAl 207
QY 766 TTTTTCATATCTGACAAACCTAGACATGATGATCTTTCTTATAC-----TATAT 816
Db 207 AsnAspArgIyLeuGlySerIyLeuArgIyLeuValAlaLeuAlaGlyAsnArgLeuAlaIyTrle 227
QY 817 TCAAACTATTTCTGTCAAAAGACTTACAGTTTCTACGTGAAGAAATCCCAAGTCAATCTCTC 876
Db 227 UGlnProAlaLeuPheSerGlyLeuAlaGluLeuArgIy----- 240
QY 877 TTTAGACCTGTCTTTAAACCAATTTGACTCCATTCAGGCCAAGCTTT---CAGGGAAT 933
Db 241 -LeuAspLeuSerArgAsnAlaLeuArgAlaIleIyAsnValPheValGlnLeuPr 260
QY 934 TAGCTCCATGAATGATGCTTAAGAGTATTTTAATAGCTCAAAATGATGAGAAATGTG 993
Db 260 ArgLeuGlnIySerLeuIyLeu----- 267
QY 994 CTTTCAAAACATGACTGTGTTTACATGTCATCGGTGATCTTGGAGAAATTTAAATGA 1053
Db 268 -----As 268
QY 1054 AAGGAATCTGAAAAGTTTGAACCGTTCTGTCAATGAGAGACTATGCAATGTAGCATTGA 1113
Db 268 PArgAsnLeu----- 271
QY 1114 TGAATTCAGGTAAATATATTAATCATTTTTCAGATGATATTTAATGCTCAATTCCT 1173
Db 272 ----- 1172
QY 1174 GGCAAAATATTTCTGCAATGTCTTTCAAGGTGTATATAAACACATAGACAGATGTTCC 1233

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Db      272 eAlaAlaValAlaProGlyAlaPheLeuGlyLeu-----283
Qy      1234 TAGGATTTCAAAATGGCAATCCTTATCATGATTAGATGTCATTAGCCTTTCCAA 1293
Db      284 -LysAlaLeuArgTyrLeuAspLeuSer-----292
Qy      1294 GCTGAGTCTACCTTTCTTAAAGTTGAGCTTAACTACCAACAGA-----1339
Db      293 -----HisAsnArgValAlaGlyLeuLe 300
Qy      1340 -GAGGATATCAGCTTTGGTCACTGGCTGCGCAAGTCCAGATATCTTAGATCTTAGTAG 1398
Db      300 uGluAspThrPheProGlyLeuLeu-----GlyLeuArgValLeuArgLeuSerH 317
Qy      1399 AAATGCCATGAGCTTTAGAGGTGCTGTTCTTATCTCATTTTGGACAAACCACTGAA 1458
Db      317 sAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu-----HisPheLeuG 335
Qy      1459 GTACTTAGACCTCAGCTTCAATGGTGC--ATCCTGATGAGTGCCCACTTCATGGGCT 1515
Db      335 uGluLeuGlnLeuGlyHisAsnArgIleArgGlnLeuAlaGluArgSerPheGluGlyLe 355
Qy      1516 AGAAGAGCTGGAATACCTGGAACCTTCAGCACTCCACTTAAAAAAGTCAAGAAATTCTC 1575
Db      355 uGlyGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnVal--LysAlaG 374
Qy      1576 AGTGTCTTATCTCTGAAAAACTTCTTACCTTCACATCTTACCTAATACCAAAAT 1635
Db      374 yAlaPheLeuGlyLeuThrAsnValAlaValMetCysLeuSerGlyAsnCysLeuArgAs 394
Qy      1636 TGACTTATGATGCAATATTTCTTGGCTTGATCAGTCCAACTTAAAAAAGGCTGGCA 1695
Db      394 nLeuProGlnGlnValPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGlnGlySe 414
Qy      1696 TTCT-----1699
Db      414 rCysLeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPh 434
Qy      1700 -TTCAAGACCAACACCTTTCAATATGC-----TTTACAAACACACAAACTT 1746
Db      434 eLeuLysAspAsnGlyLeuValGlyIleGlnGlnSerLeuTyrGlyLeuAlaGlyLe 454
Qy      1747 AACATTCCTGATCTTTTAATATGCACTGGAACAGATATAGGGGGATTTTGAACAC 1806
Db      454 uLeuGlnLeuAspLeuThrSerAsnGlnLeuThrHisLeuProHisAsnGlyLeuPheGlnG 474
Qy      1807 ACTCTACAGACTCCAGTTATTAACATGATGATCACAACAACCTACTGTTTCTGATCCATC 1866
Db      474 yLeuGlyLysLeuGlnTyrLeuLeuLeuSerArgAsnArgLeuAlaGlnLeuProAlaAs 494
Qy      1867 CCATTATTAACAGCTGTATCCCTCAGAGACTCTTGATTCAGTTCAATGCCATAGAC 1926
Db      494 pAlaLeuGlyProLeuGlnArgAlaPheTyrLeuAspValSerHisAsnArgLeuGlnAl 514
Qy      1927 ATCCAAAGGATATCGCAACATTTTCCAAAGAGTCTACCGCTTCATCTGACTAATAA 1986
Db      514 aLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArgTyrLeuSerLeuAspAs 534
Qy      1987 TTCTGTTGCTGTATATGATATCAGAAATTTCTTGACG-----TGGTCAAGACCA 2040
Db      534 nSerLeuArgThrPheThrProGlnProProGlyLeuGlnArgLeuTyrLeuGlnGly-- 553
Qy      2041 GAAAAATGTTCTTGGAATGTTGAACAAATGAATGTCATCACCCTATAGAC----- 2092
Db      554 -----AsnProTyrAspCysGlyCysProLeuLysAlaLeuArg 566
Qy      2093 -----ATGAAGGCTCCCTGGTGTGGATTTTGAATTCACACTGCT----- 2144
Db      566 gAspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCysGlyGln 586
Qy      2135 -----TATATATACAGACTATCATCAGTGTATGGTGTGCAG 2172

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Db      586 yAspAspCysGlnProAlaTyrThrTyrAsnAsnIleThrCysAlaSerProProG 606
Qy      2173 TGTGCTT 2179
Db      606 uValVal 608

RESULT 14
US-09-191-647-7
; Sequence 7, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kld, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OR INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-191-647-7

Alignment Scores:
Pred. No.: 1,12e-19 Length: 1480
Score: 282.50 Matches: 161
Percent Similarity: 33.29% Conservative: 88
Best Local Similarity: 21.52% Mismatches: 246
Query Match: 4.75% Indels: 254
DB: Gaps: 25

US-09-396-985B-5 (1-3395) x US-09-191-647-7 (1-1480)
Qy      374 TGCAATGATCAGATCTCAGCAAAATCCCTCATGATCCCTTATTCACCAAGACCTA 433
Db      308 CysArgGlnLysSerLeuThrSerValProValThrLeuProAspArgThrThrAspVal 327
Qy      434 GATGTGAGCTTCAACCCCTGGAAGATCTTAAAGCTATAGCTTACCAATTTTCAACA 493
Db      328 ArgLeuGlnGlnAsnPheIleThrGlnLeuProProLysSerPheSerPheArgArg 347
Qy      494 CTTCAAGGCTGCGATTTATTCAGGTGGAATTTGAGCAATTTGAAGCAAGGATGGCAT 553
Db      348 LeuArgArgIleAspLeuSerAsnAsnAsnIleSerArgIleAlaHisAspAlaLeuSer 367
Qy      554 GCGTTAACAAGCTCTCAACCTTGATCTGACAGAGAAACCTATCAAGAGATTTTCCCA 613
Db      368 GlyLeuLysGlnLeuThrThrLeuValLeuTyrGlyAsnLysIleLysAspLeuProSer 387
Qy      614 GAAAGTTTCTGGACTPAACAATTTAGAGAAATCTGCTGCTGAGACAAATAATGACC 673
Db      388 GlyValPheLysGlyLeuGlySerLeuArgLeuLeuAsnAlaAsnGlnIleSer 407
Qy      674 TCTCTAAGGGTTCCATATTTGACACAGCTTATATCTTAAAGAAACCTAATNGGCTCAT 733
Db      408 CysIleArgLysAspAlaPheArgAspLeuHisSerLeuSerLeuLeuTyrAsp 427
Qy      734 AATCTTATACATTCCTTAAAGTTCCTGAATATTTTCTAATCTGACAAACCTAGAACAT 793
Db      428 AsnAsnIleGlnSerLeu-----AlaAsnGlyThrPheAspAlaMetLysSerMetLysThr 446
Qy      794 GTGATCTTTCTTATTAACCTATATTCATTAACACTATTTCTGCAAGCTTACAGTTCTAC 853
Db      447 ValHisLeuAlaLysAsn-----ProPheIleCysAspCysAsnLeuArgTyrLeuAla 464

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QY      854 GAAATCCCAAGCAATCTCTTTAGACCTGTCTTAAACCCCAATTCATTCACAA 913
      465 Aspyr-----LeuH1sIysAnProlIeglUthrSerGly 476
QY      914 GCCCAAGCCTTTCAGGAAATTAGCTCCAGAAATTGACTTAAGAAGT----- 961
      477 AlArgCysGluSerProLysArgMetH1sArgArgIlegIuSerLeuArgGlu 496
QY      962 AATTATATAGCTCAAAATGACTGAAATGACCTTCAAAAACATGACTGGTTTACATGTC 1021
      497 LysPheLysCysSer----- 501
QY      1022 CATCGTTGATCTTGGAGAAATTTAAATGAAAGAAATCTGAAAGTTTGAACGGTTCT 1081
      502 -----TpgIglUleu-----ArgMet 507
QY      1082 GTCATGGAAGCACTATGCAATGTGAGCAATTGATGATTCAGGTTAACATATATATCAT 1141
      508 LysLeuSerGlyGluCysArgMetAspSerAsp----- 518
QY      1142 TTTTCAGATGATATTTATTAATCTCAATTCGTTGGCAATATTTTCGCAATGCTTTGACA 1201
      519 -----CysProAlaMetCysH1sCysGluGlyThrThrValAspCysThr 533
QY      1202 GGTGTACATATTAACAACATAT---GCAGATGTTCTTACGCAATTTCAAAATGGCAATCTTCA 1258
      534 GlyArgArgLeuLysGluIleProArgAspIleProLeuH1s----- 547
QY      1259 TCATATCTTAGATGTCATCTTAAAGCTTTTCCAAAGCTGAGTCACTTTTCTTAAAGT 1318
      548 -----Thr 548
QY      1319 TGACATTAACTACCAACAGAGATATCAGC-----TTTGGT 1357
      549 ThrGluLeuLeuLeuAsnAspAsnGluLeuGlyArgIleSerSerAspGlyLeuPheGly 568
QY      1358 CAGTGTGCTGTGCCAAGCTTCAGATATCTAGATCTTATAGTAAATGGCAGTACAGCTTTAGA 1417
      569 Arg-----LeuProH1sLeuValIlyLeuGluLeuLysArgAsnGlnLeuThr----- 584
QY      1418 GGTGTGCTGTCTTATTTCTGATTTTGGAAACAACCACTGAAGTCTTAGACCTCAGCTTC 1477
      584 ----- 584
QY      1478 AATGTGTCAATCTGATGAGTGCACAC---TTGATGGGTCTAGAAGAGCTGAATACCTG 1534
      585 ---GlyIle-----GluProAsnAlaPheGluGlyAlaSerH1sIleGlnGluLeu 600
QY      1535 GACTTTCAGCACTCCACTTTTAAAAAAGGTCAAGAAATTCCTAGTGTCTTATCTTTGAA 1594
      601 GlnLeuGlyGluAsnLysIleLysGluIleSerAsn---LysMetPheLeuGlyLeuH1s 619
QY      1595 AAATCTTCTTACCTTGCACATCTTTCACATTAATCCAAATATGACTTTGATGGCATATTT 1654
      620 GlnLeuLysThrLeuAsnLeuLysArgAsnGlnIleSerCysValMetProGlySerPhe 639
QY      1655 CTTCGGTTCAGTCACTCAACACTTTTAAAAAAGGTGCTGCACTTTCTTC----- 1702
      640 GlnH1sLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPheAsnCysAsnCys 659
QY      1702 ----- 1702
Db      660 HistLeuAlaTrpPheAlaGluCysValArgLysLysSerLeuAsnGlyAlaAlaArg 679
QY      1703 -----AAAGAC----- 1708
Db      680 CysGlyAlaProSerLysValArgAspValGlnIleLysAspLeuProH1sSerGluPhe 699
QY      1708 ----- 1708
Db      700 LysCysSerSerGluAsnSerGlyGlyCysLeuGlyAspGlyTyrcysProProSerCys 719
QY      1709 -----AACACCTTTTCAAAATGTC----- 1726

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Db      720 ThrCysThrGlyThrValValAlaCysSerArgAsnGlnLeuLysGluIleProArgGly 739
      1726 ----- 1726
QY      740 IleProAlaGluThrSerGluLeuTyrlLeuGluSerAsnGluIleGluGlnIleH1sTyrc 759
      1727 -----TTTCAACAACAACAACAACTTAACATTCCTGATCTTCTTCTTAAATGCCAATCGAA 1780
      760 GluArgIleArgH1sLeuArgSerLeuThrArgLeuAspLeuSerAsnAsnGlnIleThr 779
QY      1781 CAGATATCTAGGGGGGATTTTGCACACATCTTACAGACTCCAGTTATTAACATGATGATCAC 1840
      780 IleLeuSerAsnTyrlThrPheAlaAsnLeuThrLysLeuSerThrLeuIleIleSerTyrc 799
QY      1841 AACACCTACTGTCTTTCGATTCATCCATTAATAACAGATGATCTCCCTCAGACACTCTT 1900
      800 AsnLysLeuGlnCysLeuGlnArgH1sAlaLeuSerGlyLeuAsnAsnLeuArgValAla 819
QY      1901 GATTGCAGTTTCAATGCAATAGAG---ACATCCAAAGAAATACTGCACATTTTCCAAAG 1957
      820 SerLeuH1sGlyAsnArgIleSerMetLeuProGluGlySerPheGluAspLeu---Lys 838
QY      1958 AGTTCAGCGCTTTCATCTGACTAATTAATCTTGTCTTGTATGATGAAATTCAGAAAT 2017
      839 SerLeuThrH1sIleAlaLeuGlySerAsnProLeuTyrcysAspCysGlyLeuLysTrp 858
QY      2018 TTCTTCAGTGGGTCAAGAGCCAGAAATGTTCTTGTGAATTTGAACAATGAATGTT 2077
      859 PheSerAspTrpIle-----LysLeuAspTyrlValGluProGlyIleAlaArgCys 875
QY      2078 GCATCACTATAGACATGAAAGGCTCCTGCTGTTGGATTTTCAATTCACAC----- 2131
      876 AlaGluProGluGlnMetLysAspLysLeuIleLeuSerThrProSerSerPheVal 895
QY      2132 -----TGTATAT----- 2139
Db      896 CysArgGlyArgValArgAsnAspIleLeuAlaLysCysAsnAlaCysPheGluGlnPro 915
QY      2140 ATCAAGACTATCATGACGTATCGGT-----GGTCAAGTGTGTTGT--- 2181
      916 CysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGlyTyrcysLysCysGln 935
QY      2182 -----GGTAGCCACTGT 2193
      936 ProGlyTyrlH1sGlyLysH1sCys 943

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RESULT 15
 US-09-540-245A-7
 : Sequence 7, Application US/09540245A
 : Patent No. 6270984
 : GENERAL INFORMATION:
 : APPLICANT: Goodman, Corey
 : APPLICANT: Kid, Thomas
 : APPLICANT: Brose, Katja
 : APPLICANT: Tessier-Lavigne, Marc
 : TITLE OF INVENTION: Modulating Robo: Ligand Interactions
 : FILE REFERENCE: B98-031-3
 : CURRENT APPLICATION NUMBER: US/09/540, 245A
 : CURRENT FILING DATE: 2000-03-31
 : PRIOR APPLICATION NUMBER: 60/065,544
 : PRIOR FILING DATE: 1997-11-14
 : PRIOR APPLICATION NUMBER: 60/081,057
 : PRIOR FILING DATE: 1998-04-07
 : NUMBER OF SEQ ID NOS: 20
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 7
 : LENGTH: 1480
 : TYPE: PRT
 : ORGANISM: Drosophila melanogaster
 : US-09-540-245A-7
 Alignment Scores:

Pred. No.:	1,12e-19	Length:	1480
Score:	282.50	Matches:	161
Percent Similarity:	33.29%	Conservative:	88
Best Local Similarity:	21.52%	Mismatches:	246
Query Match:	4.75%	Indels:	254
DB:	3	Gaps:	25

US-09-396-985B-5 (1-3395) x US-09-540-245A-7 (1-1480)

QY	374	TGCATGATACGAATCTCAGCAAAAATCCCTCATGCATCCCTTATTCAACCAAGAACCTA	433
Db	308	CysArgGlnIuSerSerLeuThrIleProValThrLeuProAspSerPheThrIleAspVal	327
QY	434	GATCTGAGCTTCACACCCCTGGAAGATCTTAAGAACCTATAGCTTCAACCAATTTTCCACA	493
Db	328	ArgLeuGlnGlnAsnPheIleThrGluLeuProProIlySerPheSerSerPheArgIaG	347
QY	494	CTTCAGTGGCTGGATTTTATTCACAGGTGTGAAATTGAGACAAATTGAAAGACAAAGCATGGCAT	553
Db	348	LeuArgGlnIleAspLeuSerAsnAsnIleSerArgIleAlaHisAspAlaLeuSer	367
QY	554	GGCTTAAACCGCTCTCACAACCTTGGTATCTGACAGAAAACCTATACAGATTTTCCCA	613
Db	368	GlyLeuIysGlnLeuThrThrIleValIleuIysGlyArgIleuIysIleAspLeuProSer	387
QY	614	GGAAGTTTTCCTGCACTAACAAATTTAGAGATCTGGTGGCTGTGGAGACAAAAAATGACC	673
Db	388	GlyValPheIysGlyLeuGlySerLeuArgLeuLeuLeuAsnAlaAsnGluIleSer	407
QY	674	TCTTAGAGGGTTTCATATTTGACAGCTTATATCTTTAAAGAACTAAATGTGCTCAT	733
Db	408	CysIleArgIysAspAlaPheArgAspLeuHisSerLeuSerLeuLeuSerLeuIysIysAsp	427
QY	734	AATCTTATACATTCCTTTTAAGTGTGGCTGAATTTTTCATATCTGACAAAACCTAGAACAT	793
Db	428	AsnAsnIleGlnSerLeu--AlaAsnGlyThrPheAspAlaMetLeuSerMetIysThr	446
QY	794	GTGATCTTTCCTTATACCTATATTCACAACTATTTCTGTCAAGACCTTACAGTTTTCAGCT	853
Db	447	ValHisLeuAlaIysAsn-----ProPheIleCysAspCysAsnLeuArgTrpLeuAla	464
QY	854	GAATAATCCCAAGTCATCTCTCTTTAGACCTGTCTTTAAACCCAAATGACCTCATTTCAA	913
Db	465	AspIys-----LeuHisIysAsnProIleGluThrSerGly	476
QY	914	GCCCAAGCCTTTCAGGAATTAAGCTCCATGAATGACTCTAGAAGT-----	961
Db	477	AlaArgCysGlnSerProIysArgMetHisArgArgIleGluSerLeuArgGlnGlu	496
QY	962	AATTTTATATAGCTCAATATGTACTGAAAAATGTGCTTCAAAAACATGACGTGTTATCATGTC	1022
Db	497	LysPheIysCysSer-----	501
QY	1022	CATCGGTGATCTTGGAGAAATTAAATAAGAAAGAACTGGAAAGTTTGAACCGTTCT	1083
Db	502	-----TrpGlyGluLeu-----ArgMet	507
QY	1082	GTCATGAGAGACATATGCAATGTGAGCATATGATGATTCAGTTCATACATATTAATCAT	1144
Db	508	LysLeuSerGlyGlnCysArgMetAspSerAsp	518
QY	1142	TTTTCAGATGATATTATTAATCTCATATGCTTGGACCAATAATTCTGCAATGCTTTTCACA	1200
Db	519	-----CysProAlaMetCysHisCysGlnGlyThrThrValAspCysThr	533
QY	1202	GGGTACATATTAACACACATA--GCAGATGTTCTTACGACATTTCAAAATGGCAATCTTAA	1258
Db	534	GlyArgGlnLeuIysGlnIleProArgAspIleProLeuHis-----	547
QY	1259	TCATATCATTAATATGTCATTTAAGCCTTTCCAAAGCTGAGTCTACCTTTTCTTAAAGT	1311
Db	548	-----Thr	548

QY	1319	TGACACTTAATCAACCAAGAGAGATATCAAG-----	TTTGGT	1357
DB	549	ThrgluLeuleuleuLeuAsnAspAsnGluLeuValArgIleSerSerAspGlyLeuPheGly		568
QY	1358	CAGTTGGCTGGCCAAAGTCCAGATATCTAGATCTTGAAGATGCGCATGAGCTTTGAA		1417
		:::		
DB	559	Arg-----LeuProHISleuValIlyleuGluLeuIlyAspAsnGlnLeuThr-----		584
QY	1418	GATTGGCTGTCTTATTTCTGATTTTGGAAACAACAACCTGAAGTACTTAAGCTCAGCTTC		1477
DB	584	-----		584
QY	1478	AATGGTGCATCCCTGATGATGAGCCAAAC---TTCAATGGGCTCAAGAAAGCTGGAACTACTG		1534
DB	585	--GlyIle-----GluProAsnAlaPheGluGlyAlaSerHISileGlnGluLeu		600
QY	1535	GACTTTCAGCACTCCACTTTTAAAAAAGGTCCAGAAATTCTCAGAGTTCTTATCTTGGAA		1594
		:::		
DB	601	GlnLeuGlyGluAsnIlyIelyGlnIleSerAsn---LysMetPheLeuGlyLeuHIS		619
QY	1595	AAACTTCTTTACCTTTCACATCTCTTACACTAATACCAAAATTGACTTTCAGTGCATATT		1654
		:::		
DB	620	GlnLeuIysThrIleuAsnLeuTyAspAsnGlnIleSerCysValMetProGlySerPhe		639
QY	1655	CTTGGCTTGCATCACTCTCAACACTTTTAAAAATGGCTGCGCAATCTTTC-		1702
DB	640	GlnHISleuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPheAsnCysAsnCys		659
QY	1702	-----		1702
DB	660	HISleuAlaTrpPheAlaGluCysValArgIlyLysSerLeuAsnGlyGlyAlaAlaArg		679
QY	1703	-----AAAGAC-----		1708
DB	680	CysGlyAlaProSerIysValArgAspValGlnIleLysAspLeuProHISerGluPhe		699
QY	1708	-----		1708
DB	700	LysCysSerSerGluAsnSerGluGlyCysLeuGlyAspGlyTyCysProProSerCys		719
QY	1709	-----AACACCCCTTCAAAATGTC-----		1726
DB	720	ThrCysThrGlyThrValAlaLysSerArgAsnGlnLeuLysGlnIleProArgGly		739
QY	1726	-----		1726
DB	740	IleProAlaGluThrSerGluLeuTyLeuGluSerAsnGlnIleGluGlnIleHISerTy		759
QY	1727	-----TTTACAACAACAACAATTAACTCTGATCTTTTSTAATGCCAACTGGA		1780
		:::		
DB	760	GluArgIleArgHISleuArgSerLeuThrArgLeuAspLeuSerAsnAsnGlnIleThr		779
QY	1781	CAGATATCTAAGGGGGATTTTGAACAACACTCTACAGACTCCAGTATTAACAATGAGTCAC		1840
		:::		
DB	780	IleLeuSerAsnTyThrPheAlaAsnLeuThrLysLeuSerThrLeuIleIleSerTy		799
QY	1841	AACAACCTACTGTTTCTGATTCATCCATTTAAACAGCTTACTCCCTCAGAGACTTT		1900
DB	800	AsnIlyleuGlnCysLeuGlnAsnHISAlaIleuSerGlyLeuAsnAsnLeuAspValVal		819
QY	1901	GATTGACAGTTTCAATGCGCATAGAG---ACATCCAAAGGAATACTGCAACATTTTCCAAG		1957
DB	820	SerLeuHISgluAsnArgIleSerMetLeuProGlnIlySerPheGluAspLeu---Lys		838
QY	1958	AGCTAAGCCGCTTCATCTGACATTAATATTTCTGCTTGTATATCTGAATATCAGAAAT		2017
DB	839	SerLeuThrHISleAlaLeuGlySerAsnProLeuTyTyCysAspCysGlyLeuLysTrp		858
QY	2018	TTCTTGCAGTGGGTCAGACGACAGAAATATTTCTTGGTGAATGTTTGAACAAATGAATGT		2077
DB	859	PheSerAspTrpIle-----LysLeuAspTyValGluProGlyIleAlaArgCys		875
QY	2078	GCATCACCTTATGACATGAAGGCTCCCTGGTGTGGATTTTACGAATTCACAC-----		2131

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Db      876 AlagluProgluInMetLysAspLysLeuIleuSerThrProSerSerSerPheVal 895
QY      2132 -----TGTATAT----- 2139
Db      896 CysArgGlyArgValArgAsnAspIleuAlaLysCysAsnAlaCysPheGluInPro 915
QY      2140 ATACAAGACTATCATCAGTGTATCGGT-----GGTCAGTGTGCTTGT--- 2181
Db      916 CysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGluTyrGlnCysLeuCysGln 935
QY      2182 -----GGTAGCCACTGT 2193
Db      936 ProGlyTyrHisGlyLysHisCys 943
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Search completed: March 29, 2005, 17:38:10
Job time : 83.8263 secs

[illegible]


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QY 467 AGCTATAGCTTCACCAATTTCTCAACATTCAGTGGCTGATTTATTCAGGTGGATATT 526
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Db 70 AsnThrThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIle 89
QY 527 GAGCAATTAAGACCAAGCATGGCAGTGGCTTAAACACGCTCTCAACCTTGATCTGACA 586
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 90 TyrTrpIleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
QY 587 GGAAACCCCTATCAGAGTGTTCGCCAGAGTGTTCCTGAGCAATTAACAAATTTGAGAGAT 646
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 110 AlaAsnProLeuIlePheMetAlaGluThrAlaLeuSerGlyProValAlaLeuHis 129
QY 647 CTGGTGGCTGTGAGACAAATATGACCTCTCTAGAGGTTCATATGACACGCTTATA 706
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 130 LeuPhePheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnHis 149
QY 707 TCTTTAAAGAACTTAATATGAGCTCAATATCTTTATACATTCCTTTAACTGCTCAATAT 766
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 150 ThrLeuGlnSerLeuTyrLeuGlySerAsnHisIleSerSerIleTyrLeuProIyGly 169
QY 767 TTTTCTATCTGACAAACCTAGAACATGTGATCTTTTATATCTAATTCACAACTATT 826
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 170 PheProthr---GluLysLeuLysValLeuAspPheGlnAsnAsnAlaIleHisTyrLeu 188
QY 827 TCTGTCAAGACTTACAGTTTCTACGTGAATATCCCAAGTCAATCTCTTTAGACCTG 886
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 189 SerLysGluAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeu 206
QY 887 TCTTTAAACCAATTTGACTTCACAGCCCAAGCTTTCAAGGAAATTAGGCTCCATGAA 946
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 207 AsnGlyAsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSer 226
QY 947 TTGACTTAAGAGTATTTAATATAGCTCAATATGACTGAAGAAATGTGCTTCAAAACATG 1006
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuLeuValIlePheLysGlyLeu 242
QY 1007 ACTGGTTATACATGTCATCGGTGATCTTGAGAGATTTAAATTAAGAAAGATCTGGAA 1066
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 243 LysAsnSerThrIleGlnSerLeuThrLeuGlyThrPheGlu---AspMetAspAspIlu 261
QY 1067 AGTTTGAACCGTCTGTCAATGAGAGACTATGCAATGTGAGACTTATGAGTCAAGTTA 1126
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 262 AspIleSerProAlaValPheGlnGlyLeuCysGluMetSerValGlnSerIleAsnLeu 281
QY 1127 ACATATATATAATCATTTTTCAGATGATATTAATATCATCATGCTGGCAATATTTCT 1186
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 282 GlnLysHisTyrPhePheAsnIleSerSerAsnThrPheHisCysPheSerGlyLeuGln 301
QY 1187 GCAATGTCTTCACAGGTGTATCATATTAACAACATAGCAGAT----- 1228
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 302 GluLeuAspLeuThrAlaThrHisIleLeuSerGluLeuProSerGlyLeuValGlyLeuSer 321
QY 1229 -----GTTCTTAGGCATTTCAATGGCAATCTTATTCATCATGATTAGATGT 1273
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 322 ThrLeuLysLysLeuValLeuSerAlaAsnLysPheGluAsnLeu-----Cys 337
QY 1274 CATCTTAGACCT-----TTTCCAAAGCTGAGTCACTTTTCTTAAAGTTGACCTTTA 1327
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 338 GlnIleSerAlaSerAsnPheProSerLeuThrHisIleLeuSerIleLysGly----- 354
QY 1328 ACTACCAACAGAGAGATATACGTTTGTCAGTTGGCT-----CTGCCAAGTCTCAGATAT 1384
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 355 AsnThrLysAspGluLeuGlnGlyThrGlyCysLeuGlnLysAsnLeuGlnAsnLeuArgLys 374
QY 1385 CTAGATCTTAGTAAATGCAATGACGCTTTAGAGGCTGTGCTGTTTCTTATTCGATTTTGA 1444
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 375 LeuAspLeuSerHisAspAspIleGluThrSerAspCysCysAsnLeuGlnLeuArgAsn 394
QY 1445 ACAACCAACCTGAAGTACTAGACTCAGCTTCAATGAGTGCATC---CTAGTAGAGGCC 1501
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 395 LeuSerHisLeuGlnSerLeuAsnLeuSerTyrAsnGluProLeuSerLeuLysThrGlu 414
QY 1502 AACTTCATGGGTCTAGAAAGCTGGAATACCTGACCTTTCAGCACTTCACCTTAAAG 1561

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Db 415 AlaPheLysGluCysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuVal 434
QY 1562 GTCAACAGAAATTCACAGTGTCTTATCTGTGAAAACCTTTTACCTTGACATCTTAC 1621
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 435 LysAspAlaGlnSerProPheGlnAsnLeuHisIleLeuLysValLeuAsnLeuSerHis 454
QY 1622 ACTAATACCAAAATTTGACTTGTATGAGCATATTTCTTGAGCTTGATCAGTCAACACTTTA 1681
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 455 SerLeuLeuAspIleSerSerGlnGlnLeuPheAspIleuLeuProAlaLeuGlnHisLeu 474
QY 1682 AAAATGGCTGGCAATTTCTTCAAAAGACACACCTT-----TCAATGTCTTTACAAAC 1735
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 475 AsnLeuGlnGlyAsnHisPheProLysGlyAsnIleGlnLysThrAsnSerLeuGlnThr 494
QY 1736 ACAACAAATTAACATTCCTGAGATCTTTCTTAATTCGCAACTGGACAAACGATCTAGGGGG 1795
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 495 LeuGlyArgLeuGlnIleLeuValLeuSerPheCysAspLeuSerSerIleAspGlnHis 514
QY 1796 GTATTTGACACACTCTACAGACTCCAGTTATTAACATGAGTGCACAAACACTACTGTTT 1855
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 515 AlaPheThrSerLeuLysMetMetAsnHisValAspLeuSerHisAsnAspGlyThrSer 534
QY 1856 CTGGAT-----CCATCCCATTAATAACACCTGTACTCCCTCAGACACTTTGATGTC 1906
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 535 SerSerIleGlnAlaLeuSerHisLeuLysGlyIleTyr-----LeuAsnLeu 550
QY 1907 AGTTCAATGGCATAGAGACATCCAAAGAAATCTGCAATTTTCCAAAGAGCTTAGGCC 1966
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 551 AlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleLeuSerGlnLysArg 570
QY 1967 GTCTTCATCTGACTAATATATCTGTGCTGTATATGTAATGCAATTCGAAATTTCTTGACG 2026
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 571 ThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyrPheLeuGln 590
QY 2027 TGGGTCAAGACCAAGAAATGTTCTTGCTGAATGTGCAACAAATGAAATGTGATCACT 2086
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 591 TrpTyrLysGlnLysMetGlnLysLeuGlnAspThrGlnAspThrLeuCysGluAsnPro 610
QY 2087 ATAGACATGAAGGCTCCCGGTGGTGGATTTTACGAATTCACACCTGTAT----- 2137
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 611 ProLeuLeuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaVal 630
QY 2138 ---ATATCAAGACTATCATGATCGATCGGTGATCGGTGCTGCTGATGACCATGTA 2194
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 631 GlyIlePhePheLeuIleValIlePheLeuValPheAlaIleLeuLeuIlePheAlaVal 650
QY 2195 GCATTTCTGATATACCACTTCTATTTTACCTG 2227
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 651 LysTyrPheLeuArgTrpLysTyrGlnHisIle 661

```

RESULT 2

T08664
 Toll protein-like receptor DKFZp54710610.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08664
 R:Pousetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16466
 A:Accession: T08664
 A:Molecule type: mRNA
 A:Residues: 1-786 <POU>
 A:Cross-references: UNIPROT:Q15399; EMBL:AL050262
 A:Experimental source: fetal brain; clone DKFZp54710610
 C:Genetics:
 A>Note: DKFZp54710610.1

Alignment Scores: 1.71e-25 Length: 786
 Pred. No.: 465.50 Matches: 203
 Score: 40.83% Conservative: 131
 Percent Similarity: 40.83% Mismatches: 287
 Best Local Similarity: 24.82%

Db 663 Glymet-----GlnIleCysIeuHlsGlnIuArgAenPheValProGluYlySerIle 679

Qy 2408 GCTGCGCAATCATCATCCAGAAAGGCTTCACAAAGACCGGAAAGTATGTGTGTGCT 2467

Db 680 ValGluasnIlelle--ThCysIleGluYlySerIlyRlySerIlePheValIeuSer 698

Qy 2468 AGACACTTATCCAGAGCCGTGTGTATCTTTGAAATGAAATGCTCAGACATGGCAG 2527

Db 699 ProAenPheValGlnSerGluTrpGlyHisIlyRlyGluYlyRlyPheIleHisIAsnIeu 718

Qy 2528 TTTCTGAGTAGCCGCTCTGGCATCATCTTCAATTGTCCTTGAGAAAGT--GAGAACTCC 2584

Db 719 PheHisGluGlySerAsnSerIleuIlePheIleuGluProIleProGluIlySer 738

Qy 2585 TTGCTGAGGAGCAGCAGGTGAAATGATGCGCTTTCTTACGAAACCACTACCTGAGTGG 2644

Db 739 IleProSerSerIlyRlyHisIlySerIleuIleuSerIleuIleAAsnGlyTrpIleuGluTrp 758

Qy 2645 GAGGACAAATGCTCTGGGAGGACCATCTTCTGAGAAAGCTCAAAAAGCCCTG 2698

Db 759 ProIlySGluYlySerIlyArgGlyIleuHeTrpAlaIleuIleuArgAlaIle 776

RESULT 3

A29943
Toll protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Ashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of *Drosophila*, required for dorsal-ventral embryonic polarity, ap
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HMS>
A:Cross-references: UNIPROT:P08953; GB:M19969; GB:J02662; NID:G158640; PIDN:AAA28941.1;
C:Genetics:
A:Gene: *FLYBase:TL*
A:Cross-references: *FLYBase:PBgn0003717*
C:Keywords: transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <MAY>

Alignment Scores:

Pred. No.:	1,19e-20	Length:	1097
Score:	398.50	Matches:	210
Best Percent Similarity:	38.37%	Conservative:	125
Best Local Similarity:	24.05%	Mismatches:	317
Query Match:	6.71%	Indels:	221
DB:	2	Gaps:	34

US-09-396-985B-5 (1-3395) x A29943 (1-1097)

Qy 212 GTTCGTACATGCTTTCTCAACGCGCTCCGCTGTTGAGAAATGCCAGATG----- 262

Db 298 ValArgIeuMetAsnAsnArgValProIleuAlaThrIleuProSerArgIeuPheAlaAsn 317

Qy 263 ATGCTCTCTTCGATCATCTGGCTGGACTCTGATCATGCGATTTCTTCTCGCTGAGA 322

Db 318 GlnProGluIleuGlnIle-----LeuArgIeuArgAlaGluIleuGlnIleuSerIeu 333

Qy 323 CCAGAGAGCTGAATCCCGTCGATAGAGGATCTCCATATTATTAATCAATGATGAT 382

Db 334 ProGluAspIleu-----PheGluHisSerThrGlnIleThrAsnIleSerIeu 350

Qy 383 CAGAACTTCAGCAAA-----ATCCCTCATGACATCCCTTATTCACAC 424

Db 351 AspAenIleuIleuYleThrIeuProAlaThrIleuGluHisGlnVal-----AsnIeu 368

Qy 425 AAGAACTGATGATGAGCTTCAACCCCTGAAAGATCTTAAAGACTTAAGAGCTTACCAAT 484

Db 369 IeuSerIleuAspIeuSerAsnArgIeuThrHisIleuProAspSerIeuPheAlaHis 388

[illegible]

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QY 1517 GAAGAGCTGAATACCTGAGACTTTCAGACTCCATTAAAAAGTCAGAAATTCACA 1576
Db 656 ThnrlsvalProaglleuProasnlleuHlsylasnlmetGlnleuMeGlun----- 672
QY 1577 GTGTTCTTATCTTGAAAAAATTCTTTTACCTTGACATCTCTTACATAATACCAAAATT 1636
Db 673 -----LeuHlsleuGlnasnlHnrlleuHnrgleuProserAlasnlHnrlPro--- 689
QY 1537 GACTTTGATGGCAATATTTCTTGCTGATGATGCTGCAACATTTAAAAAGTGGCGCAT 1696
Db 690 -----GlyTylgluSerValHnrlserLeuHlsleuAlaGlyAsn 702
QY 1697 TCTTTCAAGACACACCCCTTTCAATGCTTTTCAACACACAAACTTAACATTCCTG 1756
Db 703 Asnleu-----ThnrlsleuAspAlasnlleuProHnrlasnlleuHlsleu 719
QY 1757 GATCTTTTAAATGCCAATGGAACAGATATCTAGGGGGTATTTGACACATCTACAGA 1816
Db 720 Asplleser-----TyrAsnlHls 725
QY 1817 CTCGAGTTATTAACATGAGTCACACACACCTACTGTTTGCATCCATCCCATTAATAA 1876
Db 726 LeuGlnleuLeuasn----- 730
QY 1877 CAGCTGACTCCCTCAGACTCTTGATTCAGTTTCAATCGCATAGACATCCAAAGA 1936
Db 731 -----AlathnrlValleuGly 735
QY 1937 ATACTGCACATTTTCCAAAGAGTCAGCCGCTTCAATCTGACTAATATTCCTGTTGCT 1996
Db 736 PheleuasnargHnrlmetLysTlrlPargSerVal---LysleuSerGlyAsnProTlrlMet 754
QY 1997 TGTATATGTAATTCAGAAATTTCTTGACATGGGGTCAGAGCCAGAAATTTCTTGCTG 2056
Db 755 CysaspCysHnrlAlaLysProleuLeuHnrlHnrlGlnasnlPheGlnArgHnrlleuGly 774
QY 2057 AATGTTGAACAATGAATGTGACATCACTTATGACATGAAGGCTCCCTGCTGTGGAT 2116
Db 775 AsplrganglnleuMetCysValasn---AlaGlnMetProHnrlArgMetValGlnleu 793
QY 2117 TTATGCAATTCACCTGTTATATATACAAAGCTATC--ATCAGTGTATCGGTGTC--- 2170
Db 794 SerHnrlasnlleuHlsCysProalaglnleuGlyValPheleuAlaValleuAlaValleu 813
QY 2171 -----AGTGTCTTGCTGAGTCCAGCTGATCTTCTGATATACCACTTC----- 2215
Db 814 AlaLeuHnrlGlyLeuLeuAlaGlyPheHnrlAlaLeuHnrlGlyLysPheGlnHnrlGln 833
QY 2216 -----TATTTTCAC--CTGATCTTATTCCTGCTGCTGTTAAAAAGTACAGC 2257
Db 834 IlelYsllleuHnrlleuHlsasnlleuLeuHnrlPheValHnrlGlnleuAspLeu 853
QY 2258 AGAGGAGCAATCATATGATGATGATTCATCTGAGCCAGAAATGAGACTGGGTG 2317
Db 854 AsplYsaspLysPheAspAlaPheHlsleuTlrlserHnrlsLysAspGlnSerPheleu 873
QY 2318 AGAACAAGCTGCTGAAGAAATTTAGAGAAGAGAGTCCCTTTCAGCTTTCCTTCAT 2377
Db 874 GlnAspYlrlleuValProGlnleuGlnHnrlGlyProGlnLysPheGlnleuCysValHnls 893
QY 2378 TACAGGAGCTTATTCCTGCTGAGCCATTCGTCGCAACATCAACAGGAAGGCTTCAC 2437
Db 894 GlnAspArgPrlleuValGlyGlyHnrlleuProGlnleuHnrlleuHnrlGlnleuVal 912
QY 2438 AAGAGCCGGAAGTATTCGTGTGTCTGAGACATTTATCCAGAGCCGTGTGTATTC 2497
Db 913 AsperArgargHnrlleuValleuSerGlnasnlPheleuHnrlGlnleuAlaArg 932
QY 2498 TTTGATATGAGATTCCTCAGACATGACATGATTTCTGAGTACCCGCTGCGATCATCTTC 2557
Db 933 LeuGlnPheArgAlaAlaHnrlsArgSerAlaLeuasnGlnleuGlyArgSerArgHnrlleuVal 952
QY 2558 ATTGTC-----CTTGAGAAAGTGAAGAGTCTTCGTCGAGCAGAG 2599

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Db 953 IlelTlrlserAsplleuGlyAspValGlnleuLeuAspGln----- 966
QY 2600 GTGCAATTTGATGCTTCCTTTAGCAGAAACACTCACTCGAGTGGGAGACAAATGCTCTG 2659
Db 967 ---GlnleuLysAlaTlrlleuLysMetAsnlHnrlTlrlleuLysTlrl----- 980
QY 2660 GGGAGGACATCTTCGAGAGACTCAAAAGAGCCCTG 2698
Db 981 GlyAspProTlrlPheTlrlPheAspLysleuArgPheAlaLeu 993

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Eldon, E.; Koeyer, S.; D'Veleyn, D.; Duman, M.; Lawinger, P.; Botes, J.; Bellem, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A:Reference number: Z17796; MUID:55324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <EID>
A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:G415682; PID:G1019104; PIDN:AAA7920
C:GeneticS:
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn004364

Alignment Scores:
Pred. No.: 6,56e-19 Length: 1389
Score: 374.50 Matches: 250
Percent Similarity: 35.40% Conservative: 172
Best Local Similarity: 20.97% Mismatches: 361
Query Match: 6.30% Indels: 410
DB: 2 Gaps: 54

US-09-396-985b-5 (1-3395) x T13852 (1-1389)
QY 380 GATCAGAAATTCAGCAAAATCCCTCATGACATCCCTTATTCACAAAGAACTGATCTG 439
Db 154 AsplasnHnrlleuArglnleuProGlnleuGlyValTlrlPcySerMetProSerleuGlnleu 173
QY 440 AGCTTCAACCCCTGAAGATCTTAAGAAGCTATAGCTTACCAATTC----- 487
Db 174 LeuasnleuHnrlGlnasnlArgHnrlleuArgSerAlaGlnleuGlyPheSerGlnLysleu 193
QY 488 -----TCACACTTCAG 499
Db 194 CysAlaGlySerAlaLeuSerAsnlAlaAsnGlyAlaValserGlyGlnleuGln 213
QY 500 TGGCTGATTTATCCAGGTGTAATTTGAGCAATTTAGACAAAGCATGGCATGCG--- 556
Db 214 ThrlleuAspValBerPheAsnGlnleuLysSerleuProasp---AlaTlrlGlyAlaSer 232
QY 557 ---TTAAACAGCTCTCAACCTTGATGCTGACAGAAACCTTATCAAGATTTTCCCA 613
Db 233 ArgleuArgargleuGlnHnrlleuSerleuGlnHnrlsAsnlHnrlleuHnrlleuAlaPro 252
QY 614 GGAAGTTTCTGAGATTAACAAATTTAGAGATCTGCTGCTGAGACAAAGATGACC 673
Db 253 AsnlAlaLeuAlaGlyLeuSerSerleuArgValleuAsnlleuSerTlrlAsnlHnrlleuVal 272
QY 674 TCTTCAGAGGTTTCCATATTTGACAGCTTATATCTTAAAGAACTAAATGTGCTCAT 733
Db 273 SerleuProSerGlnAlaPheAlaGlyAsnlGlnleuHnrlGlnleuHnrlleuGlnGly 292
QY 734 AATCTTATACATTCCTTTAAGTCCCTGAA----- 763
Db 293 AsnlAspLeu-----TlrlGlnleuProLysGlyLeuLeuHnrlsArgleuGlnleuLeu 310
QY 764 -----TATTTTCT 772

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Db      311 ValLeuAspLeuSerGlyAsnGlnLeuThrSerHisValAspAsnSerThrPheAla 330
Qy      773 AAATGCAAACTAGAAACATGGATCTTTCTTATACATAATTCAAATATT----- 826
Db      331 GlyLeuLeuArgLeuValLeuAsnLeuSerAsnAlaLeuThrArgGlyLeuGlySer 350
Qy      827 ----TCGTCAAGCTTACAGTTTCTACGGAATAATCCCAAGTCATCTCTCTTTAGAC 883
Db      351 LysThrPheLeuSerGluLeuTyrPheLeuGln-----IleLeuAsp 363
Qy      884 CTGTCTTTAAACCCATTCATCTCCATCAAGCCCAAGCTTTGAGGAAATT---AGGCTC 940
Db      364 MetArgAsnAsnSerIleGlyHisIleGlnGlnGlyAlaPheLeuProLeuTyrAsnLeu 383
Qy      941 CATGAATTGACTCTAGACGTAAT-----TTTAATAGC 973
Db      384 HisThrLeuAsnLeuAlaGluAsnArgLeuHisThrLeuAspAsnArgIlePheAsnGly 403
Qy      974 TCAAAATGACTG---AAATGTGCTTCAAAACATGACTGTGTTTACATGTCATCGGTG 1030
Db      404 LeuTyrValLeuThrTyrLeuThrLeuAsnAsn-----AsnLeuValSerIle 419
Qy      1031 ATCTTGAGAGAA---TTTAAAAATGAAAGGATCTGGAAGTTTTCACCGTTCT----- 1081
Db      420 ValGluSerGlnAlaPheArgAsnCysSerAspLeuTyrGluLeuAspLeuSerSerAsn 439
Qy      1082 -----GTCATGAAAGACTATGCAATGTGAGC----- 1108
Db      440 GlnLeuThrGlnValProGlnAlaValGlnAspLeuSerMetLeuTyrThrLeuAspLeu 459
Qy      1109 -----ATTGATGAGTTCAAGTTTAAATATATTAATCATTTTTCAGATGATATT 1156
Db      460 GlyGluAsnGlnIleSerGluPheLys-----AsnAsnThrPhe 472
Qy      1157 TATATATCAATATGCTTGGCAAAATATTTCGCAATGCT-----TTCACAGGTGATCAT 1210
Db      473 ArgAsnLeuAsnGlnLeuThrGlnLeuArgLeuIleAspAsnArgIleGlyAsnIleThr 492
Qy      1211 ATAAAAACATAGACATGTTCTTAGGCAATTCAAATGGCAATCTTATCATCATTTAGA 1270
Db      493 ValGlyMetPheGlnAspLeuProArg-----LeuSerValLeuAsn 506
Qy      1271 TGTGATCTTAAGCTTTTCCAAAGCTGAGTCTA---CCTTTCTTAAAGTGGAGCTTTA 1327
Db      507 LeuAlaLysAsnArgIleGlnSerIleGlnArgGlyAlaPheAspLysAsnThrGlnIle 526
Qy      1328 ACTACCAACAGAGATATCAGCTTT-----GGTCAGTTGGCT---CTG 1369
Db      527 GlnAlaIleArgLeuAspLysAsnPheLeuThrAspIleAsnGlyIlePheAlaThrLeu 546
Qy      1370 CCAAGTCTCAGATATCTTAGATCTTAGAAGAAAGCCATGAGCTTTAAGAGTGTCTTCT 1429
Db      547 AlaSerLeuLeuTrpLeuAsnLeuSerGlnAsnHisLeuValTrp-----PheAsp 563
Qy      1430 TATCTGATTTTGGAAACAAACCTGAGACTTAGACCTCAATGAGTGTATC 1489
Db      564 TyrAla---PheIleProSerAsnLeuTyrTrpLeuAspIleHisGlyAsnTyrIleGln 582
Qy      1490 CTGATGAGTGCCACTTCATGGGTCTAGAAAG-----CTGAAATACCTGAGCTTT 1540
Db      583 AlaLeu---GlyAsnTyrTyrLeuLeuGlnGlnIleArgValThrThrLeuAspAla 601
Qy      1541 CAGACATCCACTTTAAAAAGGTCAACAGATTCAGATGTTCTTATCTCTTGAAGAACTT 1600
Db      602 SerHisAsnArgIleThrGlnIleGlyAlaMetSerValProAsnSerIleGln---Leu 620
Qy      1601 CTTTACCTTGACATCTCT-----TACCTAATACG----- 1630
Db      621 LeuPheIleAsnAsnAsnIleIleGlyGlnIleGlnAlaAsnThrPheValAspLysThr 640
Qy      1631 -----AAATTGACTTTGATGCGATATTCTTGCGCTTGATCAGTCTCAACACTTTA 1681

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Db      641 ArgLeuAlaArgValAspLeuTyrAlaAsnValLeuSerLysIleSerLeuAsnAlaLeu 660
Qy      1682 AAAATGGCT-----GGCAATTCT 1699
Db      661 ArgValAlaProValSerAlaGluLysProValProGlnPheTyrLeuGlyGlyAsnPro 680
Qy      1700 TTCAAACACACACCTTTCAATGTCTTTACAAACACAACTTAACTA----- 1750
Db      681 PheGlnCysAspCysSerMetGluTrpLeuGlnArgIleAsnAsnLeuThrThrArgGln 700
Qy      1751 -----TTCCTGATCTTTCTAAA----- 1768
Db      701 HisProHisValValAspLeuGlyAsnIleGlnCysLeuMetProHisSerArgSerAla 720
Qy      1768 ----- 1768
Db      721 ProLeuArgProLeuAlaSerLeuSerAlaSerAspPheValCysLysTyrGlnSerHis 740
Qy      1769 -----TCCCAACTGGAACAG----- 1783
Db      741 CysProProThrCysHisCysCysGluTyrGlnGlnCysGlnCysGlnValIleCysPro 760
Qy      1783 ----- 1783
Db      761 GlyAsnCysSerCysPheHisAspAlaThrTrpAlaThrAsnIleValAspCysGlyArg 780
Qy      1784 -----ATATCTAGGGGGTATTTGACACACTCTAC--- 1813
Db      781 GlnAspLeuAlaAlaLeuProAsnArgIleProGlnAspValSerAsp---LeuTyrLeu 799
Qy      1814 -----AGACTCCAG 1822
Db      800 AspGlyAsnAsnMetProGlnLeuGlnValGlnHisLeuThrGlyArgArgAsnLeuArg 819
Qy      1823 TTATTTAACTAGTCAACAAACCTACTGTTTCTGAGATCCATCCATTTAAACAGCTG 1882
Db      820 AlaLeuTyrLeuAsnAlaSerAsnLeuMetThrLeuGlnAsnGlySerLeuAlaGlnLeu 839
Qy      1883 TACTCCCTAGAGCTGTGATGTCAGTTTCAATCGCATAGACATCCAAAGCA----- 1936
Db      840 ValAsnLeuArgValLeuHisLeuGlnAsnValLysLeuThrAlaLeuGlnGlnTyrGln 859
Qy      1937 -----ATACTGCAACATTTT 1951
Db      860 PheArgSerLeuGlnLysLeuAspArgGlnLeuTyrLeuHisAsnAsnMetLeuThrHisIle 879
Qy      1952 CCAAG-----AGTCAAGCGCTTCAATGACTGATAATATTCT 1990
Db      880 SerAsnAlaThrPheGlnProLeuValSerLeuGlnValLeuArgLeuAspAsnArg 899
Qy      1991 GTT----- 1993
Db      900 LeuSerSerLeuProHisLeuGlnTyrArgHisSerLeuGlnGlnLysLeuThrLeuGlnArg 919
Qy      1994 -----GCTTGATATGT---GAATATCAGAAATTTCTTGCACTGGCTCAAGGACGAG 2041
Db      920 AsnAlaTrpSerCysArgCysGlnGlnLeuAspArgGlnLeuAlaGlnPheValSerAspAsn 939
Qy      2042 AAAATGTTCTTGAGTATGTTGACAAATGATGCA---TCACTATAGACATGAGAG 2098
Db      940 AlaMetValValArgAspAlaHisAspIleTyrCysLeuAspAlaGlyIleLysArgGln 959
Qy      2099 GCCTCCCTGGGTGGATTTTACGAATTCACG----- 2131
Db      2132 -----TGTTATATATCAAG 2146
Qy      980 AlaSerAsnIleSerSerSerGlnAspLeuAlaGlyAlaIleGlyCysProCysTrpPro 999
Db      2147 ACTATCATCAGTATACGTTGCTGACGTGCTTGTGGTAGCCACTGTAGACTTTTGATA 2206
Qy      1000 AlaValLeu-----ValLeuIlePheLeuValValValLeuIleIleValPheVal 1016

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OY 2207 TACCACTTCTATTTCACATGTAFACTAATTTGGTGCC-----TGATA--- 2248
Db 1017 PheArgGluSerValArgMetTrpLeuPheAlaHisTyGlyValArgValCysGlnPro 1036
OY 2249 AAGTACACAGAGAGAAGAAACATCTATGATGCATTTGTGATCTACTCCAGGCCAGATGAG 2308
Db 1037 ArgPheGluAspAlaGlyLysLeuTyTrpAlaIleIleLeuHisSerGlnLysAspTyr 1056
OY 2309 GACTGGGTGAGAAACAGCATGTGGTAAAGATTTAGAAGAGAGTCCCCCGTTTCAGCTT 2368
Db 1057 GluPheValCysArgAsnIleAlaIleGluLeuGlnHisGlyArgProProPheArgLeu 1076
OY 2369 TGCCCTCATTTACAGGAGCTTTATTCCTGTGTAGCCATTCGTCCGAACATATCACAG--- 2425
Db 1077 CysIleGlnGlnAlaArgAspLeuProPro-----GlnAlaSerHisLeuGlnLeu 1092
OY 2426 ---GAGGCTTCCACAMAGCCCGAAGATTAATTTGATGTGTGTATGACACTTTATCCAG 2482
Db 1093 ValGlnGlyAlaArgAlaSerArgLysIleIleLeuValLeuThrArgAspLeuAla 1112
OY 2483 AGCGTTGGTGTATTTGAAATATGAGATTGCTCAGACATGCGAGTTTCTGATGACCCG 2542
Db 1113 ThrGlnTrpAsnArgIleGluPheArgAlaAla-----PheHisGluSerLeu 1128
OY 2543 TCTGATGCTCATC-----TTCATGTCTCTTGAAA----- 2572
Db 1129 ArgGlyLeuAlaGlnLysLeuValIleIleGlnGlnThrSerValSerAlaGlnAlaGlu 1148
OY 2573 -----GTGAGAAAGTCTTGTCTGAGCAGCAGGTGCAATTGTATGCGCTTTAGCAGA 2626
Db 1149 AspValAlaIleLeuSerProTyrLeuLysSerValProSerAsnArgLeuThrCys 1168
OY 2627 AACACATCTCTCGAGTGGAGAGACAATGCTCTGGGAGGACACATTTTGTGAGAAAGACTC 2686
Db 1169 AspArgTyr-----PheTrpGluLysLeu 1176
OY 2687 AAAAAGCGCTGTGATGATGAAGAACCTTGATCCAGATGAACATCA----- 2734
Db 1177 ArgTyrAlaIle-----ProIleGluLeuSerProArgGlyAsn 1189
OY 2735 -----GAGAGAAGACMAGMACAACACTTGACCTGAGAGATA----- 2773
Db 1190 AsnTyrThrLeuAspRHisHisEGluAspPheLysGlnProValSerProGlyMetIlePhe 1209
OY 2774 ---CAAACTGTGGGCTTAAAAACCATTATGTGTTACAATTTCCGAATGCTACAGTTCAATC 2830
Db 1210 ArgGlnAlaProProProProAlaTyrTyr----- 1219
OY 2831 TGGGTTTCTGCTGAGCAGGAGGCGCAGGAGCAGAGCTTCTAACT----- 2880
Db 1220 -----CysThrGlnGluMetGlnAlaAsnTyrSerSerAlaThrAlaThrProSer 1237
OY 2881 CAACGACCTCCACAGGCGCACAAGAAAGTAGACATGTG-----ATG 2919
Db 1238 ProArgProThrTrpArgProGlyGlyAlaAlaArgIleValaAspSerMetPrometPromet 1257
OY 2920 AAACCCCATCTTTCATGATGATACAGGTGATGAA 2955
Db 1258 ArgProProSerGluHisIleTyrHisSerIleGln 1269

RESULT 5
T13887
clr protein - fruit fly (*Drosophila melanogaster*)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13887
R:Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A:Title: Expression of a novel Toll-like gene spans the parasite boundary and contribut
A:Reference number: Z17805; MUID:95151581; PMID:7848870
A:Accession: T13887
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-1385 <CH>
A:Cross-References: UniProt:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383
C:Genetics:
A:Cross-References: FlyBase:FBgn0004364
A>Note: tlr

Alignment Scores:

Pred. No.:	1,08e-18	Length:	1385
Score:	371.50	Matches:	250
Percent Similarity:	35.23%	Conservative:	170
Best Local Similarity:	20.97%	Mismatches:	363
Query Match:	6,25%	Indels:	410
DB:	2	Gaps:	54

US-09-396-985B-5 (1-3395) x TL3887 (1-1385)

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QY      GATGAGAAATCTGACGAAATCCCTCATGACATCCCTATTCAACCAAGACATGATCTG 439
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      154 AspaAsnaHnllleArglnleuProgluGlYvalTtrpCysermetProseleuGlndleu 173
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      440 AGCTTCACACCCCTCGAAGATCTTAAGACGCTATAGCTTCACCAATTC----- 487
Db      174 LeuAsnleuThrGlnAsnArgllleArgserAlgluPheleuGlulPheSerGlulysleu 193
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      488 -----TCACAACTTCAG 499
Db      194 CyvalaglySerAlaleuSerAsnAlaAsnGlyAlaValserGlYglYserGlulndleu 213
QY      500 TGGCTGATTTATTCGACGATGTGTGAATTTGAGACATTTGAACAAGCAGCATGCTGC--- 556
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      214 ThrleuAspValSerPheAsnGluldeuArgserleuProAsp---AlatrpGlyAlaser 232
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      557 ---TTAAACCACTCTCAACCTTGTGACTGACAGAAACCCATCAAGAGTTTTCCTCCA 613
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      223 ArgleuArgArgleuGlnThrleuSerleuGlnHleAsnAsnllleSerThrleuAlapro 252
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      614 GGAAGTTTTCTCGGACCTAACAAATTAGAGAACTGCTGCTGCTGAGACAAATAATGACC 673
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      253 AsnAlaleuAlaleuSerleuArgValleuAsnllleSerTyraAsnHleuVal 272
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      674 TCTCTAGAGGGTTTCCATATTGGACAGCTTATATCTCTTAAGAACTAAATGCGCTCAT 733
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      273 SerleuProserGlulAlaPheAlaleuGlyAsnlyGluldeuArgGluldeuHleuGln 292
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      734 AAT-----CTTAACATTCCTTT----- 751
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      293 AsnAspLeuTyGluldeuProlysglyLeuHleuHleuArgleuGlnGlnleuValleu 312
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      752 -----AAGTTCGCTGAATAT-----TTTCTTAATGTG 778
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      313 AspLeuSerGlyAsnGlnleuThrAspHlnHleValAspAsnSerThrPheAlaleu 332
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      779 ACAAACTTAGAACATGATGATCTTTCTTATACATATCAAACTAT-----TCT 829
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      333 lLeArgleuHleValleuAsnleuSerAsnAsnAlaleuHrArgllleGlySerlyserThr 352
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      830 GTCAAAAGACTTACAGTTTCTACGTGAATAATCCCAAGTCAATCTCTTTTGAAGCTGTCT 889
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      353 PheylsgluldeuPheleuGln-----lLeuAspMetArg 365
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      890 TTAACCCCAATGACTCCATTCAGGCCCAAGCCTTTCAGGGAAT---AGGCTCCATGA 946
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      366 AsnAsnSerllleGlyHlellleGlnGlnGlyAlaPheleuProleuTyraAsnleuHleThr 385
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      947 TTGACTCTAAGAAATAT-----TTTAATAGCTCAAT 979
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      386 LeuAsnleuAlaleuAsnArgleuHleThrleuAspAsnArglllePheAsnGlyleuTyx 405
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      980 GTACTG---AAAATGCTCTTCAAAACATGACTGGTTTACATGCTCCATCGGTTGATCTTG 1036
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      406 ValleuHrlyPheuThrleuAsnAsn-----AsnleuValSerllleValGlu 421
Db      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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QY	1037	GGAGA---TTTAAATGAAAGAAATTTGGAAAGTTTGACCGTCT-----	1081
DB	422	SerGlnAlaPheArgAsnCySerSerAspLeuylSGluLeuSerLeuSerAsnGlnLeu	441
QY	1082	-----GTCAATGGAAGACTATGCAATGTGAGC-----	1108
DB	442	ThrGluValProGluAlaAlaGlnAspLeuSerMetLeuylSThrLeuAspLeuGlyGlu	461
QY	1109	-----ATTGATGAGTTTCAGGTTTAAATATATTAATCATTTTTCAGATGATATTATTAAT	1162
DB	462	AsnGlnIleSerGluPheIys-----	474
QY	1163	CTCAATTGCTTGGCAAAATATTTCTGCAATGTCT-----TTCAAGAGGTGACATATATAAA	1216
DB	475	LeuAsnGlnLeuThrGlyLeuAlaGlyLeuIleAspAsnArgIleGlyAsnIleThrValGly	494
QY	1217	CACATAGACAGATGTTCTTAGGCAATTTCAAAATGGCAATCTTCATGATCATATGATGTCAT	1276
DB	495	MetPheGlnAspLeuProArg-----	506
QY	1277	CTTAAGCCTTTTCCAAAGCTAGTCTACCTTTTCTTAAAGTTGAGCTTTAACTTACACAC	1336
DB	507	-----LeuAlaIaIysAsnArgIleGlnSerIleGluArgGlyAlaPheAspIaIysAsn	523
QY	1337	AGACAG-----	1360
DB	524	ThrGlnIleGluAlaIleArgLeuAspIaIysIaIysPheLeuThrAspIleAsnGlyIlePhe	543
QY	1361	TTGGCTTGGCAAGCTCAGATATCTATATCTTATGTGAAATATGCAATGAGCTTTAGAGGT	1420
DB	544	AlaThrLeuAlaSerLeuLeuThrLeuAsnLeuSerGluAsnIleValaIlePro-----	561
QY	1421	TGCTGTTCTTATTTCTGATTTTGGAAACAACAACCTGAGTACTTACACTTCAGCTTCAT	1480
DB	562	---PheAspIaIysAla---PheIleProSerAsnLeuIaIyStrPheAspIleIleGlyAsn	579
QY	1481	GGTGCATCTCGATGATGTCGCAACTTCATGGGTCTAGAACG-----CTGAAATAC	1531
DB	580	TyrIleGluAlaIaIe---GlyAsnIaIyStrIaIysLeuGlnGluGluIleArgValaIleThr	598
QY	1532	CTGACCTTTCAGCACTCCACTTAAAAAAGTCCACAGAAATCTCAGTGTCTTATCTCT	1591
DB	599	LeuAspAlaSerIleAsnArgIleThrGlnIleGlyAlaMetSerValProAsnSerIle	618
QY	1592	GAATAACTTTTCTTACCTTGACATCTCT-----TACACTATAATCC-----	1630
DB	619	Glu---LeuLeuPheIleAsnAsnAsnIleIleGlyGlnIleGlnAlaAsnIleThrPheVal	637
QY	1631	-----AAATATGACTTTGATGCGCATATTTCTTGCGCTGATCAGTCTC	1672
DB	638	AspIaIySThrArgLeuAlaArgValaIaIaPheLeuIaIaValaIeLeuSerIaIleSerLeu	657
QY	1673	AACACTTTTAAATAGGCT-----	1690
DB	658	AsnAlaLeuArgValaIaIaProValSerIaIaGluIaIyProValProGluPheTyrLeuGly	677
QY	1691	GCGAATTTCTTTTCAAGCAACACCTTTCAATGCTTTTACAAACAACAACAATCTTAAACA	1750
DB	678	GlyAsnProPheGlnCyAspCySerMetGluThrLeuGlnAlaGlyIleAsnAsnLeuThr	697
QY	1751	-----TTCTCGATCTTTTCTTAA-----	1768
DB	698	ThrArgGlnIleProIleValIaIaIaPheLeuGlyAsnIleGluCyLeuMetProIleSer	717
QY	1768	-----	1768
DB	718	ArgSerAlaProLeuArgProLeuAlaSerIleSerAlaSerAspPheValCysIaIyStr	737
QY	1769	-----TGCGAATCTGAAAG-----	1783
DB	738	GluSerHisCyAspProProThrCysHisCysCysGluIaIyGlnGlnCysGluCysGluVala	757
QY	1783	-----	1783

Dd	758	IlEcyvBrpoclYamvSvserCyvBrneniAvsrrAlathTrrAlathpnaenlleValasr	777
Qy	1784	-----ATAATCAAGGGGATATTGACACA	1807
Dd	778	CysglYatrglnBrvleuValalaleuProdanhgllelrrpoglmerValSerAsr---	796
Qy	1808	STSPAC-----	1813
Dd	797	LeutYrteuAsvrglYuaenAmelProglYleuGlYValGlYnlVleuthrglYatrgY	816
Qy	1814	AGATSSCAAGTATAAACAATGAGACACAACAACSTAGTCTTTGTCGATCCATGCAATTAAT	1873
Dd	817	AsmleuYrGlaleuYrGlaleuAsnAlaserAsmleuMetThrlleuGlInanpInglYserleu	836
Qy	1874	AAACAGSTGTACTCCSTCAGAGACTSTGTATGCAAGTTTCAATCGCATAGACAATCCAA	1933
Dd	837	AlaGlInleuValAsmleuYatrgValleuNlVleuGlYamYnleuYleuThrlalaleuGl	856
Qy	1934	GGA-----ATPCTG	1942
Dd	857	GlYthrglYphearGserleuGlYleuYleuAtrgGlYleuYrGlYenlVlaenAmleu	876
Qy	1943	CAACATTTTCCAAAG-----AGCTACGGCGTTCAATGTCACT	1981
Dd	877	ThrllelleserAnalathrPheglYrYoleuValSerleuGlYValleuAtrgYleuAsr	896
Qy	1982	AAATATTTCTGT-----	1993
Dd	897	AsmYnBrYleuSerleuSerleuProhlyleuGlYthrghtlsserleuGlInglYleuThr	916
Qy	1994	-----GCTGTATATGT--CAATATACAAATTTCTTGACGTGGCT	2032
Dd	917	LeuGlYatrgAnalatrSerCyatrgCyuglInglInleuYatrgleuYalaglInPheVal	936
Qy	2033	AAAGACCAAGAAATGTTCTTGTCGATGCAATGTTGAACAAATGAAATGTGCA---TCAACCATAT	2089
Dd	937	SerAsrAnalMetValValAtrgAsrAnlAnleAsrPrlleYrCyvleuAsrAlaglYle	956
Qy	2090	GACATGAAGGCTCCCTGCTGTGTGATTTGACATGCTCC---ACSTGT-----	2134
Dd	957	LyatrgGlYleuGlYleuGlleGlYAsmleuYalAsnGlYrProAsrCyvsserAsrleuYleu	976
Qy	2135	-----TATATATCAAG	2146
Dd	977	AsrAlaserAlaserenlleSerSerSerGlInAsrleuYalaglYglYtYatrgYleuPro	996
Qy	2147	ACTATCACTAGTATAGCGTGGTACAGTGTCTTGCTGTAACCACTAGACATTTCTGATA	2206
Dd	997	LeuYleuAlalaleuValleuValleuPheleuYasrValleuYleuIleValPheVal	1016
Qy	2207	TACCACTTCTATTTTCACTGATCTTATGCTGTC-----TGTAAC---	2248
Dd	1017	PhearGgluSerValatrgMetTrPleuPheAlathlstrYglYValatrgYalCyvgluPro	1036
Qy	2249	AAATACACAGAGAGAGAAAGCATGTATGATGCAATTTGTGATCTATGACACCAATGAG	2308
Dd	1037	AtrgPheglYasrAlaglYleuYleuYatrgAlatlelleuYnlsSerGlYleuAsrYrY	1056
Qy	2309	GACTGGGTGAGAAACAGACSTGTAAADAATTTGAAAGAGAGTGGCCCGCTTCACTT	2368
Dd	1057	GlYpHeValCyvatrgAnlleAlalaglYleuYnlsVglYatrgProProPheAsrGleu	1076
Qy	2369	TGCGTCAATTAACAGAGACTTATGCTCGTGGTACCAATTTGGTGCACATCATCAAG---	2425
Dd	1077	CyslleGlInglInatrgAsrleuProPro-----GlInAsrAnlVleuGlInleu	1092
Qy	2426	---AAGCGTTCACAGAGGCGGAGAAATTAATGTGGTGGTGTCTAGACATTTATCAAG	2482
Dd	1093	ValGlInglYalAatrgAlaserAtrgYleuIlelleuValleuThrlAtrgAnleuYleuAla	1112
Qy	2483	AGCGGTGTGTATCTTGAATATGAAATGCTCAGACATGCGACGTTTCTGATGAGCGGC	2542

Db 1113 ThrGIuTPraAnAGllleGIuPheArgSbnla-----PhehIGluSerIeu 1128
OY 2543 TCTGGCATCATC-----TTCATGTCTCTGAGAA----- 2572
Db 1129 ArgGIyleuAlaGlnIuLeuValIlelleGIuGluThrSerValSerAlaGluAla 1148
OY 2573 -----GTGGAGAAGTCTTTCGTAGGAGCAGCAGCAATGTATCGGCTTCTTAGCAGA 2626
Db 1149 AspValAlaGluLeuSerProTyrLeuysSerValProSerAsnArgLeuIthCys 1168
OY 2627 AACACCTTACCTCCAGAGTGAGAGACATATGCTGTGGGAGGCACATCTTCTGGAGAACTC 2686
Db 1169 AsnArgTyr-----PheTrpGluIuLeu 1176
OY 2687 AAAAAAGCCCTGTGGATGAGAAAGCCTTGATTCAGATGAACATCA----- 2734
Db 1177 ArgTyrAlaIle-----ProIleGluLeuSerProArgGlyAsn 1189
OY 2735 -----GAGAAAGAACAAAGACAAACAACTTGACTTGAGAGTA----- 2773
Db 1190 AsnTyrThrIleuAspHisHleGluArgPheIuysGlnProValSerProGlyMetIlePhe 1209
OY 2774 ---CAAACCTCGGCGCTTAAACCCATTAATGTTCATATTCGCCAATCTACAGTTATC 2830
Db 1210 ArgGlnAlaProProProProAlaTyr----- 1219
OY 2831 TGGTTTCTGTGTGTGACAGAGGAGGCCAGGAGCAGAGCTTAACT----- 2880
Db 1220 -----CysThrGluGluMetGlnAlaAsnTyrSerSerAlaThrAlaThrProser 1237
OY 2881 CAAGCACTTCACAGGCGCACAGGAAGTAGCAATGTG-----ATG 2919
Db 1238 ProArgProThrArgProGlyAlaAlaIaArgIleValaIaerMetPromePomet 1257
OY 2920 AACCCTTACCTTCATGTATCAGGTATGAA 2955
Db 1258 ArgProProSerGluHisIleTyrHisSerIleGlu 1269

RESULT 6
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: photoreceptor cell-specific membrane protein
C/Species: Drosophila melanogaster
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29944; A21123
R/Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A/Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell
A/Reference number: A29944; MUID:88135762; PMID:3124963
A/Accession: A29944
A/Molecule type: DNA
A/Residues: 1-1134 <REI>
R/Zipursky, S.L.; Venkatesh, T.R.; Teplov, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A/Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecular
A/Reference number: A21123; MUID:84106810; PMID:6420071
A/Accession: A21123
A/Molecule type: protein
A/Residues: 31-43,'HX','46-49','H' <ZIP>
C/Genetics:
A/Gene: FlyBase:chp
A/Cross-references: FlyBase:FBgn0000313
A/Intons: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C/Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C/Keywords: cell adhesion; glycoprotein; membrane protein
F/1-29/Domains: signal sequence #status predicted <SIG>
F/30-1134/Product: chaoptin #status predicted <MNT>
F/80-102/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F/103-126/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
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F.903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
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F.949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
F.973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F.996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F.1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F.1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Alignment Scores:
Pred. No.: 5.65e-16 Length: 1134
Score: 333.50 Matches: 172
Percent Similarity: 37.42% Conservative: 112
Best Local Similarity: 22.66% Mismatches: 244
Query Match: 5.61% Indels: 231
Dns: 1 Gaps: 28

US-09-396-985B-5 (1-33395) x A29944 (1-1134)

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QY   CTAATATTCCCAACGATGCATGCATGCAGATCTCACCAAAATCCCTCATGACATCCCTT    416
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DB   132 LeuileLeupProGlmsnspbleuValGIuileProserilLeuAry-His-Leug    151
      :::::|||||
QY   ATTCAACCAGAACAACCTGATCTGAGCTTCACACCCCCTGAAGATCTTTAAGAAGCTATAGCT  476
      ::::::|||||
DB   151 IntyleleuarightsleuabpbleuGIyTyrrahnhisilethrhisilelnhisabpserP  171
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QY   477 TCACCAATTT--TCACAATTCACTGAGTGCTGTGATTTATCCAGGCTGTGAAAATTGAGACA  533
      |||||
DB   171 heArgglyleuengluaabpserleuGIInthrleuileuArygluaAnCysIleserGIInL  191
      |||||
QY   TTGAAGACAGACGATCGCATGCGCTTTAAACCAAGCTCTTAACCTTGATGGTACTGACAGAAACC  593
      ::::::
DB   191 eueMseSerhisserPheserGIyleuileuileuGIIntlrhleuaspreserGIyaAna    211
      ::::::
QY   CTATCAAGATTTTTCCCAAGAAAGTTTT--TCTGACCTTAACAAATTTAGAGATCTGG        650
      ::|||
DB   211 enleupeheglulileapProhevalpheValabpGIymetProArxgleuthraAgbleu    231
      ::|||
QY   TGCGTGTGAGACAAATAATGACCTCTTAGAGGGGTTCATATTGACAGCGTTATATACCT       710
      ::::::
DB   231 euletheThrapenlileuaserGIuileProTyraPalaleuGIyProleuNysSerL     251
      ::::::
QY   TTAAGAACTAAATGCGCTCATATCTTTATACATTCCTTTAAAGTGGCTGCAATATTTT-      769
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DB   251 euarTyThrleaspliserHisasnValletlpresleuaserGIyasngluNhryrg 271
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OY	770	-----TCGAATGCAAAAGCTTAAGAACTGAGATCTTTCTATACATATATTC	818
Db	271	lulielysalaSerThrllybLeuasnleuApsanleuHlsleuGluYrtrsnHslleg	291
OY	819	AAACATATTTCTGTGCAAAAGACTTAACAGTTTCTACGTAAGAAATCCCAAGTCAATCTCTCT	878
Db	291	luvalleuProProasnSerPheUlytrPhe-----AspThrValasnHrghtrP	308
OY	879	TAGACCTGTCTTTAAACCCAAATGACTTCATTTCAAGCCCAAGCCCTTCAGGAAATTAGGC	938
Db	308	he----PheAspGlyAsnProIlenHstrHleuAUGluAAspAlaPheUlysrProAlaArgI	327
OY	939	TCCATGAATGACTCTAAGA-----	959
Db	327	leargGluHleUryrMetArgYrCySgUlyleuthrAsnHlsSerProValaAAspAsps	347
OY	960	GTAATTTTAAATAGCTCAAAATGTACTAGAAATGTGCTTCAAAACATGACTGGTTTACATG	1019
Db	347	erleuValaAsnSerleuGlnHleuAAspLeuSerGlyAsnAsnleuHrlyrUlysnHls	366
OY	1020	TCCATCGGTTG-----ATCTTG-----	1043
Db	367	--HAsUlysrPheAsnAsnAAspAAspValleuAUGValHlsSerMetArgAspAsnUlysrI	386
OY	1044	TTAAAAATGAAGAAAGACTGGAAGATTTTGAACCGTTCTGTGATGGAAGAAAGATTCATG	1103
Db	386	IelysHleGlnHlysrProHrghtrGlnHrPheAsn--AlaValHlsUryrHrHleuUlysrL	405
OY	1104	TGACCATGTAGATGACTGAGTTTAACATATATTAATCATTTTCAAGATATATTTATATC	1163
Db	405	euAAspLeuSerGlyAspArg-----AsnAspProHrAsnL	417
OY	1164	TCAATTTGCTGGCAAAATATTTCTGCAATG---TCCTTCAACAGGTGTACATTTAAACACA	1220
Db	417	eugHnHrHleuAArgAsnMetHrArgMetHrArgAsnMetArgAsnMetArgSerUlysrHsl	437
OY	1221	TAGCAAGATGT-----CTTAGCACTTTCAAA-----	1256
Db	437	eugUlysrSerSerValGlyProGluAAspPheUlysrPheGlyValGluUeuGluAAspL	457
OY	1257	TATCATATCATTAAGATG-----	1283
Db	457	eugHnHleHrHrArgAlaSerUlysrGlyHleGlnSerHlsAlaPheUlysrHslValaUGG	477
OY	1284	CTTTTCCAAAGCTGAGTCTACCTTTTCTTAAAGTGGACTTAACTACCAACAGAGAGG	1343
Db	477	lyleuUlysrArgleuAAspPhe-----SerGluAAsnGlyHleSerSerHleGluA	493
OY	1344	ATATCAGCTTTGGTCAAGTTG-----	1363
Db	493	snAspAlaPheHlsleGluHleGlyHlsSerUlysrUlysrMetSerHlsleGlyUlysr	513
OY	1364	-----GCTCTGCA-----	1399
Db	513	erGlySerAlaUeuProAlaGluProleuAUGHlsUlysrHrSerUeuGlnGluUeuAAspR	533
OY	1392	TTAGTAGAAATGSCATGAGCTTTAGAGTGTGCTTTTATTTCTGATTTT	1441
Db	533	heserAAsnAsnHlsHlsSerSerMetSerAAspHrSerPheHlsrPheUlysrAAsnUeuA	553
OY	1442	-----GGAAACA-----	1444
Db	553	rgleuUeuGluUeuHlsAAspAAsnArgHleGluGlnValleuUlysrGlyHrPheGlnGlyA	573
OY	1448	-----AACAACTGGAAGTCTTGAAGCTTCAAGCTTCAATGATGATGCTTCCGATGAGTG	1499
Db	573	srHleHlsSerUlysrUeuGlnGluUlysrUlysrUeuAArgPheAsnHlsUlysrHrSerHlsSerG	593
OY	1500	CCAAC-----	1504
Db	593	lnHlsHrPheAAspUeuGlnUlysrAlaUeuArgUlysrUlysrUlysrAAspAAsnUlysrIleA	613

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Db 613 sPLySIlleGluYArGArGAlaPheMetAsnIleuAspGluIleuGluYrIleuSerIleuAspG 633
QY 1545 ACTGCACCTTTAAAGGCAAGAAATTCAGGTGCTTATCTCTTGAAGAACTT----- 1600
Db 633 IyAsnIleuYrIleAsnIleuAlaAspGluSer--PheGlnAsnIleuProIySleuGluI 652
QY 1600 ----- 1600
Db 652 IeIeuAspMeAlaPheAsnGlnIleuProAsnPheAsnIleuAspGlyrPheAspGlnValG 672
QY 1600 ----- 1600
Db 672 IyThrIleuSerAsnIleuAsnValAsnValSerHisAsnGlnIleuArgGlnIleuMetGlyrA 692
QY 1601 -----CTTAC-----C 1607
Db 692 snSerSerTrpSerGluYrGAsnGlnIHisGlyIleuMetGlyrHisSerAsnIleuSleIel 712
QY 1608 TTGACATCTCTTACACCTTAATACCAAAATGACTTTGATGGCAATTTCTT---GGCTTGA 1664
Db 712 euaSpleuSerHisAsnAsnIleSerIleIeHisProGluYrPheAspProAlaGluI 732
QY 1665 TCAGTCTCAACACTTTAAATAGCGCTGGCAATCTTTCAAGACAAACCCCTTCAATG 1724
Db 732 IeSerIleuThrHisIleuHisIleuGluYrAsnSerIleuMet--AsnThrThrArgAspV 751
QY 1725 TCTTTACAAACCAACAAACTTAACACTTCCTGGATCTTTCTAAATGCCAATGGAAACGA 1784
Db 751 alPheGlyAsnMetProHisIleuGlnIleuTrpLeuAspIleuSerGlyrAsnTrpIleHisGluI 771
QY 1785 TATCTAGGGGGGATTTTGGACACACTCTACAGACTCCAGTATTAACATGAGTCACACA 1844
Db 771 euaSpleuAspAlaPheIyAsnIleuThrIyGlnIleuGlnIleuValPhePheGlyHisAsnT 791
QY 1845 ACCTACCTGTTTCTGGATCCATCCCATTTAAACAGCTGACTCCCTCAGACTCTTGATT 1904
Db 791 yIleuSerAspIleProGlnAspIlePheIyAspProValGlnGlyIleuArgIleValAspR 811
QY 1905 GCAGTTTCAT-----C 1916
Db 811 heSerHisAsnHisIyAsnArgIyIleuProAspAsnIleuPheYrAsnGlyIleuMetGluI 831
QY 1917 GCATAGAGACTCCAAAGCAATAGTCAACACTTTTCCAAAGACT----- 1960
Db 831 ySleuAspValSerHisAsnMetMetIleuYrIleProSerSerIleuSerSerIleuA 851
QY 1961 -----CTAGCCGCTTTCATCTGACTAATAATATCTGTGCTGTATA 2002
Db 851 IaAlaIleuThrIleuCysGluIleuHisIleuSerAsnAsnPheIleSerThrIle 868

RESULT 7
T15864
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C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15864
R:Fulcom, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of *C. elegans* cosmid C56B6.
A:Reference number: S69019
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A:Status: preliminary; translated from GB/EMBL/DDBL
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A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:G1055114; PID:G1055120; PIDN:AAA810;
C:Genetics:
A:Gene: CESP:C56B6.6
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Pred. No.: 1

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Query Match:	5.11%	Indels:	13
DB:	2	Gaps:	26

US-09-396-985B-5 (1-3395) X T15864 (1-1066)

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Oy	296	ATGGCATTTGCTCTTCCGTGGCCGTGAGACGAGAACCTTG	337
Db	87	ThrgIuIleGlnIlyMetSerLeu---ProGlnIthrLeuIlyPheLeuValIleuArgShn	105
Oy	338	CCCTGCATAGAGGTACTCTTCATAATTT	379
Db	106	AsnLeuLeuThrGlnIleProTyrValAlaLeuAsnAspLeuIlyPheThrLeuGlnSerIle	125
Oy	380	GATCGAGATCTTCAGCAAAATCCCTCAT	421
Db	126	AspLeuGlnIlyGlyAsnAsnIleThrIhIleuMetAspThrAsnGlnIValIthrPheGlnSer	145
Oy	422	ACCAAGAACTAGATCTGAGCTTCAACCCCTGGAAGACTCTTAAAGACTATAGCTTCAAC	481
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Oy	482	AATTTCTCAACAATTCACTGAGCTGGATTTATCTACAGGTGAAATTTGAGCAATTTGAAGC	541
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Oy	662	ACAAATATGACCTCTCTAGAGGTTTCCATATGTGACAGCTTATATCTTAAAGAACTA	721
Db	218	-----ThreIuIlyShThrIeu	222
Oy	722	AATGAGCTCAATCTTATACATTCCTTTAAGTTGCGCGAATATTTTCTAATGCA	781
Db	223	LysIleuAlaGlnAsnMetIleIhIAla-----ThrProGlnAlaIleuArgSerIeuArg	240
Oy	782	AACCTAGAACATGTGATCTTCTTATATACATATTTCAAACTATTTCTGTCAAAAGACTTA	841
Db	241	AsnIleuThrIhIleuAsnIleuAsnIleuAsnIlyAsnIlyIle-----AspGly	257
Oy	842	CAGTTTCTAGCTGAAATCCCAAGTCAATCTCTCTTAAAGCTGTCTTTAAACCAATT	901
Db	258	AspValIleuIlySgIlyCyAsThrAspThrIleuValGlnIleuPheIleAlaAsnIlyThrIeu	277
Oy	902	GATCTTCATTAAGCCCAAGACCTTTCAGGAAATTAG---CTCCAGATATGATGCTCAAG	958
Db	278	GlnIshIleProIhIshIlyValIleuSerGlyMetIlySgIleuGlnIhIleuAspIleSer	297
Oy	959	AGTAATTTTAATAGCTCAATAGTACTGAAATGTGCTTCAAAACATGACTGGTTTA	1015
Db	298	LysAsn-----LysIleMetSerIleuIlyProThrSerIleu	311
Oy	1016	-----CATGTCCATCGGTGATCTTG-----GGAAGATTT	1044
Db	312	SerIleThrIlySgIlnIlyThrSerThrValArgArgLeuAsnIleuAlaGlyAsnArgIle	331
Oy	1046	AAAAATGAAGAACTGGAAGAAATTTTGAACCGTTCTGCATGGAAGAACTATGACATGTG	1105
Db	332	AsnAsnMetSerAspTyrIleuIlePheGlnIhIshetProIleuLeuThrTyrValAspVal	351
Oy	1106	AGCATTTAGAGTTCAAGTTAACATATATAAATCATTTTTCAGATGATATTTATATATCTC	1165

Db	352	SerPheAsnArgIleArgPheIleSerProArgValPheGluIys-----	366
Db	1166	AATGTCCTGGGCAAAATATTTCTGCAAGCTCTTTCACAGGTGACATATATAACACATAGCA	1225
Db	367	-----LeuYsAlenLeuGluSerLeuPheLeuGlnAsnGlnIleuAlaIHisPhePro	384
Qy	1226	GATGTTCTTAGACATTTTCAAAATGGCAATCCTTATCATCATTTAGATGTCATCTTAAGCCT	1285
Db	385	SerLeuPheArgLeuAspIysLeuArgIleValMetLeuAspAsnGlnIleGlnIys	404
Qy	1286	TTTCCAAAGCTGAGT-----CTACCTTTTCTTAAAGTTGACCTTTTAATCAACAC	1336
Db	405	IleAspAsnPheSerLeuAlaAspLeuProIysLeuGlnIHisLeuSerLeuAlaGlyAsn	424
Qy	1337	AGAGAGATATC-----AGCTTTGGTCAGTTGGCTGTCGCCAAGCTCAGATAT	1384
Db	425	GlnIleuAspIleIleIleThnGlnAsnMetPheGlySerSerSerSerGlnIleuIysSer	444
Qy	1385	CTGATCTTAGTGAATAATGCCATGACCTTTAGAGGTGTCTGTCTTATCTGATTTTGA	1444
Db	445	LeuAsnLeuAlaHisLeuIysIleHisSerIleSerSerArgSerPheSerAspLeu---	463
Qy	1445	ACAAACAACCTGGAAGTACTTAGACCTCAGCTTCATGTGTGC---ATCTGATGAGTGC	1501
Db	464	--AspAsnLeuGlnGlnIleuArgLeuSerHisAsnAsnIleArgThrIleThrsMet	482
Qy	1502	AACCTTCATGGGTCTAGAAAGCTGGAATACCTGGACCTTTCAGACCTCCACCTTAAAAAG	1561
Db	483	ThrPheSerAsnLeuAspGlnAsnLeuArgItyIleuAspLeuSerHisAsnArgIleIleIys	502
Qy	1562	GTCACAGAAATCTCAGGTGTC---TTATCTCTTGAAAACTTCTTACCTTGACATCTCT	1618
Db	503	IleLeuProSerAlaIleuItyGlnIleuProAlaIleuAspValIleuHisLeuAspHisAsn	522
Qy	1619	TACATTAATACCAAAATTTGACTTTTGATGCGCATATTTCTGGCTTGATGACTCAACACT	1678
Db	523	AsnLeuAsn---GlnIleAspArgAspAla---PheArgSerPheSerAspLeuGlnSer	540
Qy	1679	TTAAAAATGGCTGGCAATCTTTTCAAA-----	1705
Db	541	LeuIysLeuSerHisAsnAlaPheArgArgPheSerCysGlnPheLeuGlySerIleSer	560
Qy	1706	-----GACACACCCCTTCA-----AATGCTTTACAAC	1735
Db	561	GlnValHisGlnLeuAspLeuSerSerAsnGlnIleAsnGlnIleAspIlePheCysIle	580
Qy	1736	ACAAACAACCTTAACATTCCTGGAATCTTTTAAATGCCAATGCAATGCAAGATTTCTAGGGG	1795
Db	581	AlaArgGlyIleArgIysLeuSerLeuAlaSerAsnSerValGluIysIleAsnArgIys	600
Qy	1796	GTAATTGACACACCTTCACAGCTCCAGTTTAAACATGATGATCAACACCTCTGTT	1855
Db	601	LeuLeuGlnAspAlaIleThnGlnIleThsSerIleAspIleSerHisAsnGlyIleIleSer	620
Qy	1856	CTGATCCATCCCTTAATTAACAGCTGACTCCCTCAGAGACTCTTGATTTGACGTTTCAAT	1915
Db	621	ValAspSerAspAlaPheCysGlnCysArgIysLeuSerHisIleIysLeuSerHisAsn	640
Qy	1916	CGCATAGACATCCAAAGAGATATCTGCAACATTTTCCAAAGAGCTTACCCGCTTCAAT	1975
Db	641	TyrIleArg-----	Asn 644
Qy	1976	CTGACTAATATATCTGTGCTGTGTATATGTGAATATGCAATTTCTTGACGTGGTCAAG	2035
Db	645	LeuItyIysGlyIleThsArgValCysIle-----ProIleIleSer	657
Qy	2036	GACCAAGAAATGTTCTTGATG-----AATGTGAACAATGAATGATGCAATCA	2083
Db	658	HisLeuThrThrPheCysPhePheIleThsGlnHisLeuGlnIleSerPheSer	677
Qy	2084	CTTATAGACATGAAGGCTCCCTGCTGTGATTTTACGAAT	2125


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QY      1612 CATCTTACACATAACAAATTGACTTGTGATGSCATTTCTTGCTTGATCACTCT 1671
Db      368 nleuSerGlyAsnCySleuArgAsnLeuProGluGlnValPheArgGlyLeuGlyLys 388
QY      1672 CAACACTTTAAATAATGGCTGCAATTCCT 1699
Db      388 whiSerLeuHisLeuGluGlySerCySleuGlyArgIleArgProHisLeuPheIleGlu 408
QY      1700 -----TTCAAGACCAACCTTTCAAATGTC----- 1726
Db      408 yLeuSerGlyLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGluGlu 428
QY      1727 -----TTTAAACAAACCAACCAACTTAACATTCCTGATCTTTCTAAAGCCACGAGAAC 1782
Db      428 nSerLeuTrpGlyLeuAlaGluLeuLeuGlnLeuAspLeuThrSerAsnGlnLeuThrHi 448
QY      1783 GATATCTAGGGGGTATTTGACACACTCTACAGACTCCAGTTATTAAACATGATGACAA 1842
Db      448 sLeuProHisGlnLeuPheGlnGlyLeuGlyLysLeuGlnLysLeuLeuLeuSerHisAs 468
QY      1843 CAACCTACTGTTTGTGATCCATCCCATTTATAACAGCTGATCTCCCTCAGACTTTGA 1902
Db      468 nArgLeuAlaGluLeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAs 488
QY      1903 TTGCACTTCAATCGACATAGACATCCAAAGAAATACCTGCAATTTTCCAAAGACTCT 1962
Db      488 pValSerHisAsnArgLeuGlnAlaLeuProGlySerLeuLeuAlaSerLeuGlyArgLe 508
QY      1963 AGCCGCTTCAATCTGACTTAATATCTGTTGCTGTATATGATAATACGAATTTCTT 2022
Db      508 uArgTyLeuLeuLeuArgAsnSerLeuArgThrPheThrProGlnProProGlyLe 528
QY      2023 GCAG-----TGGGTCAAGAGCCAGAAATATCTTGTGATGTTGAACAATGAAT 2076
Db      528 uGlnArgLeuTrpLeuGluGly-----AsnProTrpAspCy 540
QY      2077 TGCATCACTTATAGAC-----ATGAAGCCCTCCCGGTGGA 2115
Db      540 sSerCyProLeuValAlaLeuArgAspPheAlaLeuGlnAsnProSerAlaValProAr 560
QY      2116 TTTTACGAATCCACTGCT-----TATATATCAAGAC 2148
Db      560 gPheValGlnIleAlaLeuCySgluGlyAspAspCyGlnProValTyTrpTrpAsnAs 580
QY      2149 TATCATCAGTGTATCG 2164
Db      580 nIleThrCyAlaSer 585

RESULT 10
T10504
disease resistance protein Cf-2.1 - currant tomato
C/Species: Lycopersicon pimpinellifolium (currant tomato)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10504; T10515
R/Dixon: M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A/Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
A/Reference number: Z17062; MUID:96190812; PMID:8608599
A/Accession: T10504
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1112 <DIX>
A/Cross-references: UNIPROT:Q41397, EMBL:U42444; NID:g1184074; PIDN:AACT5779.1; PID:g118
A/Experimental source: cultivar Cf 2
A/Accession: T10515
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1066, '1', 1068-1085, 'E', 1087-1110, 'R', 1112 <DIX>
A/Cross-references: EMBL:U42445; NID:g1184076; PIDN:AACT5780.1; PID:g1184077
A/Experimental source: cultivar Cf 2

Alignment Scores:

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Pred. No.:	3,91e-13	Length:	1112
Score:	294.00	Matches:	185
Percent Similarity:	35.43%	Conservative:	108
Best Local Similarity:	22.37%	Mismatches:	270
Query Match:	4.95%	Indels:	264
DB:	2	Gaps:	32

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US-09-396-985b-5 (1-3395) x T10504 (1-1112)

QY      326 GGAAGCTTGAAATCCCTGCATAGAGGTATCTCTAATATTAAC-----TACCAATGATG 379
Db      397 GlySerIleProAlaSerLeuGlyAsnLeuAsnLeuSerArgLeuTyLeuTyAsn 416
QY      380 GATCAGAAATCTGCAAAATCCCTCAATGACCTCTAT-----TCAACCAAGAACCTTA 433
Db      417 AsnGlnLeuSerGlySerIleProGluGluIleGlyTyLeuSerSerLeuTrpTyLeu 436
QY      434 GATCTGAGCTTCAACCCCTGAAGATCTTAAAGAGTATAGCTTCAACCAATTTCTGACAA 493
Db      437 AspLeuSerHisAsnSerIleAsnGlyPheIleProAlaSerPheGlyAsnMetSerAsn 456
QY      494 CTTCAGTGGCTGATTTATTCAGAGGTGAATTAAGCAATTAAGCAACCAAGCATGGCAT 553
Db      457 LeuAlaPheLeuPheLeuTyArgIleAsnGlnLeuAlaSerSerValProGluGluIleGly 476
QY      554 GGCTTAAACCAAGCTCTCAACCTTGATAGTACAGAAACCTTACAAAGATTTTCCCA 613
Db      477 TyLeuArgSerLeuAsnValLeuAspLeuSerGlnAsnAlaLeuAsnGlySerIlePro 496
QY      614 GGAAGTTTCTGAGCTTAACAAATTAAGAAATCTGAGCTGTGAGACAAAGATGACC 673
Db      497 AlaSerPheGlyAsnLeuAsnLeuSerArgLeuAsnLeuValAsnAsnGlnLeuSer 516
QY      674 TCTCTAGAGGTTCCATATATGACAGACTTATATCTTAAAGAAATTAATGTGGCTCAT 733
Db      517 GlySerIleProGluGluIleGlyTyLeuArgSerLeuAsnValLeuAspLeuSerGlu 536
QY      734 AATCTTATACATCCCTTAAAGTCCGGAATATTTTCTAATGACCAACATGACAT 793
Db      537 AsnAlaLeuAsnGly---SerIleProAlaSerPheGlyAsnLeuAsnLeuSerArg 555
QY      794 GTGATCTTCTTATATACATATTAACAACATATTTCTGCAAGACTTACAGTTTCACT 853
Db      556 LeuAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIleGlyTyLeuArg 575
QY      854 GAAATCCCAAGTCAATCTCTCT----- 877
Db      576 SerLeuAsnAspLeuGlyLeuSerGluAsnAlaLeuAsnGlySerIleProAlaSerLeu 595
QY      877 ----- 877
Db      596 GlyAsnLeuAsnAsnLeuSerMetLeuTyLeuTyAsnAsnGlnLeuSerGlySerIle 615
QY      878 -----TTAGACCTGTCTTTAAACCAATT 901
Db      616 ProGluGluIleGlyTyLeuSerSerLeuThrTyLeuSerLeuGlyAsnAsnSerLeu 635
QY      902 GACTCCATTCAAGCCCAAGCTTTCAAGGGAATTAG---CTCATGAATGACTCTTACGA 958
Db      636 AsnGlyLeuIleProAlaSerPheGlyAsnMetArgAsnLeuGlnAlaLeuIleLeuAsn 655
QY      959 AGT-----AATTTTAATAGCTCAAAATGTA 982
Db      656 AspAsnAsnLeuIleGlyIleProSerSerValCyAsnLeuThrSerLeuGluVal 675
QY      983 CTGAAATG-----TGCTTCAAAACATGACT 1009
Db      676 LeuTyMetProArgAsnAsnLeuLysGlyLeuValProGlnCySleuGlyAsnIleSer 695
QY      1010 GGTTCATGTCATCGCTGATCTTGGGGAATTTAAATGAA----- 1054
Db      696 AsnLeuGlnValLeuSerMetSerSerAsnSerPheSerGlyIleLeuProSerSerIle 715

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QY	1055	AGGATCTGGAAGC-----TTGACGGTTCGTGACGAAGCACTA----	1096
Db	716	SerSsnLeuThrSerLeuGlnIleLeuAspPheGlyArgAsnAsnLeuGluGlyAlaIle	735
QY	1097	-----TGC-----AATGAGCACTTGATGAGTTCAGGTTTAACTATATATATCATTTT	1144
Db	736	ProGlnGlyPheGlyAsnIleSerSerLeuGluValPheAspMetGlnAsnAsnLysLeu	755
QY	1145	TCAGATGATATT-----TATATCTCAATTGCTCTGGCAATATATTTCTGCAGATGCTCT	1195
Db	756	SerGlyThrLeuProThrAsnPheSerIleGlyCys-----SerLeuIleSerLeuAsn	773
QY	1196	TTCCAGCGTGTACATATAAACAACATACCAAGATGTTCTCTAGGCATTTCC-----	1243
Db	774	LeuHISgLYaSnGlnLeuGlnAsp-----GluIleProArgSerLeuAspAsnCysLys	791
QY	1244	AAATGGCAATCCTTATCATCATATTAGATGTCATCTTAAG-----CCTTTTCCAAAGCTG---	1297
Db	792	LysLeuGlnValLeuAspLeuGlyAspAsnGlnLeuAsnAspThrPheProMetCysLeu	811
QY	1298	---AGCTACCTTTTCTTAAAGTTGACCTTAACTTACCAACAGAGAGAT-----	1345
Db	812	GlyThrLeuProGlnLeuArgValLeuArgLeuThrSerAsnLysLeuHISgLYProIle	831
QY	1346	---ATCAGCTTTGGTGCATGTGGCTTGGCAAGCTGCAGATATCTTGATCTTAGTGAAT	1402
Db	832	ArgSerSerArgAlaGlnIleMetPheProAspLeuArgIleIleAspLeuSerArgAsn	851
QY	1403	GCCATGACCTTTAGAGGTGTGCTTTCTATCTGATTTTGGAAACAACAACCTGAAGTAC	1462
Db	852	AlaPheSer-----GlnAspLeuProThrSerLeuPheGluHis	864
QY	1463	TTAGACCTCAGCTTCATGGTGTCTACCTGTAGAGTGGCAACTTCATGGGCTTAGAAG	1522
Db	865	Leu-----LysGlyMetArgThrValAspLysThr-----MetGluGln	877
QY	1523	CTGGAATACCTGAGACTTTCAGACATCTCCACTTTAAAAAGGTACAGAAATTCACAGTTC	1583
Db	878	ProSerTyrgLysSerTyrrAspAspSerValValValThrLys-----	893
QY	1583	TTATCTCTTGAACAACTCTTACTTACCTGACATCTCTACATATATACAAATATGACTTT	1642
Db	893	-----	893
QY	1643	GATGGCATATTTCTTGCTGTGATCTGATCTCAACACTTTAAAAATGGCTGGCAATTTCTTTC	1702
Db	894	---GlyLeuGlnLeuGlnIleValArgIleLeuSerLeu-----	905
QY	1703	AAAGCAACAACCCTTTCAAAATGCTTTTACAAACAACAACAACAACTTACATTCCTGACTTT	1762
Db	906	-----TyrThrValIleAspLeu	911
QY	1763	TTCTAATGCCAATCGAACAAGATATCTAGGGGGGATTTGACACACTTCACAGATCTCAG	1822
Db	912	SerSerAsnLysPheGlnGlyHisIleProSerValLeuGlyAspLeuIleAlaIleArg	931
QY	1823	TTATTTAAACAGAGTCACAACAACCTTACTGTCTTCAGATCTCCATTTATTAACAGCTTG	1882
Db	932	IleLeuAsnValSerHisAsnAlaLeuGlnGlyTyrIleProSerSerLeuGlySerLeu	951
QY	1883	TACTCCCTCAGAGACTCTTGATTTGACAGTTTCAATGCGCATAGAGACATCCAAAGAAATACTG	1942
Db	952	SerIleLeuGlnJusSerLeuAspLeuSerPheAsnGlnLeuSer-----	965
QY	1943	CAACATTTTCCAAAGAGTCTAGCC-----GCTTCAATCTAGCTAAT	1988
Db	966	GlyGlnIleProGlnGlnLeuAlaSerLeuThrPheLeuGlnPheLeuAsnLeuSerHis	985
QY	1985	AATCTGTGCTTGATATGTGATAATATCAAGATTTCTTCCAGTGGGTGACAGACCAAGAAA	2044
Db	986	Asn-----TyrLeuGln-GlyCys-IleProGlnGlyProGlnP	998
QY	2045	ATGTTCTTGTCGATATGTGAACAAATGAATATGTCATCACTATAGACATGAAGGCTTCC	2104

Db	998	heargThrPheIu-----SerAasSerTyrgIuGlyAana	1010
Qy	2105	CTGGTGTGGATTTC-----	2121
Db	1010	spgIyIeuaArgIyTyPrProValSerIyGlyCyGlyLysAppProValSerGIuLYSA	1030
Qy	2122	-----GAATTCACCCGTGTATATATACAGCTATC	2152
Db	1030	snTyfThrValSerAlaIeuGluAspGlnGluSerAasSerGIuPhehAasApphet	1050
Qy	2153	ATCAG-----TGTACGGGTGGTCAGTGTCTGG	2182
Db	1050	rPLyAlaIaIaIeueuGlyTyrgIySerGIyLeuCySryIegly-----	1064
Qy	2183	GTAGCAGCTGTAGCATTTCTGATATACACTTCTATATTCACCTGATACTATATTCGTGGC	2242
Db	1065	-----IleSerMetIleTyrlleuIleSerThGIyAsnIeuaArgITpL	1080
Qy	2243	TGTAAAA-----GTACAGCAGAGAGAAAGCATCTAT	2275
Db	1080	euAlaIaArgIleIleGIuLyLseuGluHlIbVsrIleIleMetGlnIaArgArgys-----	1097
Qy	2276	GATGCATTGTGATCTACTCGAGCCAGATGAGAGCTGGGTGAGAAACGAGCTGTAAAG	2335
Db	1098	-----LySgIaIaArgIyGlnaRGA	1104
Qy	2336	AATTGAGAAGAGAGT 2352	
Db	1104	snTyfArGIaArgArGaaen 1109	

RESULT 11

insulin-like growth factor-binding protein acid labile chain precursor - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C|Accession: JCI282
R|Daif, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A|Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A|Reference number: JCI282; MUID:93038676; PMID:1384485
A|Accession: JCI282
A|Molecule type: mRNA
A|Residue: 1-603 <DAI>
A|Cross-references: UNIPROT:P35859; GB:S46785; NID:G258002; PIDN:AAB3770.2; PID:G570593
A|Experimental source: liver
A|Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F11-27/Domain: signal sequence #status predicted <IG>
F128-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F1267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Alignment Scores:

Pred. No.:	6.35e-13	length:	160
Score:	290.50	Matches:	155
Percent Similarity:	37.85%	Conservative:	87
Best Local Similarity:	24.30%	Mismatches:	24
Query Match:	4.63%	Indels:	15
DB:	2	Gaps:	24

US-09-396-985B-5 (1-3395) X JC1282 (1-603)

[illegible]

DB: 2 Gaps: 34

US-09-396-985b-5 (1-3395) x T13174 (1-1051)

QY 503 CTGGATTATTCAGGCTGGAAATTGACAAATTGAAAGCAAGGCTGGCATGGCTTAAC 562

DB 297 ILeuysIleAlaAsnCysThrLeuGluThrLeuHISalagIuAlaPheHISglYLeuAsn 316

QY 563 CAGCTTCAGACCTGGTGGTCTGACAGAAACCCATCAAGAGTTTCCCGAGAAAGTTT 622

DB 317 GluLeuYrAlaValAsnLeuThrAspValGlyLeuAlaIleIleAsnProAspThrPhe 336

QY 623 TCTGAGCTAACAAATTTAGAGATCTGGTGGCTGGAGACAAATATGACCTCTAGAG 682

DB 337 ValGlyAsnLysLysLeuArgMetLeuThrIleSerGlyAsnAspLeuSerValMetSer 356

QY 683 GGTTCAT---ATTGACAGCTTATATCTTAAAGAACTPAAGTGGCTCATATGTT 739

DB 357 SerIleHISrYrLeuLeuLysSerSerIleGluGluLeuAspPheSerArgAsnAsn 376

QY 740 ATACATTCCTTAATGCTGCAATTTCTTATCTGACAAACCTGAACATGTGAT 799

DB 377 LeuMetGluLeuAsn---ProLysAlaPheSerHISLeuSerAsnValAlaIlyrIleAsn 395

QY 800 CTTTCTTAACTATATCAAACTATTTCTGCAAGACTTACAGTTTCTACGTGAAT 859

DB 396 LeuSerArgIleAsnSerLeuLysLysLeuProGluLysAlaPheGlu----- 410

QY 860 CCCCAAGTCAATCTC---TCTTAAAGCTGTCTTAAACCCAAATGACTCCATTCAA 913

DB 411 ---LysValThrLeuGluGluGluLeuAspLeuSerYrAsnSerLeuThrGluLeuPro 429

QY 914 GCCCAAGCTTCAGGAAATAGGCTCCATGATGATGACTCAAGAAAGTAT----- 964

DB 430 ArgAspIlePheAsnGlyThrThrLeuSerIleLeuHISLeuLysrYrAsnThrPheAsn 449

QY 965 -----TTTAAATGCTCAATATGCTGAATATGCTTCAAAATGCTCAAAATGCTGCT 1012

DB 450 GlyAspLeuHISrPheGlyThrIlyAspLeuGlnGlnLeuAspLeuSerPheAsnSerIle 469

QY 1013 TTACATGCTCATCGGTTGATCTGGAGAAATTTAAAAATGAAGAAATCTGAAAGTTT 1072

DB 470 ValGlnValHISHis-----SerMetPhe 477

QY 1073 GACCGTTCTGCATGGAAGCAATGCAATGAGCAAT----- 1111

DB 478 Asplys-----MetProGlyLeuThrAsnLeuAsnLeuLysglYAsnGlyIleLysLys 495

QY 1112 -----GATGAGTTCAAGTTAACATATTAATCATTTTTCAGATGATATTTATAT 1162

DB 496 IleGlnProAspSerPhe---LeuThrLeuLysAsnLeuArgHISleAspLeu---Ser 513

QY 1163 CTCATATGCTTGGCAAAATATTTCTGCAATGCTTCTTCAAGGTGATCATATAAACACATA 1222

DB 514 IleAsnAspLeuAspGlnIleSerGlyMetLeuPhe----- 525

QY 1223 GCAATGTCTTAGGCAATTTCAATGGAATCTTATCATCATATGATCTTAAAG 1282

DB 526 -----PheLysAsnSerGluLeuAspValIleArg-----LeuAsn 537

QY 1283 CCTTTTCCAAAGCTGAGT---CTACCT-----TTTCTTAAAGTTGGACCTTAACT 1330

DB 538 AspnProArgLysSerGlnLeuProThrAspGlyPheLeu---SerTrpSer----- 554

QY 1331 ACCAAGAGAGAGATATCAGCTTTGGTCAAGTTGGCTTGCAGAGTCAAGATATCTAGAT 1390

DB 555 -----GlyGluPhe-----ThrValrYrTyrLeuAsp 563

QY 1391 CTTAGTAGAATGCCATGAGCTTATAGAGTGGCTGTCTTATCTGATTTTGAACA--- 1447

DB 564 IleSerAsnCysAlaIle-----GlyProLeuGlnGlyHISLysAlaPheSerThrMet 580

QY 1448 AACAACTGAAGTACTTAGACTCAGCTTCAATGATGTGCATCTGATGATGAGTCCAACTTC 1507

DB 581 ProHISLeuThrThrLeuLysLeuAlaIleAsnAsnIle-----AsnHIS 595

QY 1508 ATGGGTCTAGAAAGAGCTGGAAATACCTGACCTTACAGACTCCACTTTAAAAAGTCA 1567

DB 596 LeuProArgGlu----- 599

QY 1568 GAATTCACAGTGTCTTATCTCTGAAAACCTCTTATCACTTGAACATCTTAACT--- 1624

DB 600 -----IlePheThrGlyLeuHISLysLeuIleAspLeuAspLeuSerAsnAsnLeu 616

QY 1625 AATACCAAAATTTGACTTGAATGAGCATTTCTGGCTTGATCAGCTTCAACACTTAAA 1684

DB 617 IleThrArgMetAsp---AspLeuIlePheMetAspAsnGlyGluLeuThrIlyLeuSer 635

QY 1685 ATGGCTGCAATCTTTCACAAAGACAAACCTTTCA---AATGTCTTACAAACACACA 1741

DB 636 LeuAlaGlyAsnProIle-----SerArgLeuSerValArgLeuPheLeuProLeuHIS 653

QY 1742 AACTTAACATTCCTGATCTTCTTAAATGCCAACTGGACAGATATCTAGGGGGTATTT 1801

DB 654 GlnLeuArgCysLeuAspValAsnAspCysGluLeuThrIleu----- 668

QY 1802 GACACACTCTACAGACTCCAGTTATTAACATGAGTCAACAAACCTACTGTCTTGAT 1861

DB 669 -----LeuSerAspArgAspLeu----- 674

QY 1862 CCATCCCATTTTAAACAGCTGACTCCCTCAGACTCTGTGATTTGCACTTCAATGCAATA 1921

DB 675 GlyAlaGlyrYrLysIlePheAspSerLeuArgSerPheAsnAlaSerGlyAsnLeuIle 694

QY 1922 ---GAGACATCAAAAGAAATCTGCACAACTTTTCCAAAGAGTCTAGCCGTCTCAATCTG 1978

DB 695 LysLysIleSerSerGluAspValLysSerPhe---LysAsnLeuArgSerLeuAspIle 713

QY 1979 ACTAATATTTCTGTGCTGTGATATGTAATATGCAATTTCTTGCAGTGGTCAAGAC 2038

DB 714 ThrAsnAsnProLeuLysCysThrProAspPheGlnGluPheIleSerYr----- 730

QY 2039 CAGAAATGTTCTTGTGATGTTGAACAATGAATGATGATCACTATAGACATGAAG 2098

DB 731 -----ValThrLeuGlnMetGlnMetThrProLysArgLeuProValLeu 745

QY 2099 GCTCCCTGCTGTGATTTTATGCAATTCACCTGTTATATATCAAGCATATCATAGT 2158

DB 746 AlaAsnLeuGluAspAspAlaIleHr----- 753

QY 2159 GTATCGGTGCTCAGTGTCTGTGTAGCCACTGTAGCAATTTCTGATATACACTTCTAT 2218

DB 754 -----IleValGlnLeuGlnThrIleuAlaGlnAlaGlyTrpSerSerIleu 768

QY 2219 TTTCACCTGATCTTATTTGCTGCTGTAAAGATGACAGACAGAGAGAAAGCATCTATGAT 2278

DB 769 AlaHISgluVal-----Cys---LysHISAlaGluGlySerAspLeuLeuAsp 783

QY 2279 GCATTTGTGATCTACGAGCCAGATGAGACCTGGGTGAGAAAGAGCTGTAAAGAT 2338

DB 784 -----GluLysLysAlaAspSerAlaGluAlaLysLeuGluLysArg 797

QY 2339 TTAGAGAGAGAGTGGCCCGC 2359

DB 798 LeuLysGluSerValLysLys 804

RESULT 13

B3665

slit protein 2 precursor - fruit fly (Drosophila melanogaster)

C1Species: Drosophila melanogaster

C1Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C1Accession: B3665

R1Rocheberg, J.M.; Jacobe, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

Gene Dev. 4, 2169-2187, 1990

A1Title: slit: an extracellular protein necessary for development of midline glia and co

A1Reference number: A3665; MUID:91099665; PMID:2176636


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Qy 1708 ----- 1708
Db 700 LysCysSerSerGluAsnSerGluGlyCysLeuGlyAspGlyTyrCysProProSerCys 719
Qy 1709 ----- AACCCCTTCAATGTC----- 1726
Db 720 ThrCysThrGlyThrValAlaCysSerArgAsnLeuGlyGluIleProArgGly 739
Qy 1726 ----- 1726
Db 740 IleProAlaGluThrSerGluLeuTyrLeuGluSerAsnGluIleGluGluIleHisTyr 759
Qy 1727 -----TTTACAAACACAACTTAACATTCCTGATCTTTGTAATGCCAATGGAA 1780
Db 760 GluArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAsnAsnGlnIleThr 779
Qy 1781 CAGATATCTAGGGGGGATTTTGACACACTCTACAGACTCCAGTTATTAACATGATGAC 1840
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Qy 1901 GATTGCAAGTTTCATTCGATAGAG--ACATCCAAAGGAATATCGCAACATTTCCAAAG 1957
Db 820 SerLeuHisGlyAsnArgIleSerMetLeuProGluGlySerPheGluAspLeu--Lys 838
Qy 1958 AGCTGACCGCTTCTCAATCTGACTAATTAATCTGTGCTGTTATATGTAATATCAGAT 2017
Db 839 SerLeuThrHisIleAlaLeuGlySerAsnProLeuTyrCysAspCysGlyLeuLeuTyr 858
Qy 2018 TTCTTGCAAGTGGGTCAGAGACCAAAATGTTCTTGGAATGTTGAACAATGAATGT 2077
Db 859 PheSerAspTyrIle-----LysLeuAspTyrValGluProGlyIleAlaArgCys 875
Qy 2078 GCATCACCCTTATAGATGAAGAGCCCTCCCTGTTGGATTTTACGAATTCACAC----- 2131
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Qy 2132 -----TGTATAT----- 2139
Db 896 CysArgGlyArgValArgAsnAspIleLeuAlaLysCysAsnAlaCysPheGluGlnPro 915
Qy 2140 ATACAGACTATCTCAGTGTATCGGT-----GGTCACTGTGCTTGT-- 2181
Db 916 CysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGluTyrGlnCysLeuCysGln 935
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Db 936 ProGlyTyrHisGlyLysHisCys 943

RESULT 14
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Apr-1991 #sequence: revision 30-Apr-1991 #text: change 02-Aug-2002
C/Accession: A36665; A31640; S13523
R:Rocheberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A>Title: slit: an extracellular protein necessary for development of midline glia and cc
A:Reference number: A36665; MUID:91099665; PMID:2176636
A:Accession: A36665
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1480 <ROT>
A:Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98615
R:Rocheberg, J.M.; Hattley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A>Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A:Reference number: A31640; MUID:89077533; PMID:3144436
A:Accession: A31640

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A:Molecule type: DNA
A:Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', <RO2>
A:Cross-references: GB:M23543; NID:9340939; PID:9514357
C:GeneticCB:
A:Gene: FlyBase:slit
A:Cross-references: FlyBase:FBgn0003425
A:Introns: 1351/3
C:Superfamily: fruit fly slit protein; EGF homology; Leucine-rich alpha-2-glycoprotein x
C:Keywords: alternative splicing; growth factor
F:66-91/Domain: proteoglycan amino-terminal homology <PAH1>
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F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
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F:288-316/Domain: proteoglycan amino-terminal homology <PAH2>
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F:547-571/Domain: proteoglycan amino-terminal homology <PAH3>
F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
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F:708-733/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F:791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F:815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>
F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:1028-1061/Domain: EGF homology <EGF>
F:1068-1099/Domain: EGF homology <EGF2>
F:1115-1148/Domain: EGF homology <EGF1>

Alignment Scores:
Pred. No.: 2,74e-12 Length: 1480
Score: 282.50 Matches: 161
Percent Similarity: 33.29% Conservative: 88
Best Local Similarity: 21.52% Mismatches: 246
Query Match: 4.75% Indels: 254
DB: 2 Gaps: 25

US-09-396-985b-5 (1-3395) x A36665 (1-1480)
Qy 374 TGCATGATGATGAGATCTCAGACAAATGCCCTCATGACATCCCTTATTCACCAAGACTTA 433
Db 308 CysArgGluLysSerLeuThrSerValProValThrLeuProAspAspThrThrAspVal 327
Qy 434 GATCTGAGCTTCAACCCCTGAAGATCTTAAGAAGCTATAGTCTTCAACCAATTTCTCAAA 493
Db 328 ArgLeuGlnAlaAsnPheIleThrGluLeuProProLysSerPheSerPheArgArg 347
Qy 494 CTTCACTGCTGATTTATTCAGGTGTGAATTTGAGCAATTTGAAGCAAGCAAGCATGGCAT 553
Db 348 LeuArgGlyLeuAspLeuSerAsnAsnIleSerArgIleAlaHisAspAlaLeuSer 367
Qy 554 GCGTTAAACAGCTTCAACCTTGATCTGATCAAGAAACCCCTTCAAGATTTTCCCA 613
Db 368 GlyLeuLysGlnLeuThrThrLeuValLeuTyrGlyAsnLysIleLysAspLeuProSer 387
Qy 614 GGAAGTTTCTGCACTTAACAATTTAGAAATCTGGTGGCTGGAGACAAATAATGACC 673
Db 388 GlyValPheLysGlyLeuGlySerLeuArgLeuLeuLeuLeuLeuAlaAsnGluIleSer 407
Qy 674 TCTCTAAGAGGGTTTCAATATTTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCAT 733
Db 408 CysIleArgLysAspAlaPheArgAspLeuHisSerLeuSerLeuLeuSerLeuTyrAsp 427

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Db 745 ThrIeuProIysGlyMetProIysAspValThrGluIeuTyrLeuGluGlyAsnHisIeu 764
QY 1799 -----TTTGACACACTCTACAGACTCCAGTTATTTAAACATGACTCAC 1840
Db 765 ThrAlaValProIysGluIeuSerThrPheArgGlnIeuThrIleAspIeuSerAsn 784
QY 1841 AACAACTTACTGTTTCTGATTCATCCATTATTAACAGCTGACTCCCTCAGGACTCTT 1900
Db 785 AsnSerIleSerMetIeuThrAsnHisThrPheSerAsnMetSerHisIeuSerThrIeu 804
QY 1901 GATTGACGTTTCATCGC-----ATAGACATCCAAAGGAATACGTCAA 1945
Db 805 IleuSerTyrAsnArgIeuArgCysIleProValHisAlaPheAsnGlyIeu----- 822
QY 1946 CATTTCCAAAGAGCTTACGCGCTTTCATCTGACTAATAATTCTGTGCT----- 1996
Db 823 -----ArgSerIeuArgValIeuThrIeuHisGlyAsnAspIleSerSerValPro 839
QY 1996 ----- 1996
Db 840 GluGlySerPheAsnAspIeuThrSerIeuSerHisIeuAlaIeuGlyIleAsnProIeu 859
QY 1997 ---TGTATATGTGAATATCAGAAATTTCTGCAGTGGGTCAAG----- 2035
Db 860 HisCysAspCysSerIeuArgTyrIleuSerGluTyrIleValArgIleGlyTyrGluPro 879
QY 2036 -----GACCAGAAATGTTCTTGTTGAAT 2059
Db 880 GlyIleAlaArgCysSerSerProGluSerMetAlaAspArgIeuIeuThrPro 899
QY 2060 GTTGACAAATGAATGTGCATCATTATAGACATG-----AAGGCTCCCTG 2107
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QY 2108 GTGTGGATTT-----ACGAATTCACCTGT----- 2134
Db 920 CysIeuSerSerProCysIysAsnAsnGlyThrCysSerGlnAspProValGluGlnTyr 939
QY 2135 -----TATATTTACAGAC-----TATCATCAGTGT 2160
Db 940 ArgCysThrCysProTyrSerTyrIysGlyLysAspCysThrValProIleAsnThrCys 959
QY 2161 ATCGGTGATCAGTGTGCTTGATGAGCCACTGTAGCAATTTCTGATATACACTTCTATT 2220
Db 960 ValGlnAsnProCysGlnHisGlyGlyThrCysHisIeuSer----- 973
QY 2221 TCACCTGATCTTATTCGTGCTGTAAAGATACAGACAGAGAAAGCATATGATGC 2280
Db 974 -----GluSerHisArgAspGlyPheSerCys 982
QY 2281 ATTTGTGATCTA-----CTCGAGCCAGAAATGAGACTGGGT 2316
Db 983 SerCysProIeuGlyPheGluGlyGlnArgCysGlnIleAsnProAsp----- 998
QY 2317 GAGAAACGAGCTGTAAAGATTAGAAAGAGAGTGCCCGCTTTCAGCTTTCCTTCA 2376
Db 999 -----AspCysGlnAspAsnAspCysGlnAsnSerAla---ThrCys 1011
QY 2377 TTACAGGAGACTTATTCCTGTGTAGCCATTGCTCCAAATCATCCAGAAAGGCTTCCA 2436
Db 1012 ValAspGlyIleAsnAsnTyrAlaCysValCysProProAsnTyrThrGlyGluIeuCys 1031
QY 2437 CAAGAGCCGGAAGTTATGT 2457
Db 1032 AspGluValIleAspTyrCys 1038

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

[illegible]

QY 1460 TACTTAGACCTCAGCTTCAATGATGTCATCTCGATGAGTGCACCTTCATGAGTCTAGAA 1519
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 QY 1520 GAGCTGAATACCTGAGACTTCAGACTCCACTTTAAAAAGGTACAGAAATTCAGTG 1579
 DB 421 GluleugluTyrlleuAapPheGlnHiserThrlleuTyrlValThrlupheserVal 440
 QY 1580 TTCTTACTCTTGAAGAACTTCTTACCTTACATCTCTTACATTAATACCAAAATTCAC 1639
 DB 441 PheleuserleuGluTyrlleuTyrlleuapHleSerTyrlThraThrlLysIleasp 460
 QY 1640 TTGTATGAGCATATTTCTGCTGATCAGTCTCAACACTTTAAAAAGGTGCGCAATTC 1699
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 DB 481 PheTyrlapantThrlleuserAsnValPheThraThrlThraThraThrlPheleuasp 500
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 QY 2120 ACGAATTCACCTGTTATATATACAGACTTATCATCAGTATATGCTGCTGCTT 2179
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 AC Q8K2T5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029856; AA429856.1; -;
 DR HSSP; O60603; 1077.
 DR MGD; MGI:96824; Tlr4.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; IDA.
 DR GO; GO:0007249; F:1-kappab kinase/NF-kappab cascade; IDA.
 DR GO; GO:0008063; P:Toll signaling pathway; IDA.
 DR InterPro; IPR000887; Aldlee_KDPG_KHG.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRT, 1.

DR SMART; SM00255; TIR; 1.
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KW Receptor.
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Alignment Scores:

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US-09-396-985b-5 (1-3395) x Q8KZT5 (1-835)

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QY 380 GATCAGAACTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTGATCTG 439
Db 41 AspGlnIysLeuSerIysValProAspAspIleProSerThrIlyAsnIleAspLeu 60
QY 440 AGCTTCAACCCCTGAAAGATTAGAAGCTAAGCTTACCAATTTCTGACACTTCAG 499
Db 61 SerPheAsnProLeuIysIleLeuIysSerIysSerPheSerAsnPheSerGluLeuGln 80
QY 500 TGGTGATATTATTCAGGTGTGAATTTGAGACATTTGAACAAGGATGGCATGGCTTA 559
Db 81 TrpLeuAspLeuSerIysArgCysGlnIleGlnThrIleGlnAspIlyAlaTrpHisGlyLeu 100
QY 560 AACGAGCTCTCAACCTTGTAAGTACAGCAAAACCTTACAAAGATTTTTCCCGAGAACT 619
Db 101 HisIleIleuSerAsnLeuIleLeuThrGlyAsnProIleGlnSerPheSerProGlySer 120
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QY 680 GAGGCTTTCATATTTGACAGCTTATATCCCTTAAGAACTTAATGGCTCATTAATCTT 739
Db 141 GluSerPheProIleGlyGlnLeuIleThrLeuIysIysLeuAsnValAlaHisAsnPhe 160
QY 740 ATACATTCTTTAAGTGGCTGAATATTTTCTAATCTGACAAACCTGAAACATGTGGAT 799
Db 161 IleHisSerCysIysLeuProIaIlyrPheSerAsnLeuThrAsnLeuValHisValAsp 180
QY 800 CTTTCTTATAACATATTTCAAACTAATTTCTGTCAAAGACTTACAGTTTCTTACGTAAAT 859
Db 181 LeuSerIlyrAsnIlyrIleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGluAsn 200
QY 860 CCCCAGTCAATCTCTTTAGACCTGTCTTTAAACCCAAATGACTCCATTCAGCCCAA 919
Db 201 ProGlnValAsnLeuSerLeuAspIleSerLeuAsnProIleAspPheIleGlnAspGln 220
QY 920 GCTTTAGAGGAATTAAGGCTCATGAATTAAGTCTTAAGAAATTAATTAATAGTCAAT 979
Db 221 AlaPheGlnIlyIleIysIysLeuHisGlnLeuThrLeuArgGlyAsnPheAsnSerSerAsn 240
QY 980 GTACGAAATATGTCCTTCAAAACATGACGTGTTTACATGTCCATCGGTGATCTTGGGA 1039
Db 241 IleMetIysThrCysLeuGlnAsnLeuAlaGlyLeuHisValHisArgLeuIleLeuGly 260
QY 1040 GAATTTAAAAATGAAGAATCTGAAAAGTTTGAACGCTTGTGCATGGAAGAACTATGC 1099
Db 261 GluPheIysAspGluArgAsnLeuGlnIlePheGlnProSerIleMetGluGlyLeuCys 280
QY 1100 AATGTGAGCATGTATGATTCAGGTTAAACATATTAATCATTTTTCAGATGATTAATTAT 1159
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QY 1220 ATAGCAGATGTTCCATGGCATTTCAATGAGCAATCTTATTCATCAATTAATGATGCTTCT 1279
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QY 1280 AACCTTTTCCAAAGCTGAGTCTACCTTTTCTTAAAAGTTGACCTTTAACTACCAACAG 1339
Db 341 LysGlnPheProThrLeuAspLeuProPheLeuIysSerIleuThrLeuThrMetAsnIys 360
QY 1340 GAGGATATCAGCTTTGTCAGTTGGCTGCGCCAAAGTCCAGATATCTAGATCTTATTAAG 1399
Db 361 GlySerIleSerPheIysIysValAlaLeuProSerLeuSerIlyrLeuAspLeuSerArg 380
QY 1400 AATGCCATGAGCTTTAGAGGTGCTGTCTTATTTGATTTTGAACAAACACTGAAG 1459
Db 381 AsnAlaLeuSerPheSerGlyCysCysSerIlyrSerAspLeuGlnIlyrAsnSerLeuArg 400
QY 1460 TACTAGACCTCAGCTTCAATGCTGTGCATCTGATGAGTGCACCACTTCAATGGCTTAGAA 1519
Db 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerHisAsnPheMetGlyLeuGln 420
QY 1520 GAGCTGGAATCCTGACCTTTCAGCACTCCACTTTAAAAAGCTCAGAGATTTCTGATG 1579
Db 421 GluLeuGlnHisIleuAspPheGlnHisSerThrLeuIlyAsArgValThrGluPheSerAla 440
QY 1580 TTCTTATCTCTTAAAAAAGCTTCTTTCATGACATCTCTTACCTAATACCAAAATGAC 1639
Db 441 PheLeuSerLeuGlnIlyuSerLeuIlyrLeuAspIleSerIlyrThrAsnThrIlyLeAsp 460
QY 1640 TTTGATGCAATATTTCTGGCTTATGATCAGTCTCAACACTTTAAAAATGGCTGCAATTC 1699
Db 461 PheAspGlyIlePheLeuGlyLeuThrSerLeuAsnThrLeuIysMetAlaGlyAsnSer 480
QY 1700 TTCAAAAGACAAACCTTTCAAAATGCTTTTCAAAACAAACAAACCTTAATCTCGAT 1759
Db 481 PheIlyAspAsnThrIleuSerAsnValPheAlaAsnThrThrAsnLeuThrIlyPheLeuAsp 500
QY 1760 CTTTCTTAATAGCAACCTGGAACAGATATCTAGGGGGGTATTTGACACACTCTACAGACTC 1819
Db 501 LeuSerIlyCysGlnLeuGlnGlnIleSerIlyGlyValPheAspThrLeuHisArgLeu 520
QY 1820 CAGTTATTAACATGAGTCACAACAACTAAGTTTCTGGATCCATCCCATTTAAACAG 1879
Db 521 GlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisIlyrAsnGln 540
QY 1880 CTGTACTCCCTCAGGACTCTTGAATTCAGTTTAAATCGCATAGAGCATTCGAAAGAAAT 1939
Db 541 LeuIlyrSerLeuSerThrIleuAspCysSerPheAsnArgIleGlnThrSerIysGlyIle 560
QY 1940 CTGCAACATTTTCCAAAGAGCTGAGCGTCTTAACCTGACTAATTAATCTGTGCTGT 1999
Db 561 LeuGlnHisPheProIySerSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
QY 2000 ATATGTGAATATGCAATTTCTTGAGTGGGTCAAGAGCCAGAAAATGTTCTGTGTAAT 2059
Db 581 IleCysGlnHisGlnIysPheLeuGlnTrpValIlyAspGlnIysGlnPheLeuValAsn 600
QY 2060 GTTGAACAAATGAATGTGCATCACTATAGACATGAAGGCTCCCTGCTGTGGAATTT 2119
Db 601 ValGlnGlnMetThrCysAlaIlyrProValGlnMetAsnThrSerLeuValIleuAspPhe 620
QY 2120 AGCAATTCACCTGTATATATACAGACATATATAGCTATACGGTGTGCTGCTGCTT 2179
Db 621 AsnAsnSerThrCysIlyrMetIlyrIlyrThrIleIleSerValSerValIleSerValIle 640
QY 2180 GTGTAGCCACTATGACATTTCTGATATACCACTTCAATTTCACTGATTAATGCT 2239
```


CC	Blnde lY96 via the extracellular domain.. Bnde MYD88 and TIRAP via
CC	their respective TIR domains.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and
CC	muscle. Lower levels are found in liver and kidney.
CC	-1- POLYMORPHISM: Interstrain analysis reveals that TIR4 is a
CC	polymorphic protein and that the extracellular domain is far more
CC	variable than the cytoplasmic domain, which is variable at the C-
CC	terminal.
CC	-1- DISEASE: The protein is encoded by the lps locus, an important
CC	susceptibility locus, influencing the propensity to develop a
CC	disseminated Gram-negative infection.
CC	-1- SIMILARITY: Belongs to the Toll-like receptor family.
CC	-1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC	-1- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	entities requires a license agreement (See http://www.isdb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF095353; AAC99411.1; -
DR	EMBL; AF185285; AAF04278.1; -
DR	EMBL; AF101033; AAD92272.1; -
DR	EMBL; AF17767; AAF05317.1; -
DR	EMBL; AK014533; -; NOT_ANNOTATED_CDS.
DR	HSSP; Q15399; 1FYV.
DR	MED; MGI:96834; Tlr4.
DR	GO; GO:0046686; C:lipopolysaccharide receptor complex; ISS.
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR	GO; GO:0004888; P:transmembrane receptor activity; ISS.
DR	GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
DR	GO; GO:0016045; P:detection of fungi; ISS.
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR	GO; GO:0042116; P:macrophage activation; NAS.
DR	GO; GO:0045576; P:mast cell activation; NAS.
DR	GO; GO:0045671; P:negative regulation of osteoclast different. . ; ISS.
DR	GO; GO:0045365; P:negative regulation of interleukin-1 biosyn. . ; ISS.
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosy. . ; ISS.
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosy. . ; NAS.
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . ; NAS.
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR000157; TIR.
DR	Pfam; PF00560; LRR; 10.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICRPT.
DR	SMART; SMO0082; LRRCT; 1.
DR	SMART; SMO0255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KM	Disease mutation: Glycoprotein; Immune response;
KM	Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;
KM	Signal; Transmembrane.
FT	REPEAT 1 25 Potential.
FT	CHAIN 26 835 Toll-like receptor 4.
FT	DOMAIN 26 638 Extracellular (Potential).
FT	TRANSMEM 639 659 Potential.
FT	DOMAIN 660 835 Cytoplasmic (Potential).
FT	REPEAT 29 52 LRR 1.
FT	REPEAT 53 75 LRR 2.
FT	REPEAT 76 99 LRR 3.
FT	REPEAT 127 123 LRR 4.
FT	REPEAT 149 148 LRR 5.
FT	REPEAT 173 172 LRR 6.
FT	REPEAT 201 196 LRR 7.
FT	REPEAT 224 224 LRR 8.
FT	REPEAT 227 251 LRR 9.
FT	REPEAT 305 330 LRR 10.
FT	REPEAT 348 370 LRR 11.

Query	Subject	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	260 ATGATGCTCTTCTTTCATCTGGCTGGAGACTGTGATCAGTGTCTTCTGCTG 319	3e-263	835	715				
Db	1 MetMetProProTrrLeuEnlAargThrLeuIlleMetAlaLeuPheSerCysLeu 20	3745.00						
QY	320 AGACGAGAGAGCTTGAATCCCTGCATGAGGACTTCCATATATATCCAGCAATGCAT 379	91.74%			51			
Db	21 ThrProGlySerLeuAsnProCysIleGluValAlaProAsnIleThrTyrgInCysMet 40	85.63%			69			
QY	380 GATCAGAACTTCAGCAAAATCCCTCATGATCCCTTATTCACCAAGAACCTAGATCTG 439	63.02%			0			
Db	41 AsgInLysLeuSerLysValaProAspPheIleProSerSerThrLysAsnIleAspLeu 60							
QY	440 AGCTTCAACCCCTGAGAGATCTTGAAGACTATAGCTTCACCAATTTCTCACAACTTCAG 459							
Db	61 SerPheAsnProLeuLysIleLeuLysSerTyrrSerPheSerAsnPheserGluLeuGln 80							
QY	500 TGGCTGAGATTATCCAGGTGTGAATTTAGAGACATTTGAACAGCAAGCATGGCTGCTTA 555							
Db	81 TrpleuAspLeuSerArgCysGluIleGluTrIleGluAspLysAlaTrpHisGlyLeu 100							
QY	560 AAGCAGCTCTCAACCTGGTACGTGACAGGAAACCTATCAAGAGTGTTCCTCCAGAGAGT 619							
Db	101 HisHisLeuSerAsnLeuIleLeuTrgIysAsnProIleGlnSerPheSerProGlySer 120							
QY	620 TTTTCTGACATAACAATTTAGAGATCTGTGGCTGTGAGAGCAAAAATGACCTCTTA 679							
Db	121 PheSerGlyLeuThrSerLeuGluAsnLeuValAlaIvalGluThrLysLeuAlaSerLeu 140							
QY	680 GAGGCTTTCATATTTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCATATCTT 739							
Db	141 GlusPheProIleGlyGlnLeuIleTrIleuLysLysLeuAsnValAlaHisAsnPhe 160							
QY	740 ATACATCTCTTAAGTGGCTGAATATTTTCTAATCTGACAAACCTAGAACATGGGAT 799							
Db	161 IleHisSerCysLysLeuProAlaTyrrPheSerAsnLeuThrAsnLeuValHisValAsp 180							
QY	800 CTTTCTTAACTATATTCACAACTATTTCTGCAAGACTTACAGTTTCTTACGTAAGAAAT 859							
Db	181 LeuSerTyrrAsnTyrrIleGlnThrIleThrValAsnAspLeuGlnPheLeuAspGlyAsn 200							
QY	860 CCCGAGTCATATCTCTTTTAGACCTGTCTTTAAACCAATTAGACTTCATTCAGGCCAA 919							


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Db      321 LeuGIyLeuLeuLysAspPheProIyGlyPheGIyTrpGlnAspPheGluLeuValAsn 340
Qy      1271 TGTCATCTTAAGCCTTTTCCAAAGCTAGTCTACCTTTCTTAAAGTTGACCTTAACT 1330
Db      341 CysArgIleGIyGluPheProThrLeuGluLeuThrSerLeuLysArgLeuValPheThr 360
Qy      1331 ACCAAGAGAGAGATATCACTTGTGTCAGTGGCTGCGCAAGTCTCAGATATCTAGAT 1390
Db      361 SerAsnLysAspMetLysSerPheAsnGluValLysLeuProSerLeuGluPheLeuAsp 380
Qy      1391 CTTAGTGAATAATGCCATGAGCTTTAGAGGTGCTGTTCTTATCTGATTTTGAACAAC 1450
Db      381 LeuSerArgPheAsnArgLeuSerPheLysSerCysCysSerGluValAspLeuLysThr 400
Qy      1451 AACTGGAAGTACTTAAGACCTTCAATGTGTCTCATCTCGATGAGTGCACACTTCAATG 1510
Db      401 ArgLeuLysHisLeuAspLeuSerPheAsnAspValIleSerMetSerSerAspPheMet 420
Qy      1511 GGTCAGAGAGCTGGAATACCTGAACTTTCAGACCTCACTTAAAGGTCACAGAA 1570
Db      421 GLyLeuGluGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnAlaSerAsp 440
Qy      1571 TTCTCAGTGTCTTATCTCTTGAAGAACTTCTTACCTTGAACATCTCTTACACTAATACC 1630
Db      441 PheProValPheLeuSerLeuLysAsnLeuArgTrpLeuAspIleSerTrpThrAsnThr 460
Qy      1631 AAAATTGACTTGAATGGCATTTTCTGGCTTGAATCACTCAACACTTAAAGTGGCT 1690
Db      461 ArgValValPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuLysMetGlnA 480
Qy      1691 GGCAATTCCTTCAAGAGCAACACCTTCAAGTCTTCAACAAACAAACACTTAAACA 1750
Db      481 GlyAsnSerPheLysAspAsnPheLeuProAsnIlePheArgGluMetThrAsnLeuThr 500
Qy      1751 TTCCTGATCTTTCTTAAATGCCAACTGGAACAGATATCTAGGGGGGTATTTGACACATC 1810
Db      501 ThrLeuAspLeuSerLysCysAsnLeuGlnValSerGlnGluAlaPheCysLeuLeu 520
Qy      1811 TACGAGCTCCAGTATTAAATGATGATGACAAACAACTACTGTTTCTGGATCCATCCCAT 1870
Db      521 ProArgLeuArgValIleAsnMetSerHisAsnAsnLeuLeuPheLeuAspMetLeuPro 540
Qy      1871 TATAACAGCTGTAATCCCTCAGACCTTGAATGGAGTTTCAATGCGATGAGACATCC 1930
Db      541 TyrLysProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe 560
Qy      1931 AAA---GGAAATACCTGCAACATTTTCCAAAGAGTACGCGCTTCAATCTGACTAATATAT 1987
Db      561 LysTrpGlnGluLeuGlnHisPheProSerSerLeuAlaSerLeuAsnLeuThrGlnAsn 580
Qy      1988 TCTGCTGCTGTATATGTGAATATACAAATTTCTGACGTGGTCAAGGACCAAGAAATG 2047
Db      581 AspPheAlaCysValCysGluTrpGlnSerPheLeuGlnTrpValLysAspGlnArgGln 600
Qy      2048 TTCTGGGATGTTGAACAATGAATGTCATCACCTATAGACATGAAAGCGCTCCCTG 2107
Db      601 LeuLeuValGluValGlnHisLeuValCysAlaIleProLeuGlnMetArgGlyMetPro 620
Qy      2108 GTGTGATTTTGAAGATTCACCTGTTATATATATACAGATCAATCATCATGATTCGGTG 2167
Db      621 ValLeuGlyPheAsnAlaIleThrCysGlnIleSerLysThrIleValGlyGlySerVal 640
Qy      2168 GTCAAGTGTCTGTGTGAGCAGCTGTGACATTTCTGATATACCACTTATTTTCACTG 2227
Db      641 PheSerIleLeuMetValSerValIleAlaValLeuValTrpLysPheTrpPheHisLeu 660
Qy      2228 ATACTTATGCTGCTGTAAAGAAAGTACAGAGAGAAAGCAATCTATGATGACCTTGTG 2287
Db      661 MetLeuLeuAlaGlyCysLysLysTrpIleArgGlyGlnSerIleTrpAspAlaPheAla 680
Qy      2288 ATCTACTGACGACGATGAGAGCTGGGTGAGAAACGAGCTGTAAAGAAATTTGAGAA 2347

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Db      681 IleTrpSerSerGlnAspGlnAspTrpValArgAsnGluLeuValLysAsnLeuGlu 700
Qy      2348 GGAGTCCCGCGCTTTCAGCTTTGCTTCATTAACAGGAGCTTATTCGGTGGTACCAT 2407
Db      701 GlyValProProPheGlnLeuCysLeuHisTrpArgAspPheIleProGlyValAlaIle 720
Qy      2408 GCTGCCAATCATATCCAGAAAGGCTTCCACAGAGCCGGAAGATTAATGTTGGTGTCT 2467
Db      721 AlaAlaMetIleIleGlnGluGlyPheHisLysSerArgValIleValIleValSer 740
Qy      2468 AGACACTTTATCCAGACCGCTGTGTATCTTGAATATGAGATGCTTCACACTGCGAG 2527
Db      741 GlnHisPheIleGlnSerArgTrpCysIlePheGluTrpGluIleAlaGlnThrTrpGln 760
Qy      2528 TTTCAGTGTGCGCTGCGCATCATCTTATGCTTTCAGAAAGTGAAGTGAAGTCCCTG 2587
Db      761 PheLeuSerSerArgAlaGlyIleIlePheIleValLeuHisLysLysGluLysSerLeu 780
Qy      2588 CTGAGCAGCAGCTGCAATGTATCGCTTCTTACAGAAACACTTACCTGAGTGGAG 2647
Db      781 LeuArgGlnGlnValGluLeuTrpArgLeuLeuAsnArgAsnThrTrpLeuGluTrpGln 800
Qy      2648 GACAACTCTTGGGAGGCAACATCTTGGAGAAAGACTCAAAAAGCCCTGTTGATGGA 2707
Db      801 AspSerValLeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGly 820
Qy      2708 AAGGCTTGANTCA-----GATGAACAATCAGAGAGAAACAAGAACAA 2755
Db      821 LysProTrpSerProAlaGlyThrAlaAspAlaAlaGluSerArgGlnHisAspAlaGlu 840
Qy      2756 ACTTTGAC 2764
Db      841 ThrSerThr 843

RESULT 6
TLR4_PAPAN STANDARD; PRT; 826 AA.
ID TLR4_PAPAN
AC 09TSP2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Papio ambis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC
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CC -----

DR EMBL; AF180964; AAF07059.1; .

DR EMBL; AF180962; AAF07059.1; JOINED.

DR EMBL; AF180963; AAF07059.1; JOINED.

DR HSSP; Q15399; 1FV.

DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.

DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO; GO:0001888; F:transmembrane receptor activity; ISS.

DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.

DR GO; GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:macrophage activation; ISS.

DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.

DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.

DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.

DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.

DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.

DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR00483; LRR_Cterm.

DR InterPro; IPR003591; LRR_Typ.

DR InterPro; IPR00157; TIR.

DR Pfam; PF00560; LRR; 13.

DR Pfam; PF01582; LRRCT; 1.

DR Pfam; PF01582; TIR; 1.

DR PRINTS; PR00019; LEURICHRPT.

DR SMART; SM00369; LRR_TYP; 2.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00255; TIR; 1.

DR PROSITE; PS50104; TIR; 1.

DR GlycoProtein; Immune response; Inflammatory response; Lactoferrin; Receptor; Signal; Transmembrane.

KT Leucine-rich repeat; Receptor; Signal; Transmembrane.

FT SIGNAL 1 23 Potential.

FT CHAIN 24 826 Extracellular (Potential).

FT DOMAIN 24 631 Potential.

FT TRANSMEM 632 652 Cytoplasmic (Potential).

FT DOMAIN 653 826 LRR 1.

FT REPEAT 53 76 LRR 2.

FT REPEAT 77 100 LRR 3.

FT REPEAT 101 124 LRR 4.

FT REPEAT 128 149 LRR 5.

FT REPEAT 150 173 LRR 6.

FT REPEAT 174 197 LRR 7.

FT REPEAT 203 225 LRR 8.

FT REPEAT 228 252 LRR 9.

FT REPEAT 277 303 LRR 10.

FT REPEAT 327 350 LRR 11.

FT REPEAT 351 372 LRR 12.

FT REPEAT 373 398 LRR 13.

FT REPEAT 400 421 LRR 14.

FT REPEAT 422 445 LRR 15.

FT REPEAT 447 469 LRR 16.

FT REPEAT 470 494 LRR 17.

FT REPEAT 495 518 LRR 18.

FT REPEAT 520 541 LRR 19.

FT REPEAT 543 569 LRR 20.

FT REPEAT 571 592 TIR.

FT DOMAIN 672 818

FT CARBOHYD 35 35 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 173 173 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 205 205 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 282 282 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 309 309 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 497 497 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 526 526 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 575 575 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 624 624 N-linked (G1cNAc . . .) (Potential).

FT CARBOHYD 630 630 N-linked (G1cNAc . . .) (Potential).

FT SEQUENCE 826 AA; 94678 MM; 42277318B5F1769 CRC64;

Alignment Scores:

Pred. No.: 1,51e-199

Score: 2668.00

Percent Similarity: 80.63%

Best Local Similarity: 67.43%

Query Match: 48.26%

DB: 1 Gaps: 4

US-09-396-985b-5 (1-3395) x TLR4_PAPAN (1-826)

QY 260 ATATGCTCTCTTTCATCTGCTGAGCTCTGATCATGGCATTTGCTTTCTCTGC 316

DB 1 MetThrSerAlaLeuArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20

QY 317 CTGAGACGAGAGCTTGAATCCCTGATGAGTACTCTTCAATATTACTTCAATGTC 376

DB 21 ValArgProIleSerThrGluProCysValGlnValValProSerIleThrTrpGlnCys 40

QY 377 ATGATCAGATCTCAGCAAAATCCCTCATGATCCCTTATTCACCAAGAACTTATGAT 436

DB 41 MetGlnLeuAsnPheTrpTrpIleProAspAsnIleProPheSerThrTrpValLeuAsp 60

QY 437 CTGAGCTTCAACCCCTGAAAGATCTTGAAGCTTATGCTTCAACCAATTTCTCAACTT 496

DB 61 LeuSerPheAsnProLeuArgHisLeuGlySerTrpSerPheLeuArgPheProGluLeu 80

QY 497 CAGTGGCTGATTTATTCAGAGTGTGAATTTGAACAATTGAACAAGCATGGCATGGC 556

DB 81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGlnAspGlyAlaTrpGlnSer 100

QY 557 TTAACCAAGCTTCAACCTTGTACTGACAGAAACCTTCAAGATTTTCCCCAGCA 616

DB 101 LeuSerHisLeuSerThrLeuIleLeuThrCysAsnProIleGlnSerLeuAlaLeuGly 120

QY 617 AGTTTTCTGACTTACAAATTTGAAGATCTGAGCTGTGAGACAAATGACCTCT 676

DB 121 AlaPheSerGlyLeuSerSerLeuGlnValAlaValGlnThrAsnLeuAlaSer 140

QY 677 CTGAGAGCTTCCATATTTGAGACGCTTATTCCTTAAAGAACTTAAATGAGCTCATAT 736

DB 141 LeuGlnAsnPheProIleGlnHisLeuTrpLeuLeuSerLeuValAlaHisAsn 160

QY 737 CTTATCATCTCTTAAAGTCCCTGAATATTTTCTATCTGACAAACCTTGAACATGTC 796

DB 161 LeuIleGlnSerPheLeuProGluTrpPheSerAsnLeuHisLeuGlnHisLeu 180

QY 797 GATCTTCTTATTAATCTATATTAACATATTCTGTGCAAGACTTACAGTTTCACTGAA 856

DB 181 AspLeuSerSerAsnGlyIleGlnAsnIleTrpCysLeuAspLeuGlnValLeuHisGln 200

QY 857 AATCCCAAGTCAATCTCTTTTGAACCTGCTTTTAAACCAATGATCTGCATTCAGCC 916

DB 201 MetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnPheIleGlnPro 220

QY 917 CAAGCTTTCAAGGGAATTTAGGCTCCATGATGACTTGAAGTAATTTTAAATGACTCA 976

DB 221 GlyAlaPheLeuGluIleArgLeuHisLeuLeuThrLeuArgSerAsnPheAspLeu 240

QY 977 AATGACTGAAATGTCCTTCAAAACATGATGCTTTTACATGTCATCGATGATCTTG 1036

DB 241 AsnValMetLeuSerThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 260

QY 1037 GGAGAAATTTAAATGAAGAATCTCGAAGTTTGAACCGTCTGTCAGGAAGGACTA 1096

DB 261 GlnGlnPheArgAsnGlnArgAsnLeuGlnGlnPheAspLeuSerAlaLeuGlnGlyLeu 280

QY 1097 TGCATCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1156

DB 281 CysAsnLeuThrIleGlnGlnPheArgLeuThrTrpLeuAspTrpTrpLeuAspAsnIle 300

QY 1157 TATATATCTC--AATGCTTGGCAAAATATTCTGCAATGCTTTTCAAGGTTGATCATATA 1213

DB 301 IleAspLeuPheAsnCysLeuAlaAsnAlaSerSerPheSerLeuValSerValAsnIle 320

RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in humans." ;
 RL Nat. Genet. 25:187-191(2000).
 RN [5]
 RP SEQUENCE OF 24-38.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites." ;
 RL Protein Sci. 13:2819-2824(2004).
 RN [6]
 RP MUTAGENESIS OF GLU-697; ARG-710; ASP-711 AND PRO-714.
 RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
 RA Xu Y., Tao X., Shen B., Hornig T., Medzhitov R., Manley U.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domains." ;
 RL Nature 408:111-115(2000).
 RN [7]
 RP CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-536 AND ASN-575.
 RX MEDLINE=21649731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
 RA da Silva Correia J., Ulevitch R.J.;
 RT "MD-2 and TLR4 N-linked glycosylations are important for a functional lipopolysaccharide receptor." ;
 RL J Biol. Chem. 277:1845-1854(2002).
 RN [8]
 RP VARIANTS ARG-188; SER-246; GLY-299; SER-329; ILE-399; LEU-443; LYS-474; HIS-510; ARG-694; HIS-763 AND HIS-834.
 RX MEDLINE=21405531; PubMed=11514453;
 RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4 in humans." ;
 RL Genetics 158:1657-1664(2001).
 CC -I- FUNCTION: Cooperates with ly96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response.
 CC -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, ly96 and TLR4. Binds ly96 via the extracellular domain. Binds MYD88 and TRAP via their respective TIR domains.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- TISSUE SPECIFICITY: Highly expressed in placenta, spleen and peripheral blood leukocytes. Detected in monocytes, macrophages, dendritic cells and several types of T-cells.
 CC -I- PTM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to be necessary for the expression of TLR4 on the cell surface and the LPS-response. Likewise, mutants lacking two or more of the other N-glycosylation sites were deficient in interaction with LPS.
 CC -I- POLYMORPHISM: Allele TLR4*B (Gly-299, Ile-399) is associated with a blunted response to inhaled LPS.
 CC -I- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -I- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -I- SIMILARITY: Contains 1 TIR domain.
 CC -----
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 CC -----
 CC EMBL; U93091; AAC80227.1; -;
 DR EMBL; U98880; AAC34135.1; -;
 DR EMBL; AF177765; AAF05316.1; -;
 DR EMBL; AF177766; AAF07823.1; -;
 DR EMBL; AF172171; AAF89753.1; -;
 DR EMBL; AF172169; AAF89753.1; JOINED.
 DR EMBL; AF172170; AAF89753.1; JOINED.
 DR HSSP; O60603; IFTY.
 DR Genem; HGNC:11850; TLR4.
 DR MIM; 603030; -;

DR	GO: 0000587	C: integral to plasma membrane; TAs.	
DR	GO: 0046866	C: lipopolysaccharide receptor complex; NAS.	
DR	GO: 0001530	F: lipopolysaccharide binding; NAS.	
DR	GO: 0004888	F: transmembrane receptor activity; NAS.	
DR	GO: 0007250	P: activation of NF-kappaB-inducing kinase; ISS.	
DR	GO: 0001606	P: detection of fungi; NAS.	
DR	GO: 0000958	P: detection of pathogenic bacteria; NAS.	
DR	GO: 0006955	P: immune response; TAs.	
DR	GO: 0004216	P: macrophage activation; IMP.	
DR	GO: 0004576	P: mast cell activation; ISS.	
DR	GO: 0004567	P: negative regulation of osteoclast different. . ; NAS	
DR	GO: 0004536	P: positive regulation of interleukin-1 biosyn. . ; ISS	
DR	GO: 0004508	P: positive regulation of interleukin-13 biosyn. . ; NAS	
DR	GO: 0045388	P: positive regulation of interleukin-13 biosyn. . ; ISS	
DR	GO: 0004540	P: positive regulation of interleukin-6 biosyn. . ; ISS	
DR	GO: 0007165	P: signal transduction; TAs.	
DR	GO: 0004208	P: T-helper 1 type immune response; NAS.	
DR	InterPro: IPR001611	LRR.	
DR	InterPro: IPR000483	LRR_Cterm.	
DR	InterPro: IPR003591	LRR_Cyp.	
DR	InterPro: IPR00157	TIR.	
DR	Pfam: PF00560	LRR; 12.	
DR	Pfam: PF01463	LRRCT; 1.	
DR	Pfam: PF01582	TIR; 1.	
DR	PRINTS: PR00019	LEURICHRPT.	
DR	SMART: SM00369	LRR_Typ; 2.	
DR	SMART: SM00082	LRRCT; 1.	
DR	SMART: SM00255	TIR; 1.	
DR	PROSITE: PS50104	TIR; 1.	
KW	Direct protein sequencing; Glycoprotein; Immune response; Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;		
KW	Repeat; Signal; Transmembrane.		
PT	SIGNAL	1	23
PT	CHAIN	24	839
PT	DOMAIN	24	631
PT	TRANSMEM	632	652
PT	DOMAIN	653	839
PT	REPEAT	52	76
PT	REPEAT	77	100
PT	REPEAT	101	124
PT	REPEAT	128	149
PT	REPEAT	150	173
PT	REPEAT	174	197
PT	REPEAT	203	225
PT	REPEAT	228	252
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PT	REPEAT	307	330
PT	REPEAT	332	350
PT	REPEAT	351	372
PT	REPEAT	373	398
PT	REPEAT	400	421
PT	REPEAT	422	445
PT	REPEAT	447	469
PT	REPEAT	470	494
PT	REPEAT	495	518
PT	REPEAT	520	541
PT	REPEAT	543	566
PT	REPEAT	568	592
PT	DOMAIN	672	818
PT	CARBOHYD	35	35
PT	CARBOHYD	173	173
PT	CARBOHYD	205	205
PT	CARBOHYD	282	282
PT	CARBOHYD	309	309
PT	CARBOHYD	497	497
PT	CARBOHYD	526	526
PT	CARBOHYD	575	575
PT	CARBOHYD	624	624
PT	CARBOHYD	630	630
PT	VARIANT	188	188
PT	VARIANT	246	246

FT VARIANT 299 299 D -> G (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986790) .
 /Frid=VAR_012739.
 FT VARIANT 329 329 N -> S.
 /Frid=VAR_018731.
 FT VARIANT 399 399 T -> I (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986791) .
 /Frid=VAR_012740.
 FT VARIANT 443 443 F -> L.
 /Frid=VAR_018732.
 FT VARIANT 474 474 E -> K.
 /Frid=VAR_018733.
 FT VARIANT 510 510 Q -> H.
 /Frid=VAR_018734.
 FT VARIANT 694 694 K -> R.
 Alignment Scores:
 Pred. No.: 5.31e-199 Length: 839
 Score: 2860.50 Matches: 559
 Percent Similarity: 80.24% Conservative: 115
 Best Local Similarity: 66.55% Mismatches: 159
 Query Match: 48.13% Indels: 7
 DB: 1 Gaps: 5
 US-09-396-985b-5 (1-3395) x TLR4_HUMAN (1-839)
 QY 260 ATGATGCTCTTCGATCTGGGAGGAGCTGATCATGCGATG---TTCCCTTCCTGC 316
 DB 1 Metceteralaseratgleualaglythrleuileproalawetalapheleusercys 20
 QY 317 CTGAGACAGAGAACTTGAATCCCTGATAGAGGACTCTTAATATTAATCTTACCAATGC 376
 DB 21 ValArgprogluinsertprgluiprocysvalgluivalproanillethrlyglnlys 40
 QY 377 ATGATATGAAATCTCAGCAAAATCCCTCATGACATCCCTTATTAACCAAGACTTATGAT 436
 DB 41 Metgluileuinspethyrllysileproaspasinsleuoproheserthrlyasinsleuasp 60
 QY 437 CTGAGCTTCAACCCCTGAGATCTTAAGAAGCTTATGAGCTTCAACCAATTTCTCAACTT 496
 DB 61 Leuserheasnprouleuarghnsleuglyserlyserpneheserpheprogluileu 80
 QY 497 CAGTGCGATTTATTCAGGTGTGAATTTGAGACAATTTGAGACAAGCATGCGATGCG 556
 DB 81 GluValleuasprouleuserargcysgluileglnthrilegluasparglyalatyglins 100
 QY 557 TTAACCAAGCTTCAACCTTGTGATGACAGAAACCTTATCAAGAGTTTTCCTCCAGGA 616
 DB 101 Leuserhisleuserthrleuileleuthrcllyasnprouleuglnserleuallaleugly 120
 QY 617 AGTTTTCTGACCTTAACAATTTTGAAGATCTGGTGGCTGTGAGACAAAATGACCTCT 676
 DB 121 Alapheaserglyleuserserleuglnlyleuvalalavalglutrhinsleuallaser 140
 QY 677 CTAGAGGGTTTCCATTTGACAGCTTATATCTTAAAGAACTTAATGCGTCATAT 736
 DB 141 Leuglinsprouleuileglnhileuylserthrleuylsergluileuvalalansh 160
 QY 737 CTATATCATCTTTAAGTGGCTGAATATTTTCTATGTCACAACTTGAACATGATG 796
 DB 161 Leuileglnserpheylsleuprouglutyrpneheserinsleuthraenleuglnhileu 180
 QY 797 GATCTTCTTATATCTATTAACAATTTCTGTCAAGACTTTCAGTTTCTGACGAA 856
 DB 181 Aspleuseraserinsyllelglnseriletyrcysthrleuaspargvalleuinsleu 200
 QY 857 AATCCCAAGTCAATCTCTCTTGAACCTGTCTTAAACCAATTTGATCCTCAAGCC 916
 DB 201 Metprouleuinsleuinsleuasprouleuserinsleuinsproumetanpheileglnpro 220
 QY 917 CAAGCTTTCAAGGAATTTAGGCTCCATGAATTTGATTAAGAACTTAATTTATAGTCA 976
 DB 221 GlyAlapheylsergluileargleuinsleuylserthrleuasparginsprouleu 240

QY 977 AATGTAAGAAATGTCCTTCAAAACATGACTGGTTTATGATCCATCGGTTGATCTTG 1036
 DB 241 AsnValmetylserthrlycysileglnsleuallaleuglnleuvalhlsargleuvalleu 260
 QY 1037 GGAGATTTTAAATGAAGAACTTGGAAAGTTTGAACCGTTTGTTCATGAAAGACTA 1096
 DB 261 Glygluuphearginsleuglnlyasinsleuglnlypneheserleualaleuglnlyleu 280
 QY 1097 TGCAATGTGAGCATGATGATGAGTTCAAGTTAATATATATTTTTCAGATGATTT 1156
 DB 281 Cysasinsleuthrileglnleuargleuallatyrlleuaspnylytyrleuaspaspille 300
 QY 1157 TATATCTC---AATTCCTTGCAAAATATTTTCTGCAATCTTTCACAGGTGTCATATA 1213
 DB 301 Ileasprouleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 320
 QY 1214 AAACACATGACAGATGTTCTTGAAGCATTTGCAATGCAATCTTATCATATTAGATG 1273
 DB 321 GluArgVallyaspneheserlyrasnphegllytrpghinsleuinsleuvalasncys 340
 QY 1274 CATCTTGAAGCTTTCCAAAGCTGAGTCATCTTTTCTTAAAGTTGAGCTTATACACC 1333
 DB 341 Lysphegllyglinsprouthrleuylsleuylserleuylsargleuthrthrser 360
 QY 1334 AACAGAGAGATATACAGCTTGTGACATGCTGCGCAAGTCTCAGATATCTGATCTT 1393
 DB 361 Asnysgllyglinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 380
 QY 1394 AGTGAATGCAATGAGCTTTAGAGTGTGCTTCTTATTTCTGATTTTGAACCAACAC 1453
 DB 381 Sertrgansglyleuserpheylslycyscysersinsleuasphegllythrthrser 400
 QY 1454 CTGAAGTACTTAAACCTCAGCTTCAATGAGTGTCTCTGATGATGCGCACTTATAGGT 1513
 DB 401 Leuylserlyleuasprouleuserpheasnglyvalillethmetserleuaspheleugly 420
 QY 1514 CTGAAGAGCTTGAATCTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1573
 DB 421 Leuglninsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 440
 QY 1574 TCAAGTCTTATCTTCTTGAACAACTTCTTACCTGACATCTTCACTAATACCAA 1633
 DB 441 SerValpneuserleuaspansleuiletyrleuaspriieserhsthrhlsThrArg 460
 QY 1634 ATTGACTTATGAGCATATTTCTTGCTTGAATGATGATGATGATGATGATGATGATG 1693
 DB 461 ValAlapheasnglyleupneasnglyleuserserleuinsleuinsleuinsleuinsleu 480
 QY 1694 AATTCCTTCAAGCAACACCTTCAATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1753
 DB 481 Asnserpheglnsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 500
 QY 1754 CTGATCTTCTTAAATGCAACCTGGAACAGATATCTGAGGGGATTTTGAACACACTTAC 1813
 DB 501 Leuasprouleuserglnsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 520
 QY 1814 AAGCTCAAGTTATTAACATGAGTACACACACCTTACTGTTTCTGATCCATTCAT 1873
 DB 521 Serleuglninsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 540
 QY 1874 AAACAGCTGATCCCTCCAGACTCTGATGATGATGATGATGATGATGATGATGATG 1930
 DB 541 Lyscysleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 560
 QY 1931 AAAGATATCTGACAACTTTTCCAAAGAGTCTAGCCGCTTCTTCAATCTGATTAATATCT 1990
 DB 561 Lysglnglnleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 580
 QY 1991 GTTGCTTGTATATGTAATATCAAGATTTCTTGACATGAGGTCAAGACCGCAAAATGTTTC 2050
 DB 581 PheAlcysthrlycysgluinsleuinsleuinsleuinsleuinsleuinsleuinsleuinsleu 600

ID	TLR4_PANPA	STANDARD;	PRT;	839 AA.
CC	2051	TTGGTGAATGTTTGAACAAATGAAATGTGCATCACCCTATAGCATGAAAGGCTCCCTGTG	2110	
Db	601	LeuValGIuValGIuValxMetGlcCysAlaThrProSerAspLysGlnGlyMetProVal	620	
Oy	2111	TTGGAATTTTACGAATTCACCTGGTTATCTTATACAAAGATATATCATCAGTGATCGATGTC	2170	
Db	621	LeuSerLeu---AsnIleThrCysGlnMetCAsnLysThrIleIleGlyValSerValLeu	639	
Oy	2171	AGTGTGCTTGTGTGGTAGGACCTGTAGACATTTCTGTATATACACCTTCTATTTTTCACCTGATA	2230	
Db	640	SeValLeuValSerValSerValAlaValLeuValTyrLysPheTyrPheHISLeuMet	659	
Oy	2231	CTTATATGCTGTGCTGTGAAAAAAGTATACAGCAGAGAAAGAACACTATAGATGATTTGTATC	2290	
Db	660	LeuLeuAlaGlyCysVleIleTyrTolYArgGlyGluMetAsnIleTyrAspAlaPheValIle	679	
Oy	2291	TACTGAGACCGAATAGAGACACTGGGTGAGAAACGAGCTGTAAAGATTTATGAAAGAAAGA	2350	
Db	680	TyrSerSerGlnAspGlnAspTrpValAlaArgAsnGluLeuValIlyAsnLeuGlnGlnGly	699	
Oy	2351	GTGCCCCGCTTTCAGCTTGTGCTTCATATACAGGAGACTTATTTCTGTGTAGCCATTGCT	2410	
Db	700	ValProProPheGlnLeuCysLeuHISLysThrArgAspPheIleProGlyValAlaIleLeu	719	
Oy	2411	GCCAATCATCATCCAGAAAGCTTCCACAAGACCGGAAAGTTATTTGTGTGTGTCTAGA	2470	
Db	720	AlaAsnIleIleHISGlnGlyPheHISLysSerArgLysValIleValAlaValSerGln	739	
Oy	2471	CACTTTATTCACAGACCGTGTGTATCTTTTAAATATGAGATTTGCTCAGACATGGCAGTTT	2530	
Db	740	HisPheIleGlnSerArgTrpCysIlePheGlnTyrGluIleAlaGlnThrTTrpGlnPhe	759	
Oy	2531	CTGAGTAGCCGCTGTGATCATCTTTCATTTGCTTCTTGTGAAAGTGAAGTCCCTGTGCTG	2590	
Db	760	LeuSerSerArgAlaGlyIleIlePheHISLeuValLeuGlnLysValGlnLysThrLeuLeu	779	
Oy	2591	AGGCAGCAGCGTGAATTTGTATGTCCTTTTACAGAAACACTTACTTGAGTGGAGGAC	2650	
Db	780	ArgGlnGlnValAlaGluLeuTyrArgPheLeuSerArgAsnThrTyrLeuGlnTTrpGlnAsp	799	
Oy	2651	AATGCTCTGGGGAGGACATCTTCTCGAGGAAGACTCAAAAAGCCCTGTGAGTGGAAAA	2710	
Db	800	SerValLeuGlnGlyArgHisIlePheThrArgLeuAlaGlyValAlaLeuMetAspLys	819	
Oy	2711	GCTTGAATTCACAGAT-----GAAACATCAGAGAAAGAAAGAAAGCAACACTTGTG	2761	
Db	820	SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle	839	

CC		multi-protein complex containing at least CD14, LY96 and TLR4.
CC		Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
CC		their respective TIR domains (By similarity).
CC	-1-	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1-	SIMILARITY: Belongs to the Toll-like receptor family.
CC	-1-	SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
CC	-1-	SIMILARITY: Contains 1 TIR domain.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb.ch/announce/
CC		or send an email to license@isb-sib.ch).
CC		-----
DR	EMBL; AF179220; AAF05330.1; .	
DR	EMBL; AF179218; AAF05330.1; JOINED.	
DR	EMBL; AF179219; AAF05320.1; JOINED.	
DR	HSSBP; Q15399; IPFYV.	
DR	GO; GO:0046666; C:lipopolysaccharide receptor complex; ISS.	
DR	GO; GO:0001530; F:lipo polysaccharide binding; ISS.	
DR	GO; GO:0004888; P:transmembrane receptor activity; ISS.	
DR	GO; GO:0007280; P:activation of NF-kappaB-inducing kinase; ISS.	
DR	GO; GO:0016046; P:detection of fungi; ISS.	
DR	GO; GO:0009598; P:activation of pathogenic bacteria; ISS.	
DR	GO; GO:0042116; P:macrophage activation; ISS.	
DR	GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.	
DR	GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.	
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.	
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR000483; LRR_Cterm.	
DR	InterPro; IPR003591; LRR_Typ.	
DR	InterPro; IPR000157; TIR.	
DR	Pfam; PF00560; LRR; 12.	
DR	Pfam; PF01463; LRCT; 1.	
DR	Pfam; PF01583; TIR; 1.	
DR	PRINTS; PR00019; LEURICHRPT.	
DR	SMART; SM00369; LRR_Typ; 2.	
DR	SMART; SM00082; LRCT; 1.	
DR	SMART; SM00255; TIR; 1.	
DR	PROSITE; PS50104; TIR; 1.	
KW	Glycoprotein; Immune response; Inflammatory response;	
	Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1..23 Potential.
FT	CHAIN	24..839 Toll-like receptor 4.
FT	DOMAIN	24..631 Extracellular (Potential).
FT	TRANSMEM	632..652 Potential.
FT	DOMAIN	653..839 Cytoplasmic (Potential).
FT	REPEAT	52..76 LRR 1.
FT	REPEAT	77..100 LRR 2.
FT	REPEAT	101..124 LRR 3.
FT	REPEAT	128..149 LRR 4.
FT	REPEAT	150..173 LRR 5.
FT	REPEAT	174..197 LRR 6.
FT	REPEAT	203..225 LRR 7.
FT	REPEAT	228..252 LRR 8.
FT	REPEAT	277..303 LRR 9.
FT	REPEAT	307..330 LRR 10.
FT	REPEAT	332..350 LRR 11.
FT	REPEAT	351..372 LRR 12.
FT	REPEAT	373..398 LRR 13.
FT	REPEAT	400..421 LRR 14.
FT	REPEAT	422..445 LRR 15.
FT	REPEAT	447..469 LRR 16.
FT	REPEAT	470..494 LRR 17.
FT	REPEAT	495..518 LRR 18.
FT	REPEAT	520..541 LRR 19.
FT	REPEAT	543..566 LRR 20.

FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 839 AA; 95637 MW; 38328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 6,28e-199 Length: 839
 Score: 2859.50 Matches: 559
 Percent Similarity: 80.24% Conservative: 115
 Best Local Similarity: 66.55% Mismatches: 159
 Query Match: 48.12% Indels: 7
 DB: 1 Gaps: 5

US-09-396-985B-5 (1-3395) x TLR4_PANRA (1-839)

QY 260 ATGATGCTCTTTCATCTTGGTGGGAACTGATGATGCGATTG--TTGCTTTCTGTC 316
 DB 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 317 CTGAGCAGGAACTGATGATCCCTGCACTAGAGGTACTCTTATATATTACTTACCAATGC 376
 DB 21 ValArgProGluSerTrpGluProCysValGluValAlaProAlaMetIleThrTyrGlnCys 40
 QY 377 ATGATGAGATCTCAGGAAATCCCTCATGATCCCTTATGACCAAGAACCTTGAT 436
 DB 41 MetGluLeuAsnProIleTyrLysIleProAspAsnIleProPheSerThrLysAsnLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGAGAGATCTTAGAAGCTTAGAGCTTCAACCAATTTCTCAACT 496
 DB 61 LeuSerPheAsnProLeuArgIleLeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 497 CAGTGGGTGATTTATCCAGGTGGAATTTAGACAAATTGAAACAAAGGATGGCATGGC 556
 DB 81 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspArgLysAlaTyrGlnSer 100
 QY 557 TTAACAGAGCTTCAACCTTGGTCTAGCAGGAAACCTTACAGAGTTTTCSCCAGGA 616
 DB 101 LeuSerIleLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 617 AGTTTTCCTGAGTACAAATTTAGAGATCTGGTGGCTGAGACAAATGACCTCT 676
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValAlaGluThrAsnLeuAlaSer 140
 QY 677 CTAGAGGGTTTCCATATTGACAGCTTATATCTTAAAGAACTAAATGTCGTCATAT 736
 DB 141 LeuGlnAsnPheProIleGlyAsnIleLeuLysThrLeuLysGluLeuAsnValAlaAsnIleAsn 160
 QY 737 CTATATACATCTCTTAGAGTGGCTGAAATATTTTCTATCTGACAAACCTAGAACATGTC 796
 DB 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnIleLeu 180
 QY 797 GATCTTCTTATTAATCTATATCAACTATTCTGCAAGACTTACAGTTTCTAGCTGAA 856
 DB 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuAspValIleAsnGln 200
 QY 857 AATCCCAATCATCTCTCTTAAAGCTGCTCTTAAACCAATGATCATGATCAAGCC 916
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 917 CAAGCCTTTCAGGGAATTAGGCTCATGATGATGACTTAGAAGATATTTTAATAGTCA 976
 DB 221 GlyAlaPheLysGluIleArgLeuAsnIleLysLeuThrLeuLysAsnAsnPheAspSerLeu 240
 QY 977 AATGTACTGAATAATGTCCTTCAAAACATGATGATGATGATGATGATGATGATGATGAT 1036

DB 241 AsnValMetLysThrCysIleGlnGlyLeuValAlaGlyLeuValIleAspArgLeuValLeu 260
 QY 1037 GGAATAATTTAAATGAAAGAAATCTGGAAAGTTTGAACGCTTCTGCATGAAAGACTA 1096
 DB 261 GlyIleLysPheArgGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 1097 TGCATGTGAGCATGTGATGAGTTACAGGTTAACTATATTAATCTATTTTTCAGATGATTT 1156
 DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspLysTyrTyrLeuAspAspIle 300
 QY 1157 TATATATCTC--AATTCCTGGCAAAATATTTCTGCAATGTCTTTCACAGGTGTACATTA 1213
 DB 301 IleAspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1214 AAACATACATGACATGTCTTCCATGACATTTCAATGCAATCTTATCATATATGATGT 1273
 DB 321 LysSerValLysAspPheSerTyrAsnPheGlyTyrGlnIleLeuGluLeuValAsnCys 340
 QY 1274 CATCTTAAGCCTTTCGAAAGCTGAGTCACTCTTTCTTAAAGTTGAGCTTAACTTAC 1333
 DB 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
 QY 1334 AACAGAGAGATATACACTTTGCTCAGTTGGCTTGCACAACTCAGATATCTGATCTT 1393
 DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1394 AGTTGAATGCCATGAGCTTAAAGCTGCTGCTTTATTTCTGATTTTGGAAACAAACAC 1453
 DB 381 SerArgAsnLysLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGTACTTAAAGCTCAGCTTCAATGAGTGTCATCTGATGAGTGCAACTTATGAGGT 1513
 DB 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheGly 420
 QY 1514 CTGAAGAGCTGGAATCTGGAATCTTCAACACTTCACTTCACTTAAAGGTCACAGAAATC 1573
 DB 421 LeuGlnIleLeuGlnIleAsnAspPheGlnIleSerAsnLeuLysGlnMetSerGluPhe 440
 QY 1574 TCAAGTCTTCTTATCTTGAAGAACTCTTACCTTCACTCTTCACTTCACTAATACCAA 1633
 DB 441 SerValPheLeuSerLeuAspAsnLeuIleTyrLeuAspIleSerIleThrIleAspArg 460
 QY 1634 ATTGACTTGTAGGCAATATTTCTGGCTGATGATGATGATGATGATGATGATGATGAT 1693
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLysLysMetAlaGly 480
 QY 1694 AATCTTTCAAAGCAACACCTTTCAATGCTTTTCAAAACCAACCAACTTAAACATTC 1753
 DB 481 AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlyLeuAspGlnLeuThrPhe 500
 QY 1754 CTGATCTTCTTAAATGCCAATGGAACAGATATCTAGGGGGGATTTTGAACACACTTAC 1813
 DB 501 LeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1814 AGATCCAGTATTAACATGAGTGCACCAACCACTATGTTTCTGATGATGCCATAT 1873
 DB 521 SerLeuGlnValLeuAsnMetSerThrAsnAsnPhePheSerLeuAspThrPheProTyr 540
 QY 1874 AAACAGCTTACTCCCTCAGAGCTTGTGATGCAATTTGATGCAATGACATGACATCC-- 1930
 DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnIleIleMetClnThrSerLys 560
 QY 1931 AAAGAAATCTGAAACATTTTCCAAAGCTAGCCGCTTCAATGCTGATGATTAATTTCT 1990
 DB 561 LysGlnGluLeuGlnIleAspProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1991 GTTCTGTGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2050
 DB 581 PheAlaCysThrCysGlnIleGlnIleSerPheLeuGlnIleThrIleLysAspGlnIleGln 600
 QY 2051 TTGGAATGTTTGAACAAATGAAATGTCATCACTTATGACATGAAGGCTCCCTGGTG 2110

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Db      601 LeuValGluValGluArgMetGluCysAlaThrProSerAspIySgIngluMetProVal 620
QY      2111 TTGGATTTCAGCAATTCACCTGTATATATACAAAGCTATCATGATGATGGTGC 2170
Db      621 LeuSerLeu--AsnIleThrCysGlnMetAsnIySthrIleIleGlyValSerValLeu 639
QY      2171 AGTGTGCTGTGGTAGGACCTGTAGCAATTCATATACCACTTATTTTCACTGATA 2230
Db      640 SerValLeuValValSerValValAlaValLeuValIyTrpIySphetyrPheHISleuMet 659
QY      2231 CTATTGCTGTGGCTGTAAAAAGTACAGAGAGAGAAAGCATCTATGATGATTTGTATC 2290
Db      660 LeuLeuIleGlyCysIleIySyrGlyArgGlyGluAsnIleIyTrpAlaIlePheValIle 679
QY      2291 TACTCGACGACAGATGAGCATGGGTGAGAAACGAGCTGGTAAAGATTTAGAGAAAGA 2350
Db      680 TyrSerSerGlnAspGlnAspIyTrpValAlaArgAsnGluLeuValIySAsnIleGluGly 699
QY      2351 GTCGCCGCTTTCAGCTTTCCTTCATTCAGAGGACCTTATTCCTGTGTAGCCATTGCT 2410
Db      700 ValProProPheGlnLeuGluCysLeuHISIyTrpArgAspPheIleProGlyValAlaIleAla 719
QY      2411 GCCAATCATTCACAGAGAGCTTCCACAGAGCCGAGAAAGTTATGTGTGTGTCTAGA 2470
Db      720 AlaAsnIleIleHISgluGlyPheHISlySerArgIySValIleValIleValIleValIle 739
QY      2471 CACTTATTCAGAGCCGTGTGTATCTTGAATATGATGATGCTGACATGGCACTTT 2530
Db      740 HisPheIleIleGlnSerArgIyTrpCysIlePheGluIyGluIleAlaGlnIleIleIlePhe 759
QY      2531 CTGAGTAGCCGCTTTCAGCATCATCTTCATTCCTTCCTGAGAAAGTGAAGTCCCTTCG 2590
Db      760 LeuSerSerArgIleGlyIleIlePheIleValLeuGlnIySValIleGluIySThrLeuLeu 779
QY      2591 AGGCAGAGAGGTGCAATGTATTCGCTTTCAGAGAAACCTTACCTGAGTGGAGAGAC 2650
Db      780 ArgArgGlnValGluLeuIyTrpArgLeuLeuSerArgAsnIyTrpLeuGluIyTrpGluAsp 799
QY      2651 AATGCTCTGGGAGGAGCATCTTCCTGAGAGAACTCAAAAAGCCCTGTGTGATGAAA 2710
Db      800 SerValLeuGlyArgHisIlePheIleIlePheIleValLeuGlnIySValIleAspGlyLys 819
QY      2711 GCCTTGATTCAGAT-----GAAACATCAGAGAGAGAAACAGAGCAACTTTG 2761
Db      820 SerTrpAsnProGluGlyThrValGlyThrGlyCysAsnIyTrpGlnIleValIleIleSerIle 839
RESULT 9
Q8SPB8 PRELIMINARY; PRT; 837 AA.
AC Q8SPB8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9593;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=2140531; PubMed=11514453;
RA Smitnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RT in humans."
RL Genetics 158:1657-1664 (2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Beutler B., Smitnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497565; AAM18617.1; -
DR EMBL; AF497563; AAM18617.1; JOINED.
DR EMBL; AF497564; AAM18617.1; JOINED.

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DR HSP; 060603; 1077.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; F:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045676; P:mast cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Ctyp.
DR InterPro; IPR000157; TIR.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF05560; LRR_1; 10.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR Receptor.
DR KW Receptor.
SQ SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;

Alignment Scores:
Pred. No.: 1,12e-196 Length: 837
Score: 2828.50 Matches: 556
Percent Similarity: 79.76% Conservative: 114
Best Local Similarity: 66.19% Mismatches: 161
Query Match: 47.59% Indels: 9
DB: 2 Gaps: 6
US-09-396-985b-5 (1-3395) x Q8SPB8 (1-837)
QY 260 ATGATGCTTCTTCGATCTGCTGGAGCTCTGATCATGCAATG--TTCCTTTCTGTC 316
Db 1 MetMetSerIleSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 317 CTGAGACCAAGAGAGCTTGAATCCCTGATAGAGTACTTCTAATATTACCAATATGC 376
Db 21 ValArgProGluSerIyTrpGluProCys-----ValValProAsnIleIleIyTrpGlnCys 38
QY 377 ATGATCAGAAATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTAGAT 436
Db 39 MetGluLeuAsnIlePheIyTrpIleProAspAsnLeuProPheSerIySAsnLeuAsp 58
QY 437 CTGAGCTTCAACCCCTGGAAGATCTTAAGAAGCTATAGCTTTCACCAATTTCTACAATT 496
Db 59 LeuSerPheAsnProLeuArgHisIleuGlySerIySerPhePheSerPheProGluLeu 78
QY 497 CAGTGTGATTTATTCACAGGTGTAATTAATGAGCAATTTAGAGACAAAGCATGATGGC 556
Db 79 GlnValLeuAspIleuSerArgCysGluIleGlnIleIleIleuAspGlyAlaIyTrpGlnSer 98
QY 557 TTAAACGAGCTTCAACCTTGTACTGACAGAAACCTTATCAAGATTTTCCCGAGA 616
Db 99 LeuSerHisIleuSerIyTrpIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 118
QY 617 AGTTTTCTGAGCTTAACAAATTTAGAGATCTGTGTGCTGTGAGACAAATAGACTCT 676
Db 119 AlaPheSerGlyLeuSerSerIleuGlnIyLeuValAlaValGluIleIleuIleuIleuIleu 138
QY 677 CTAGAGGCTTTCATATTCAGACAGCTTATATCTTAAAGAACTTAATGAGCTCATAT 736
Db 139 LeuGluAsnIlePheProIleGlyHisIleuIySThrLeuIySgluLeuIleuIleuIleuIleu 158
QY 737 CTATACATTCCTTTAAGTTGCTGAAATATTTTCTTATCTGACAAACCTAGAACATGTG 796

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Db      159 Leu1Leu1SerPheLysLeuProGluTyrPheSerLeuThrAsnLeuGluTyrLeu 178
Qy      797 GATCTTCTTATTAATCAACTATTTCTGTCAAAGACTTAAAGTTTCTACGGTCA 856
Db      179 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuValLeuIleGln 198
Qy      857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCCAAATGACCTCCATCAAGCC 916
Db      199 MetProLeuLeuAsnLeuSerLeuAspSerLeuAsnProMetClnPheIleGlnPro 218
Qy      917 CAAGCTTTGAGGAAATTTAGGCTCCATGAATTCCTAGAGTAATTTTAAATGCTCA 976
Db      219 GlyAlaPheLysGluIleArgLeuIleLysLeuThrLeuArgAsnAsnPheAspSerLeu 238
Qy      977 AATGCTTGAATATGTCCTTCAAAACATGATGCTGTTTACATGTCACATCGGTGATCTG 1036
Db      239 AsnValMetLysThrCysIleGlnGlyLeuValAspLeuGluValArgArgLeuValLeu 258
Qy      1037 GAGAAATTTAAATGAAGAATCTGAAAGTTTGAACGCTGTCTGATGAGAGACTA 1096
Db      259 GlyGluPheArgAsnGluIleAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 278
Qy      1097 TGCATGTGAGCATGATGATGATGATGATTAATATTAATCAATTTTTCAGATGATTT 1156
Db      279 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 298
Qy      1157 TATPATCTC---AATGCTGGGCAATATTTCTGCATATGCTTTTCAACAGGTGTCATATA 1213
Db      299 IleAspLeuPheAsnCysLeuThrAsnValSerSerSerLeuValSerValThrIle 318
Qy      1214 AAACATACATGACAGATGTTCTAGACATTTCAATGAGCAATCTTATCATCATTAAGATGT 1273
Db      319 GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnIleSleuGluLeuValAsnCys 338
Qy      1274 CATCTTAAGCTTTTCCAAAGCTGATCTCACTTTTAAAGTTGAGCTTTAACTACC 1333
Db      339 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 358
Qy      1334 AACAGACAGATATACAGCTTTGTCAGTGGCTGTCAGATGCTCAATATCTAGATCTT 1393
Db      359 AsnLysLeuGlyLysAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 378
Qy      1394 AGTAGAATCCATGACGCTTAAAGTGTGCTGTTCTTATCTGATTTTGAACAACAAC 1453
Db      379 SerArgAsnLysLeuSerPheLysGlyCysCysSerIleAsnAspPheGlyThrThrSer 398
Qy      1454 CTGAAGTACTTAACTCAGCTTCAATGTGTCTATCTGATGAGTGCACATTCATGGGT 1513
Db      399 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 418
Qy      1514 CTGAAGAGCTGGAATATCTGGAATCTTACAGACTCCCATTTAAAGGTCACAGAAATTC 1573
Db      419 LeuGluGlnLeuGlnIleAsnAspPheGlnIleSerSerLeuLysGlnMetSerGluPhe 438
Qy      1574 TCAGTGTCTTATCTCTTGAAGAAATCTTATCACTTGAACATCTTCACTTAATACCAA 1633
Db      439 SerValPheLeuSerIleuArgAsnLeuIleTyrLeuAspIleSerIleStrnHisThrArg 458
Qy      1634 ATTGACTTGATGAGCATATTTCTTGCTGATGATGATGATCAACATTTAAAGTGGCTGGC 1693
Db      459 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 478
Qy      1694 AATTTCTTCAAAACAACACCTTCAAAATGCTTTTCAAAACAACAACAACTTAACATTC 1753
Db      479 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrIleuLysArgAsnLeuThrPhe 498
Qy      1754 CTGAGATCTTCTTAATGCAACTGAAACAGATATCTAGGGGGGATTTTGAACACTGTAC 1813
Db      499 LeuAspLeuSerIleCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 518
Qy      1814 AGACTCAGTTATTAACATGAGTCACACAACTCACTGTTTGTGATTCATCCATTAAT 1873

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Db      519 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 538
Qy      1874 AAACAGCTGATACCTCCACAGACTCTGATTTGACGTTTCAATGCCATAGACATCC--- 1930
Db      539 LysCysLeuAsnSerLeuArgValLeuAspTyrSerLeuAsnHisIleIleThrSerLys 558
Qy      1931 AAAGAAATCTGCAACATTTTCCAAAGACTAGCCGCTCTTCAATCTGACTAATTAATCTT 1990
Db      559 LysGlnIleuLeuGlnIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 578
Qy      1991 GTTGCTGTATATGTGAATATCAAGATTTCTTGACGTGGCTCAAGAACACAGAAATGCTC 2050
Db      579 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrIleLysAspGlnArgGlnLeu 598
Qy      2051 TTGGTGAATGTGAACAATGAATGCAATGCACTTCATAGACATGAAGGCTCCCTGGTG 2110
Db      599 LeuValGluValGluValGluMetGluCysValThrProSerAspLysGlnGlyMetProVal 618
Qy      2111 TTGGATTTTGAATTCACCTGTTATATATACAAAGCTATTCATGATGATCGGTGTC 2170
Db      619 LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 637
Qy      2171 AGTGTCTGTGTAGCCACTGTAGCATTTCTGATATATCAACTTATTTTCACTGATA 2230
Db      638 SerValLeuValIleSerValIleAlaValLeuValTyrLysPheTyrPheIleLeuMet 657
Qy      2231 CTATATGCTGTGCTTAAAGTACAGACAGAGAAAGCATCTATGATGCTTTGTGATC 2290
Db      658 LeuLeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnValTyrAspAlaPheValIle 677
Qy      2291 TACTGACGACAGATGAGACTGAGGTGAGAAACAGCTGTGTAAGATTTAGAAAGAGA 2350
Db      678 TyrSerSerIleAspGluAspTyrValArgAsnGluLeuValLysAsnLeuGluGly 697
Qy      2351 GTGCCCGCTTTCAGCTTCTGCTTATTCAGAGCATTTATTCCTGTGTAGCCATTTGCT 2410
Db      698 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 717
Qy      2411 GCCAACATCATCCAGAGAGCTCCCAAGAGCCGAAATTTTGTGTGTGTCTAGAGA 2470
Db      718 AlaAsnIleIleHisGluGlyPheHisLysSerArgLysValIleValIleValSerGln 737
Qy      2471 CACTTATCCAGAGCCGTTGTGATCTTGAATATGAGATTTGCTCAGATGACAGATTT 2530
Db      738 HisPheIleGlnSerArgTyrCysIlePheGluTyrGluIleAlaGlnThrIlePhe 757
Qy      2531 CTGATGACCGCTGTGACATCTTCATTTGCTTGAAGAAAGTGAAGAGTCTTGCTG 2590
Db      758 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeu 777
Qy      2591 AGGCACAGGTGCAATTTGATGCTTCTTGAAGAAACCTTACCTCCAGTGGAGAGAC 2650
Db      778 ArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluIleThrAsp 797
Qy      2651 AATGCTGTGGGAGGACACTCTCTGAGAGAACTCAAAAAGCCCTGTTGATGAGAAA 2710
Db      798 SerValLeuGlyArgHisIlePheThrArgValLeuArgLysAlaLeuLeuAspGlyLys 817
Qy      2711 GCCTGAATCCAGAT-----GAACATCAGAGAAAGAACAGAAAGCAACACTTGG 2761
Db      818 SerTyrAsnProGluGlyThrValGlyThrGlyCysAsnTyrGlnGluIleThrSerIle 837

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RESULT 10
TLR4_FELCA STANDARD; PRT; 833 AA.
AC P58727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Felis silvestris catus (Cat).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Genetics 158:1657-1664 (2001).

- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response (by similarity).

- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TRAF4. Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via their respective TIR domains (by similarity).

- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

- SIMILARITY: Belongs to the Toll-like receptor family.

- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

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CC EMBL; AF497562; AAM18616.1; .

CC EMBL; AF497560; AAM18616.1; JOINED.

CC EMBL; AF497561; AAM18616.1; JOINED.

CC HSSP; O60603; LPYM.

DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.

DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO; GO:0004888; F:transmembrane receptor activity; ISS.

DR GO; GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.

DR GO; GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:osteoclast activation; ISS.

DR GO; GO:0045571; P:negative regulation of osteoclast different. . . ; ISS.

DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.

DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.

DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.

DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.

DR GO; GO:0042088; P:helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR_Cterm.

DR InterPro; IPR003591; LRR_Typ.

DR InterPro; IPR001517; TIR.

DR Pfam; PF00560; LRR; 12.

DR Pfam; PF01463; LRRCT; 1.

DR Pfam; PF01582; TIR; 1.

DR PRINTS; PR00019; LEURICHRPT.

DR SMART; SM00369; LRR_Typ; 1.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00255; TIR; 1.

DR PROSITE; PS50104; TIR; 1.

DR GlycoProtein; Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Signal; Transmembrane.

KW SIGINL 1 23

FT CHAIN 24 828

FT DOMAIN 24 629

FT TRANSMEM 630 650

FT DOMAIN 651 828

FT REPEAT 50 74

FT REPEAT 75 98

FT REPEAT 99 122

FT REPEAT 126 147

FT REPEAT 148 171

FT REPEAT 172 195

FT REPEAT 201 223

FT REPEAT 226 250

FT REPEAT 275 301

FT REPEAT 325 348

FT REPEAT 349 370

FT REPEAT 371 396

FT REPEAT 398 419

FT REPEAT 420 443

LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 8.

LRR 9.

LRR 10.

LRR 11.

LRR 12.

LRR 13.

LRR 14.

FT REPEAT 445 467

FT REPEAT 468 492

FT REPEAT 493 516

FT REPEAT 518 539

FT REPEAT 541 564

FT REPEAT 566 590

FT DOMAIN 670 816

FT CARBOHYD 33 33

FT CARBOHYD 171 171

FT CARBOHYD 203 203

FT CARBOHYD 280 280

FT CARBOHYD 307 307

FT CARBOHYD 495 495

FT CARBOHYD 524 524

FT CARBOHYD 573 573

FT CARBOHYD 622 622

FT CARBOHYD 628 628

SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DFD CRC64;

FT REPEAT 445 467 LRR 15.

FT REPEAT 468 492 LRR 16.

FT REPEAT 493 516 LRR 17.

FT REPEAT 518 539 LRR 18.

FT REPEAT 541 564 LRR 19.

FT REPEAT 566 590 LRR 20.

FT DOMAIN 670 816 TIR.

FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 280 280 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 573 573 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 628 628 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DFD CRC64;

Alignment Scores:

Prod. No.: 9,05e-196 Length: 828

Score: 2816.00 Matches: 550

Percent Similarity: 79.93% Conservative: 111

Best Local Similarity: 66.51% Mismatches: 160

Query Match: 47.38% Indels: 6

DB: 1 Gaps: 5

US-09-396-985b-5 (1-3395) x TIR4_PONRY (1-828)

QY 260 ATGATGCTCTTGTGATCTGGTGGACTGTGATGAGCATG--TTCTTTCTGTC 316

1 MetMetSerAlaSerArgLeuAlaGlyThrLeuLeProAlaMetAlaPheLeuSerCys 20

QY 317 CTGAGACCGAAGAGCTTGAATCCCTGCATGAGTACTTCTTAATATTACTTCCATGCG 376

21 ValAlaArgProGluSerThrGluProCys-----ValValProAlaSerIleThrTyGlnCys 38

QY 377 ATGATCAGAAATCTGACGAAATCCCTCATGATCCCTTATTCACCAAGACCTAGAT 436

39 MetGluLeuAlaSerThrLeuTyIleProAlaSerLeuProPheSerThrIleAlaLeuAsp 58

QY 437 CTGAGCTTCAACCCCTGAAGATCTTAAGAAGCTTATAGCTTCACAATTTCTCACACTT 496

59 LeuSerPheLeuProLeuAlaGlnIleSerTySerPhePheSerPheProGluLeu 78

QY 497 CAGTGCCTGATTTATCCAGGTGTGAATTTGAACAAATTGAACAAGCATGGCATGGC 556

79 GlnValLeuAlaSerLeuSerArgCysGluIleGlnThrIleGluAlaSerGlnAlaTyGlnSer 98

QY 557 TTAACACAGCTCAACCTTGTAGTACAGAAACCTTATCAAGATTTTCCACAGA 616

99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAlaSerProIleGlnAlaLeuAlaLeuGly 118

QY 617 AGTTTCTTGAGTAACAAAATTGAAGATCTGTGGCTGTGAGACAAAAATGACCTCT 676

119 AlaPheSerGlyLeuSerSerLeuGlnTyLeuValAlaValGluThrAlaLeuAlaSer 138

QY 677 CTGAGAGGTTCCATATTTGACAGCTTATTCCTTAAGAACTTAATGGGCTCATAT 736

139 LeuGluAlaSerPheProIleGlyHisLeuTyIleThrLeuSerGluLeuAlaValAlaHisAsn 158

QY 737 CTATATCATCTCTTAAAGTGGCTGAATATTTTCTTAATCTGACAAACCTAGAACATGTTG 796

159 LeuIleGlnSerPheLeuSerProGluTyIlePheSerAlaSerLeuThrAlaSerGluHisLeu 178

QY 797 GATCTTCTTATATCATATATTTCAACTATTTCTGTCAAGACTTACAGTTTCTAGCTGAA 856

179 AsnLeuSerSerAlaSerAlaGlnSerIleTyCysValAspArgLeuGlnValAlaHisGln 198

QY 857 AATGCCAGTCAATCTCTTTAGACCTGTCTTAAACCAATTCATGCTCATTCAGCC 916

199 MetProLeuLeuAlaSerLeuAlaSerLeuAlaSerLeuAlaSerAlaMetAlaPheIleGlnPro 218

QY	917	CAAGCGCTTTGGGGAATTAGAGCTGCATGAAATTGACTGTCAAGAAAGTAATTTTAAATGGCTCA	976
Db	219	GlYalAphElySGluIleArgLeuH1slySeuNtrILyAaGAsrPheAspSerLeu	238
QY	977	AATGTACTGAATAATGTGCCTTCAAAACAATGACTGGATTTCATGTCACATCGGTTGACTTGTG	1038
Db	239	AsnValMetIySbTrnCysIleGlnIyLeuH1aGlyLeuGluValH1bH1cIleValLeu	258
QY	1037	GGAGAAATTTAAAAATGAAGAAGATCTGGAAAGTTTGAACCGTTCTGTCAATGAGAGACTA	1096
Db	259	GlyIuPheArgAsnGluIyAsnLeuGluIySAspPheAspTrnSerAlaLeuGluIyLeu	278
QY	1097	TGCAGATGAGACATTTAGAGTTCACGTTTACATATATTAATTCATTTTTCAGATGATATTT	1155
Db	279	CysAsnNeutrH1IleGluIyPheArgLeuAlaTyIleAspTyIeTyIeAsnAspIle	298
QY	1157	TATATATCTC---AATTGCTGTGGCAAAATATTTCTGCAGAAAGTCTTTCACAGGTGATCATATA	1213
Db	299	IleAspLeuPheAsnCysLeuH1aAsnValSerSerPheSerLeuValSerAlaThrIle	318
QY	1214	AAACACATAGACAGATGTTTCTTAGCGATTTCAAATGGCAACATCTTATCAATCATTAGATGT	1273
Db	319	LysSerValIyAspPheSerTyIeAsnPheGlyTrpGlnH1sLeuGluIyLeuValAsnCys	338
QY	1274	CATCTTAAAGCCTTTTCCAAAGCTGAGTCTACCTTTTCTTAAAGTTGAGACTTTAACTACC	1333
Db	339	LysPheGlyGluIyPheProThrLeuGluIyLeuIySsrLeuIyAspGlyLeuThrIle	358
QY	1334	AACGAGAGATATTCAGCTTGGTGCATGGTGCTGCGCAAGTCCAGATATCTAGATCTT	1393
Db	359	AsnIySgIyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluIyPheLeuAspLeu	378
QY	1394	AGTAGAAATGCCATGAGCCTTTAGAGAGTTCGTGTTCTTATGTTGATTTTGGAAACAACAC	1453
Db	379	SerArgAsnGlyLeuSerPheIyGlyCysCysSerGlnSerAspPheGlyThrThrSer	398
QY	1454	CTGAAGTACTTAAAGCTTACGCTTCAATGCGTCAATCTTCATGAGTGGCCAACTTATGGGT	1513
Db	399	LeuIyTyIeLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuIy	418
QY	1514	CTAGAAGAGCTGGAATATCTGAGACTTTCACAGACTCCACTTTTAAAAAGTCCAGAAATTC	1573
Db	419	LeuGluGlnLeuGluH1bLeuAspPheGlnH1sSerAsnLeuIySgIleMetSerGluIyPhe	438
QY	1574	TCAGTGTCTTATCTCTTGA AAAAATCTTTCATCTTGAACATCTCTTCACTAATATCCAA	1633
Db	439	SerAlaPheLeuSerLeuAlaGAsnLeuIeTyIeAsnAspIleSerH1sThrH1cIleThrArg	458
QY	1634	ATTGACTTGTGATGGCATATTTCTTGCGCTTATACAGTCCAACTTAAATAATGGCTGCC	1693
Db	459	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuIySValLeuIyMetAlaIy	478
QY	1694	AATCTTTCAAAAGCAACACCTTTCAAATGCTTTTCAAAACAACAACAACTTAAACATTC	1753
Db	479	AsnSerPheGlnGluAsnPheLeuProAspIlePheTrnGlyLeuAlaGAsnLeuThrPhe	498
QY	1754	CTGAGATCTTTTAAATGCCAATGGAAACAGATATTCAGGGGGGTATTTTGAACAATCTTAC	1813
Db	499	LeuAspLeuSerGlnCysGlnLeuGluIyLeuSerProThrAlaPheAsnSerLeuSer	518
QY	1814	AGACTCCAGTATTAACATAGATGCACAACAACCTACTGTTTCTTGAGTCAATCCATAT	1873
Db	519	SerLeuGlnValIleLeuAsnMetSerH1sAsnAsnPhePheSerLeuAspThrPheProTy	538
QY	1874	AAACAGCGTATCTCCCTCAGAGACTCTTGATTCAGATTTCATTCGGATAGAAATCC---	1933
Db	539	LysCysLeuAsnSerLeuGlnValLeuAspTyIeSerLeuAsnH1cIleMetThrSerIyS	558
QY	1931	AAAGGAATATCTGCAAACTTTTCCAAAGAGTCTAGCCGCTTCAATCTGACATTAATCTT	1990
Db	559	LysGlnGluIyLeuGlnH1bPheProSerSerLeuAlaPheLeuAsnLeuThrGluAsnAsp	578
QY	1991	GTTGCTGTATATGTAATATCAAGATTTCTTGACAGTGGGTCAAGACCAAGAAATGTTTC	2056

Db	PhaellacythrCysglnHisGlnSerPheLeuGlnTrpIleuValSerGlnArgGlnLeu	598
Qy	2051 TTGGTGAATGTTGAACAATGAAATGATGCACTTAAGACATGAAGGCTCCCTGGTG	2110
Db	599 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAerlybGlnGlyMetProVal	618
Qy	2111 TTGGATTTTACGAATTCGACCTGTATATATATACAAAGCATCATCAGTGTATGGGTGCT	2170
Db	619 LeuSerLeu--AsnIleThrCysGlnMetAsnIlyThrValIleGlyValSerValPhe	637
Qy	2171 AGTGTGCTGTGGTGGACATGTAGACATTTCTGTATATACCACTCTATTTTCACTGTATA	2230
Db	638 SerValLeuValValSerValValAlaValLeuValIlyTrpValPheTrpPheHisLeuMetC	657
Qy	2231 CTATATGCTGTGCTGTAAAAAGTATACAGACAGAGAAAGCACTATATGTATGTCAATTTGTATC	2290
Db	658 LeuLeuValGlyCysIleIyValTyClyArgGlyGlnSerThrTrpZarPalPheValIle	677
Qy	2291 TACTTCAGCCGAATGAGACTGGGTGTAGAAACAGCTGGTAAGAATTTAGAAGAAAGGA	2350
Db	678 TyrSerSerGlnAerGlnAerTrpValAlaArgAsnGlnLeuValIlyAsnLeuGlnGly	697
Qy	2351 GTGGCCCGGCTTTCAGCTTGGCTTCATTTACAGGGACTTTATTCCTGGTGTAGCAATGCT	2410
Db	698 ValProThrPheGlnIlyCysValenIlyTrpArgPheIleProGlyValAlaIleAla	717
Qy	2411 GCCAACAATCATCCAGAAAGGCTTCCACAAGAGCCGGAAGCTTATTTGCTGGTGTCTAGA	2470
Db	718 AlaSerIleIleHisGlnGlyPheHisIlybSerArgIyValIleValIyValSerGln	737
Qy	2471 CACTTTATCCAGAGCCGTTGGTGTATTTTGAAATATAGATTTGCTCAGACATGGCAGTTT	2530
Db	738 HisPheIleGlnSerArgTrpCysIlePheGlnIlyTrpGlnIleAlaGlnThrTrpGlnPhe	757
Qy	2531 CTGAGTGAACCGCTCTGGGATCATCTTGTATGTCTCTTGAAGAAAGTGAAGAGTCTCTGCT	2590
Db	758 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIlyValGlnIlybThrLeuLeu	777
Qy	2591 AGCAGACAGGTCGAATTTGTATCGCTTCTTAGCAAAACACCTACCTCGAGTGGAGAGAC	2650
Db	778 ArgGlnGlnValGlnIlyLeuTrpArgLeuLeuSerArgSerThrTrpIlyLeuGlnIlybTrp	797
Qy	2651 AATGCTGTGGGAGGACATCTTCTGTGAGAAAGACTCAAAAAGCCCTGTGTGATGAGAAA	2710
Db	798 SerValLeuGlyArgHisIlePheTrpArgArgLeuArgIyAlaIleLeuAerGlyIlyb	817
Qy	2711 GCCTTGAATCCAGATGAACA 2731	
Db	818 SerTrpAsnProGlnGlyThr 824	

RESULT 12

ID	TLR4_BOVIN	STANDARD;	PRT;	841 AA.
AC	09GL65;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor.			
GN	Name=TLR4;			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovine; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Guionaud C.T., Dubey C., Jungi T.W.;			
RL	"Bovine Toll-like receptor 4 (TLR4).";			
RT	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
CC	-I- FUNCTION: Cooperates with Iy65 and Cld4 to mediate the innate			
CC	immune response to bacterial lipopolysaccharide (Lps). Acts via			
CC	MyD88, TRAF6, leading to NF-kappa-B activation, cytokine			

CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TIR4. Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----
 DR HSSP: AF310952; AAG32061.2; -.
 DR HSSP: O66003; 1FYX.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:mast cell activation; ISS.
 DR GO: GO:0045571; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR0010157; TIR.
 DR Pfam: PF00560; LRR: 13.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00369; LRR_Typ; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR GlycoProfile: Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Signal; Transmembrane.
 KW SIGNAL. 23 Potential.
 FT CHAIN. 24 841 Toll-like receptor 4.
 FT DOMAIN. 24 632 Extracellular (Potential).
 FT TRANSMEM. 633 653 Potential.
 FT DOMAIN. 654 841 Cytoplasmic (Potential).
 FT REPEAT. 53 76 LRR 1.
 FT REPEAT. 77 100 LRR 2.
 FT REPEAT. 102 124 LRR 3.
 FT REPEAT. 124 149 LRR 4.
 FT REPEAT. 149 173 LRR 5.
 FT REPEAT. 173 197 LRR 6.
 FT REPEAT. 197 203 LRR 7.
 FT REPEAT. 203 225 LRR 8.
 FT REPEAT. 225 277 LRR 9.
 FT REPEAT. 277 300 LRR 10.
 FT REPEAT. 300 334 LRR 11.
 FT REPEAT. 334 350 LRR 12.
 FT REPEAT. 350 372 LRR 13.
 FT REPEAT. 372 398 LRR 14.
 FT REPEAT. 398 421 LRR 15.
 FT REPEAT. 421 445 LRR 16.
 FT REPEAT. 445 469 LRR 17.
 FT REPEAT. 469 494 LRR 18.
 FT REPEAT. 494 518 LRR 19.
 FT REPEAT. 518 542 LRR 20.
 FT REPEAT. 542 566 LRR 21.
 FT REPEAT. 566 592 LRR 22.
 FT REPEAT. 592 619 LRR 23.
 FT DOMAIN. 619 819 TIR.
 FT CARBOHYD. 819 835 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD. 835 841 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 73 73 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 841 AA; 96026 MW; CSEI7CB9C798CD16 CRC64;
 Alignment Scores:
 Pred. No.: 1,5e-195 Length: 841
 Score: 2813.00 Matches: 548
 Percent Similarity: 79.19% Conservative: 118
 Best Local Similarity: 65.16% Mismatches: 169
 Query Match: 47.33% Indels: 6
 DB: 1 Gaps: 4

US-09-396-985b-5 (1-3395) x TIR4_BOVIN (1-841)

QY 260 ATGATGCTCTCTTGCATCTGCTGGAGCTCTGATCATGCA--TTGTTCTTCTCTGC 316
 1 MetMetAlaArgLaaArgLeuAlaAlaLeuLeuProAlaThrAlaLeuSerCys 20
 QY 317 CTGAGCAAGGAGGATCCCTGATGAGGATCTCTTAATATTAACCAATGC 376
 21 LeuArgThrGluSerThrPheProCysValGlnValAlaProAsnIleSerTrpGlnCys 40
 QY 377 ATGATCAGAAATCTCAGCAAAATCCCTCATGACATCCCTTAATCAACCAAGACCTAGAT 436
 41 MetGluLeuAsnLeuTrpIleLeuProAsnIleProIleSerThrIleMetLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGGAAGATCTTAAGAGCTTAAGCTTACCAATTTCTCACAATT 496
 61 LeuSerPheAsnTrpLeuArgIleLeuGlySerHisAsnPheSerPheProGluLeu 80
 QY 497 CAGTGGCTGATTTATTCAGAGTGTGAATGAGACAAATTAAGACCAAGGATGCGATGCG 556
 81 GlnValLeuAsnProLeuSerArgCysGlnIleLeuIleLeuAsnProIleGlnIle 100
 QY 557 TTAACAGCTCTCAACCTTGTACTGACAGAAACCTTAACAAGTTTTCCTCCAGCA 616
 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaTrpGly 120
 QY 617 AGTTTCTGCAATTAACAATTTAGAGAACTGTGGCTGTGAGACAAAATGACCTCT 676
 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuValSer 140
 QY 677 CTGAGGCTTCCATATTTGAGAGCTTATCTTAAGAACTTAAGTGGCTCATAT 736
 141 LeuAsnAspPheProIleGlyHisLeuValAsnLeuValLeuValAlaHisAsn 160
 QY 737 CTATATCATTCCTTAAGTCCCTGAATATTTTCTAATCTGACAAACCTAGAACATGTG 796
 161 PheIleHisSerPheValLeuProGluTrpPheSerAsnLeuProAsnIleGluHisLeu 180
 QY 797 GATCTTCTTATTAACATTAATTAACACTATTTCTGCAAACTTACAGTTTCAAGTGA 856
 181 AspLeuSerAsnAsnIleGlnAsnIleTrpGlyAsnValValLeuHisGln 200
 QY 857 AATGCCAATCAATCTCTTGAACCTGCTTAACCAACCAATGACCTTCAAGCC 916
 201 MetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProLeuAsnProIleGluPro 220
 QY 917 CAAGCTTTGAGGAAATTAGCTTCATGATGACTTAAGAAATTAATTAATAGCTCA 976
 221 GlyThrPheValGluLeuValLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSer 240
 QY 977 AATGACTGAATAATGCTTCAAAACATGACGTGTTATACATGTCATCGGTGATTTG 1036
 241 HisValMetLeuSerThrCysIleGlnGlyLeuAlaGlyLeuValSerThrAsnArgLeuValLeu 260

QY 1037 GGAGAAATTTAAAGGAAATCTGGAAGTTTGAACCGTCTGTCATGAAGACTA 1096
 DB 261 Gtlygupheylsaainglularglyleuclnargrheapargserpheleuglclyleu 280
 QY 1097 TGCATGTGACATTTGATGAGTTCAGGTTAAATATTAATCAATTTTGA--GATGAT 1153
 DB 281 Cysasnleuthrlleglulgnlpheargllealtlryleuasplysphesercllyaspasp 300
 QY 1154 ATTTATATCTCATTTGCTTGCAAAATTTCTGGAATGCTTTTCACAGGCTACATTA 1213
 DB 301 ThraspheupheasnCysleualasbnvalserValIleSerLeuLeuSerIleSerleu 320
 QY 1214 AAACACATAGCAGATGTTCTTACGATTTCAATGCAATGCTTATCAATCATTAAGAT 1273
 DB 321 GlyserleuenglalaleuLeuLysaspheargtrgrlnhlsleuGlulIleIleasnCys 340
 QY 1274 CATCTTAAGCCTTTTCCAAAGCTGAGTACCTTTTCTTAAAGTTGAGCTTTAACTAAC 1333
 DB 341 AspheasplysphproalaleuLysleuSerSerleuLyslysphValIlePheThrAsp 360
 QY 1334 AACGAGAGATATCAGCTTTGTCACAGTTCGCTGCGCAATGCTCAAGATATCTGATCTT 1393
 DB 361 AsnLysaspIleSerThrPheThrGlnPheGlnLeuProSerLeuGlnTyrLeuaspLeu 380
 QY 1394 AGTAGAAATGCCATGAGCTTTAGAGTGTCTGTTCTTATTTGATTTTGAACAACACAC 1453
 DB 381 LysargasnhsleuSerPheLyscllyCysCysSerhsthraPheGlyThrThrAsn 400
 QY 1454 CTGAAGTATCTTAAGCCTTCAAGCTTCAATGCTGATCTGATGAGTCCCACTTACGCTG 1513
 DB 401 LeuLysasnlsleuaspLeuSerPheasnaspValIleThrLeuGlnLysSerAsnPhemecGly 420
 QY 1514 CTAGAAGCGGAGAAATCCTGAGCTTTGAGACCTCCACTTAAAGAGTACAGAAATTC 1573
 DB 421 LeuGlnGlnLeuGlnLysLeuaspPheGlnIleSerThrLeuLysGlnIleasnIlePhe 440
 QY 1574 TCAGTGTCTTATCTCTTGAAGAACTTTTACCTTGCATCTCTTACATTAATACCAA 1633
 DB 441 SerIlePheLeuSerLeuArgasnLeuArgTyrLeuaspIleSerTyrThrAsnIleArg 460
 QY 1634 ATTGACTTGAATGTCATATTTCTTGCTTGAATGATCTCAACCTTTAAAGAGCTGCGC 1693
 DB 461 IleValIlePhehlsiglyIlePheThrGlyleuValSerleuGlnThrLeuLysMetAlaGly 480
 QY 1694 AATCTTTCAAGACACACCTTTCAAAATGCTTTTACAAACACAAACTTAACTTACATTC 1753
 DB 481 AsnSerPheGlnAsnAsnLeuLeuProaspIlePheThrGlnLeuThrAsnLeuThrVal 500
 QY 1754 CTGATCTTTCTTAATGCGCACTGGAACAGATATCTAGGGGATATTGACACACTCTAC 1813
 DB 501 LeuaspLeuSerLysCysGlnleuGlnIleValIleGlnThrAlaPhehlsSerleuSer 520
 QY 1814 AGACTCCAGTATTAACATGAGTACAAACACTACTGTTTCTGATCCATCCCATAT 1873
 DB 521 SerleuGlnValIleuAsnMetSerhlsAsnLysleuSerleuAspThrPheLeuTyr 540
 QY 1874 AAAAGCTGTACTCCCTCAGACTCTTGATGCGATTTGCATCGCATAGACATCCAA 1933
 DB 541 GlnProleuLysSerleuArgIleleuaspCysSerPheasnArgIleMetAlaSerLys 560
 QY 1934 ---GGAATACTGCAACATTTTCCAAAGAGTCTAGCCGCTTCAATGCACTGAATTAATCT 1990
 DB 561 GlnGlnGlnleuGlnAsnLeuProargSerleuThrTrpLeuAsnLeuThrGlnAsnAla 580
 QY 1991 GTTGCTGTATATGATGATATCAGAAATTTCTTGAGTGGGTCAAGAACAGAAATGCTTC 2050
 DB 581 PheAlaCysValCysGlnhlsGlnSerPheleuGlnThrValLysArgGlnArgGlnLeu 600
 QY 2051 TTGCTGATGTTTGAACAATGAATGTCATCACCATTAGACATGAAGGCTCCCTGCTG 2110
 DB 601 LeuValGlnArgGlnGlnMetMetCysAlaGlnProleuaspMetGlnAspMetProVal 620
 QY 2111 TTGATTTTGAATTCACCTGTTATATATATACAAAGCTATCAGTGTGCTGCTGCTC 2170

DB 621 LeuSerPheargasnIleatThrCysGlnLeuSerLysThrIleIleSerValSerVal 640
 QY 2171 AGTGTGCTTGTGTGAGCACTGTAGCATTTCTGATATACCACTTCTATTTTCACTGATA 2230
 DB 641 ThrValLeuLeuValSerValIleValGlyValLeuValTyrLysPheTyrPhehlsleuMet 660
 QY 2231 CTATGTGCTGCTGTATAAAGATACAGCAGAGAGAAAGCATCTATGATGATTTGTGATC 2290
 DB 661 LeuLeuAlaGlyCysLysLysTyrGlyArgGlyGlnSerIleTyrAspAlaPheValIle 680
 QY 2291 TACTCGACCCAGATGAGACTGCGTGTGAGAAACAGCTGTGTAAAGATTTAGAAAGAGA 2350
 DB 681 TyrSerSerGlnaspGlnaspTyrPvalArgAsnGlnleuValLysAsnleuGlnGly 700
 QY 2351 GTGCCCCCTTTTCACTGCTTCTTCAATTAACAGGACCTTATCTGCTGTAGCCATGCT 2410
 DB 701 ValProProPheGlnLeuCysLeuAlaTyrArgAspPheIleProGlyValAlaIleAla 720
 QY 2411 GCCAATCATCCAGAGAGGCTTCCACAGAGCGGAAAGTTATTTGTGTGTGTCTAGA 2470
 DB 721 AlaAsnIleIleGlnGlnGlnPhehlsLysSerArgLysValIleValIleValSerGln 740
 QY 2471 CACTTATCCAGAGCCGTGTGTATCTTTGAATATGAGATTGCTCAGACATGCACTTT 2530
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 AC OS055;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ito T., Morimatsu M.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056444; BAB86840.1; -;
 DR HSP: OS0603; 1077
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.

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Db	561	PheAlaCySValCyGIuInHISerLeuSerPheLeuGIInTPValIyAspGIInArgInIleu	600	
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QY	2111	TTTGATTTTACGAATTTCCACCTGTTATATATACAGAACTATATACAGTATCGGTGGT	2170	
Db	621	LeuSerPheAspAlaThrCysGIInIleuSerIlySthrIleIleSerValSerValI	640	
QY	2171	AGTGGCTGTGTGGTACCACTGTAGCATTTTTCGATATACACTTATTTTTCACCTGTAT	2230	
Db	641	ThrValIleuLeuValSerValValIGIyAlaIleuValIlyLysPheIlyPheHISerMet	660	
QY	2231	CTTATTTGCTGGCTGTAAAAAGTACAGACAGAGAGAAACATCTATATGCAATTTGTGATC	2290	
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DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Toll-like receptor 4.			
GN	Name=TLR4;			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;			
OC	Bovinae; Bos.			

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RX	MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnae.1333957100;
RA	White S.N., Taylor K.H., Abbey C.A., Gill C.A., Monack J.E.;
RT	"Haplotype variation in bovine Toll-like receptor 4 and computational prediction of a positively selected ligand-binding domain.";
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
DR	EMBL; AY237040; AAQ62700.1; -
DR	GO; GO:0016020; C:membrane; IEA.
DR	InterPro; IPR001611; LRR.
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DR	InterPro; IPR003591; LRR_Typ.
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DR	Pfam; PF00560; LRR_1; 12.
DR	Pfam; PF01582; TIR; 1.
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Db	21 LeuArgThrGlnSerTrpAspProCysValGlnValAlaProAsnIleSerTygGlnCys 40
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OY	437 CTGAGACTTCACCCCCCTGAAGAATCTTAAGAACTTAGGCTTGACCACATTTCTTCACACTT 496
Db	61 LeuSerPheAsnTYrLeuArgHisLeuGlySerHisAsnPhsSerSerPheProGluLeu 80
OY	497 CAGTGGCTGAATTTATCCAGGTGTGAATTTGAGACATTTGAAGACAAAGGACATGGATGG 556
Db	81 GlnValLeuAspLeuSerArgCysGluLeuLysIleIleGluAspAspThrPheGlnGly 100
OY	557 TTAAACCAAGCTCTCAACTGTGATCTGACAGAAAACCTTATCAAGAGTTTTCGCCACGA 616
Db	101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaTrpGly 120
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Db	141 LeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGlnLeuAsnValAlaHisAsn 160
OY	737 CTATATCACTTCTTAAAGTGGCTGAAATATTTTTCTAATCTGACAAACCTTAGAACCTGTG 796
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QY 977 AATGATCGAAATGTGCTTCAAAAACATGACTGGTTTACATGTCATCGGTGATCTTG 1036
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QY 1097 TGCATGTGACATTTGATGAGTTCAGGTTAAACATATTAATCAATTTTCA--GATGAT 1153
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QY 1514 CTAGAAGCTGGAATACCTGAGACTTCAGACCTCCACTTAAAAAAGGTCACAGAAATTC 1573
DB 421 LeuGluGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnIleAsnAlaPhe 440
QY 1574 TCAGATGTTCTTATCTTGAATAAACTTTTACCTTGAATCTCTTACATTAATACAAA 1633
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DB 481 AsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeuThrAsnLeuThrVal 500
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DB 501 LeuAspLeuSerLysCysGlnLeuGluGlnValAlaGlnThrAlaPheHisSerLeuSer 520
QY 1814 AGACTCCAGTTATTTAAATGATGATCAACAACACTGATCTTTGGATGATCCCATATAT 1873
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DT 05-JUN-2004 (TRMBLrel. 27, Created)

DT 05-JUN-2004 (TRMBLrel. 27, last sequence update)

DT 05-JUL-2004 (TRMBLrel. 27, last annotation update)

DE Toll-like receptor 4.

GN Name=TLR4;

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Db 841 Thr 841

GenCore version 5.1.6
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Listing first 45 summaries

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19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	4335.5	50.5	837	10	US-09-950-041-26
2	4141	48.3	799	10	US-09-950-041-8
3	4141	48.3	799	14	US-10-128-166-7
4	4141	48.3	799	16	US-10-732-563-8
5	4141	48.3	799	16	US-10-732-796A-8
6	663	7.7	661	15	US-10-038-854-135
7	663	7.7	661	15	US-10-037-417-107
8	629.5	7.3	661	13	US-10-114-893-10
9	629.5	7.3	661	13	US-10-038-854-134
10	603.5	7.0	784	15	US-09-950-041-4
11	603.5	7.0	784	15	US-10-456-947-46
12	602.5	7.0	784	14	US-10-095-627-12
13	602.5	7.0	784	16	US-10-732-563-4
14	602.5	7.0	784	16	US-10-732-796A-4
15	602.5	7.0	784	17	US-10-741-600-1390
16	602.5	7.0	784	17	US-10-741-600-1391
17	599.5	7.0	784	13	US-10-145-014-23
18	580.5	6.8	1032	10	US-09-954-987B-192
19	580.5	6.8	1032	14	US-10-272-502A-31
20	580.5	6.8	1032	15	US-10-407-952-32
21	567	6.6	1050	10	US-09-954-987B-175
22	567	6.6	1050	14	US-10-272-502A-22
23	567	6.6	1050	15	US-10-407-952-26
24	534	6.2	1032	9	US-09-950-041-37
25	534	6.2	1032	9	US-09-864-761-38325
26	534	6.2	1041	10	US-09-954-987B-184
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28	534	6.2	1041	14	US-10-272-502A-26
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40	533	6.2	1041	10	US-09-978-191A-498
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43	533	6.2	1041	10	US-09-999-833A-498
44	533	6.2	1041	10	US-09-981-915A-498
45	533	6.2	1041	10	US-09-978-824-498

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rook, Fernando U.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DK0724XK1
CURRENT APPLICATION NUMBER: US/09/950, 041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728, 540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207, 558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073, 363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044, 293

; PRIOR FILING DATE: 1997-05-07
 ; PRIOR APPLICATION NUMBER: 60/072,212
 ; PRIOR FILING DATE: 1998-01-22
 ; PRIOR APPLICATION NUMBER: 60/076,947
 ; PRIOR FILING DATE: 1998-03-05
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 26
 ; LENGTH: 837
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-09-950-041-26

Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4335.50 Matches: 837
 Percent Similarity: 99.88% Conservative: 0
 Best Local Similarity: 99.88% Mismatches: 0
 Query Match: 50.54% Indels: 1
 DB: 10 Gaps: 1

US-09-396-985b-1 (1-4868) x US-09-950-041-26 (1-837)

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 Db 120 PheSerGlyLeuSerSerIleuGlnIleuValAlaValGluThrAsnIleuAlaSerIleu 139
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Db 780 GlnAlaGlnLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 799
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Score: 0
Percent Similarity: 4141.00
Best Local Similarity: 100.00%
Query Match: 48.27%
DB: 10

US-09-396-985b-1 (1-4868) x US-09-950-041-8 (1-799)

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QY 404 CTAGCCACCTCTTACCTTAATTAATGACAGAAACCCCATCCAGATTTAGCCCTGGA 463
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QY 464 GCCTTTCTGACATTAATGATTTACAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
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Db 141 AsnLeuSerSerAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 160
QY 704 ATGCCCTCAATCTCTTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
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QY 824 AATGTAATGAAACTTGTATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
Db 201 AsnValMetIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 220
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QY 1004 ATGACTTATTTATTTGTTGAAGAAATGTTCTTCAATTTTCCCTGCTGAGTGTGACTATTT 1063
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DB	321	AsnYsGLysGluYASnAlaPheSerGluValAlaPLeuProSerLeuGluPheLeuAspLeu	340
QY	1244	AGTAAATATGGCTTGAGTTTCAAAGGTGCTGTTCTCAAAATGATTTTGGACAACAAGC	1303
DB	341	SerHsArgAnGLysLeuSerPheYsGLysCySserGlnSerAspPheGLYThrThrSer	360
QY	1304	CTAAAGTATTAGATCTGAGCTTCAATGGTGTTATTACATGAGTTCAAACTTCTTGGGCGC	1363
DB	361	LeuYsTYrLeuAspLeuSerPheAsnGLYValIleThrMetSerAspPheAsnGLY	380
QY	1364	TTGAAACAATAGAACATCTGGATTTCCAGATTTCCAAATTTGAAACAATAGATGATTT	1423
DB	381	LeuGLInGlnLeuGlnHLSleuAspPheGlnHLSerAsnLeuYsGlnMetSerGluPhe	400
QY	1424	TCAGTATTCTATCACTAGAAACCTCATTTACCTTGACATTTTCTCATCTCAACACAGA	1483
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QY	1484	GTTGGCTTCAATGGCATCTTCAATGGCTTGTCGAGTCTCGAAGTCTTGAAAAATGGCTGGC	1543
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DB	441	AsnSerPheGlnGlnJAsnPheLeuProAspRIlePheThrGluLeuAspAlaAsnLeuThrPhe	460
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DB	501	LysCySLeuAsnSerLeuGlnValLeuAspTYrSerLeuAsnHLSIleMetThrSerYs	520
QY	1784	AAACAGGAATACAGACATTTTCCAGATAGTCTAGCTTTCTTAAATCTTACTCAGATGAC	1843
DB	521	LysGlnGlnJLeuGlnHLSIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	540
QY	1844	TTTTGCTTGAATTTGGACAACAAGGTTTCCGGAATGATTCGAAGAACAAGAGGAGCTTC	1903
DB	541	PheAlaCySthCySGLInHLSGlnMetPheLeuGlnTPRIleLYAspGlnHsArgInLeu	560
QY	1904	TTCGTGGAAGTTGAACGAATGGAATGGCAACACTTGACATTAACAGAGGCAATGCTGTG	1963
DB	561	LeuValGluValGlnHsArgMetCylCySAlaThrProSerAspLYsGlnGLYMetProVal	580
QY	1964	CTGAGTTTGAATATCACTGTCCAGATGAATTAAGACATCATTTGGTGTGGCTCTCACT	2023
DB	581	LeuSerLeuAsnHLSthCySGLInMetAsnYsThrIleIleGLYValSerValLeuSer	600
QY	2024	GTGCTTTAGTATCTGTTTACAGATCTCGGCTCTTAAGTTCTATTTCACTATGCTT	2083
DB	601	ValLeuValValSerValValAlaValLeuValTYrLysPheTYrPheHLSleuMetLeu	620
QY	2084	CTTTCGCGGTGATATAAGATGATGATGGTGAAGGATGAACATCTATGATGCGCTTGTATCTAC	2143
DB	621	IleAlaIleGLYCyAlIleLysTYrGluYsArgJGluAsnHLSIleTYrAspAlaPheValIleTYr	640
QY	2144	TCAAAGCCAGATGAGACTGGGTAAAGATGACTAGTAAGATTTAGAAAGAGGGGTG	2203

Dd	641	SeSerGIaSPgluAsePTPrValAlArGansGluLeuVallybAnleuGluGluGlyVal	660
Qy	2204	CCGCCATTTCAGCTCTGCGCTTCACTACAGAGACTTTATCCCGGTGGCCATTGCTGCC	2263
Dd	661	ProProPheGlnLeuCybLeuH1sTyArGAsPheHeProGlyValAlaIleAla1a	680
Qy	2264	AACATCATCCATGAAGGTTTCCATPAAAGCCGAAGGATGATTTGTTGGTGGTCCAGAC	2322
Dd	681	AenIleIleH1sGluGlyPheH1sLyseArGlybValIleValaValaSerGlnH1s	700
Qy	2324	TTGATCCAGAGCCCGGTGGTGTATCTTTGAATATGATGATTGGCTAGACCTGGCATTTGCTG	2383
Dd	701	PheIleGlnSerArGTPCyAllePheGluTyrguIleAlaGlnInThrTPrGlnPheLeu	720
Qy	2384	AGCAGTCGTGCTGATCATCTTCAATGCTCTGCAGAAAGGTGAGAGAACCTGCTCAGG	2443
Dd	721	SeSerArGAlaGlyIleIlePheIleValLeuGlnLybValGluTyThrLeuLeuArg	740
Qy	2444	CAGCAGGTGAGAGCTGTAACCGCTTCTCAGCAGGAACATTACCTGGAGTGGAGACAGT	2503
Dd	741	GlnGlnValGluLeuTyArgLeuLeuSerArGAsnThrTyLeuGluTPrGluAspSer	760
Qy	2504	GTCCTGGGGGGGCACATCTTCGGAGAGACCTCGAAGAAAGCCCTGCGATGTAATCA	2563
Dd	761	ValleuGlyArGHisIlePheThrPrGArGLeuArgLybAlaLeuLeuAspGlybSer	780
Qy	2564	TGGAATCCAGAGGAACAGTGGGTACAGAGATGCAATTGGCAGGAAGCAACATCTATC	2620
Dd	781	TrpAnPProGluGlyThrValGlyThrcIlyCybAsnThrGlnGluAlaThrSerIle	799
RESULT 3			
US-10-128-166-7			
; Sequence 7, Application US/10128166			
; Publication No. US2003007279A1			
; GENERAL INFORMATION:			
; APPLICANT: ARDITI, MOSHE			
; APPLICANT: RAUVASHISTH, TRIPATHI			
; APPLICANT: SHAH, PREBIMAN K.			
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING			
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4			
; FILE REFERENCE: 81476-0255398			
; CURRENT APPLICATION NUMBER: US/10/128, 166			
; CURRENT FILING DATE: 2002-04-23			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 7			
; LENGTH: 799			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-128-166-7			
Alignment Scores:			
Pred. No.: 0 Length: 799			
Score: 4141.00 Matches: 799			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 48.27% Indels: 0			
DB: 14 Gaps: 0			
US-09-396-985B-1 (1-4868) x US-10-128-166-7 (1-799)			
Qy	224	ATGAGAGTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACAAGACCTGAC	283
Dd	1	MetGluLeuAsnPheTyLysIleProAspAnLeuProPheSerThrIlybAnLeuAsp	20
Qy	284	CTGAGCTTTAATCCCTTGAAGCATTTAGGACAGCTATAGCTTCTTCAATTCCAGAACTG	343
Dd	21	LeuSerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGluLeu	40
Qy	344	CAGGTGCTGGATTATCCAGGTGTGAATCCAGACAAATGAGAGATGGGCAATATCAGAC	403
Dd	41	GlnValLeuAspLeuSerArGlyCybGluIleGlnInThrIleGluAspGlyAlaTyrgGlnSer	60

QY 404 CTAAGCCACCTCTCTAATTAATTTGACAGAAACCCCATCCAGAGTTAGCCCTGGGA 463
Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY 464 GCCTTTTCTGACATATCAAGTTTACAGAACTGGTGGCTGGAGACAAATCTAGCATCT 523
Db 81 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 100
QY 524 CTAGAGACTTCCCATTTGACATCTCAAACTTTGAAGAAGAACTTAAGTGGCTCACAT 583
Db 101 LeuGluAsnPheProIleGlyHisLeuLeuThrLeuGlyGluLeuAsnValAlaHisAsn 120
QY 584 CTATATCCATCTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 643
Db 121 LeuIleGlnSerPheLeuLeuProGluThrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
QY 644 GACCTTTCAGACAAAGATTCAAAGTATTTATTTGACAGAACTTGCGGGTCTTACATCAA 703
Db 141 AspleuSerSerAsnLeuIleGlnSerIleGlyCysThrAspLeuArgValLeuHisGln 160
QY 704 ATGCCCTCACTCAATCTCTTTTGAACCTGTGCCGTGATCTTATGAACTTATTCACACA 763
Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY 764 GGTGCAATTAAGAAATTAAGCTTCATAGCTGACTTAAAGCAATTAATTTGATAGTTTA 823
Db 181 GlyAlaPheLeuGlyIleArgLeuHisGlyLeuThrLeuArgAsnAsnPheAspSerLeu 200
QY 824 AATGTAATGAAGAACTTGTATTCAGAGTCTGGCTGGTGTATTAAGATCCATCGTTGGTCTG 883
Db 201 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 220
QY 884 GGAAGATTTTAAAGATGAAGAACTTGGAAAGTTTGAAGAACTTCGCTCTAGAGGCTTG 943
Db 221 GlyIuPheArgAsnGlyGlyAsnLeuGlyIuPheAspLeuSerAlaLeuGlnGlyLeu 240
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QY 1004 ATTTGATTAATTAATTTGTTGAAGAAATGTTTCTTCAATTTCCCTGGAGTGTGATAT 1063
Db 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
QY 1064 GAAAGGGTAAAGAACTTTCTTATTAATTCGATGGCAACTTTAGATTTAGTTACTGT 1123
Db 281 GluArgValIuPheAspPheSerGlyAsnPheGlyIleArgGlnHisLeuGluLeuValAsnCys 300
QY 1124 AAATTTGACAGTTTCCACATTTGAAGCTCAAAATCTCAAAAGGCTTACTTTCACCTCC 1183
Db 301 LysPheGlyGlnPheProThrLeuLeuLysSerLeuLysArgLeuThrPheThrSer 320
QY 1184 AACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTC 1243
Db 321 AsnLysGlyIuAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
QY 1244 AGTGAAGATGGCTTGAAGTTTCAAGGTTGCTGTTTCAAGATGATTTGGGCAACCGCC 1303
Db 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
QY 1304 CTAAGATTTTAAGATCTGAGCTTCAATGGTGTATTAACATGAGTTTCAACCTTCTGGGC 1363
Db 361 LeuLysIleThrLeuAspLeuSerPheAsnGlyValIleHisMetSerSerAsnPheLeuIle 380
QY 1364 TTAGAACAACTAGAACATCTGGATTTCCAGATTCGAATTTGAACAAATGAGTGAATTT 1423
Db 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
QY 1424 TCAAGATTCCTATCACTCAAGAACTCAATTTACCTTGAACATTTCTCAATCACTCAACGA 1483
Db 401 SerValPheLeuSerLeuArgAsnLeuIleGlyThrLeuAspIleSerHisIleThrHisArg 420

QY 1484 GTTGCTTCAATGGCACTTTCATATGGCTTTGCCAGTCTCGAAGTCTTGAAGAAATGGCTGGC 1543
Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 440
QY 1544 AATTTCTTCCAGGAAATCTTCTTCCAGATATCTTTCACAGAGCTGAGAAATCTTGAACCTTC 1603
Db 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
QY 1604 CTGGACCTCTCCAGTGTCACTGGAGAGTGTCTCCAAAGCACTTAACTTAACTCTCC 1663
Db 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProHisAlaPheAsnLeuSer 480
QY 1664 AGTCTTCAAGTACTTAATATGAGCCACAACTTCTTTTCAATGATACGTTCTTAT 1723
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QY 1784 AAACAGAACTACAGCAATTTTCCAAAGTACTAGCTTCTTAATCTTACTCAGAAATGAC 1843
Db 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY 1844 TTTGCTTGTACTTGTGAACACAGAGTTTCTTGCATATGATCAAGACAGGAGCTC 1903
Db 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
QY 1904 TTGGTGAAGTTGAACGAATGAATGTGCAACACTTCAATTAAGCAGGAGGACTGTG 1963
Db 561 LeuValGluValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 580
QY 1964 CTGAGTTGAATATCACCTGTCAGATGAATGAAGCAATCTTGGTGTGGCTCGCTCAGT 2023
Db 581 LeuSerLeuAsnIleThrCysGlnMetCysAsnLysThrIleIleGlyValSerValLeuSer 600
QY 2024 GTTGCTGTAGTATCGTTGTGAGAGTTCTGTGCTATTAAGTTCTAATTTCACTGATGCTT 2083
Db 601 ValLeuValIleSerValAlaValLeuValIleLysLysPheIlePheHisLeuMetLeu 620
QY 2084 CTTCGTGGCTGCAATTAAGTATGTGAGGTGAAGAAACATCTATGATGCTTTGTTATCTAC 2143
Db 621 LeuAlaGlyCysIleLysIleGlyArgGlyGluAsnIleGlyAspAlaPheValIleLys 640
QY 2144 TCAAGCAGAGTGAAGCACTGGGTAAAGATGCAATGAAGATTTTGAAGAGGGGTG 2203
Db 641 SerSerGlnAspGluAspThrValArgAsnGluLeuValLysAsnLeuGlnGlyVal 660
QY 2204 CCTGCATTTCAAGCTGTGGCTTCACTACAGAGACTTTATTCGGGTGGCCATTTGCTGCC 2263
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QY 2264 AACATCATCATGAAGGTTTCCATTAAGCCGAAAGGTGATTTGTTGGTGTCCAGAC 2323
Db 681 AsnIleIleHisGluGlyPheHisIleLysSerArgValIleValIleValIleSerGlnHis 700
QY 2324 TTTCATCCAGAGCCCTGGGTGATCTTTGAATATGAATGTGTCAGACCTGGCAGTTTCTG 2383
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QY 2384 AGCAGTGTGTGTATCATCTTCAATTTGCTTGTGCAAGAGGTGAGAGAACCTGTCTCAG 2443
Db 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArg 740
QY 2444 CAGAGGTGAGCTGTACCGCTTCTCAGACAGAAACCTTACCTGAGTGGAGAGACGT 2503
Db 741 GlnGlnValGluLeuGlyArgLeuLeuSerArgAsnThrIleGluGluThrGluAspSer 760
QY 2504 GTCTGTGGGGGGGCAATCTTCTGAGACGACTCAGAAAGCCCTGGCTGAGTGAATTCA 2563
Db 761 ValLeuGlyArgHisIlePheThrArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
QY 2564 TGAATCCAGAAAGAAAGTGGGTACAGATGCAATTTGGCAGAGCAACATCTATC 2620

Db 781 TrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799
RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-563-8
Alignment Scores:
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Score: 4141.00 Matches: 799
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 21 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY 344 CAGGTGCTGATTTATCCAGGTGTGAATCCAGACAATTGAAGATGGGCAATATCAGAGC 403
Db 41 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 60
QY 404 CTAAGCACTCTCTACCTTAATATGACAGAGAAACCCATCCAGAGTTTAGCCCTGGGA 463
Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY 464 GCCTTTCTGACATCAAGTTTACAGAAAGCTGGGCTGTGGAGACAAATCTAGCACT 523
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Db 141 AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 160
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QY 764 GGTGCATTTAAAGAAATTAAGGCTTCATAGAGTGAATTAAGAAATATTTTGATGTTTA 823
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QY 884 GAGAAATTTGAAGAAAGAACTTGAAAGATTGACAAATCTGCTCTAGAGGCGCTTG 943
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QY 1664 AGCTTGAGGATCAATTAATGAGCCACACAACTTCTTTCATGATGATAGCTTCTTAT 1723
Db 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrProTyr 500
QY 1724 AAGTGTCAAGCTCCCTCCAGGTTCTGATTAAGTCACTCAATCAATATGACTTCCAA 1783
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QY 1784 AACAGAACTACAGCAATTTTCCAGATGCTAGCTTTCTTAAATCTTACTCAGATGAC 1843
Db 521 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY 1844 TTTCCTTGATCTTTGAAACCAAGATTTCTGAAAGATTCAGACCAAGAGCAGCTC 1903
Db 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleLysAspGlnAspGlnLeu 560
QY 1904 TTGCTGAAGTTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGACATGCTGTG 1963


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Db      ||| 341 SerArgSenglyLeuSerPheLySGLYCyecSerSergInserAepPheGlyThrThrSer 360
Qy      ||| 1304 CTAAGATTAATTAAGTCTGAGCTTCATAGTGTTTATTCACATGAGTTCAACTTCTGGGC 1363
Db      ||| 361 LeuLySerLeuAepLeuSerPheAaNglyValIleThrMetSerSerAaPheLeuGly 380
Qy      ||| 1364 TTGAACAACATAGACATCTGATTTCTCAGCATTCATATTCATTAAGAAATAGAGAGTTT 1423
Db      ||| 381 LeuGlnGlnLeuGlnIleAaPhePheGlnIleSerSerLeuLySGLIMetSerGluPhe 400
Qy      ||| 1424 TCAGATATTCCTAGCTCAGAAACCTCATTTACCTTGAACATTTCTCATCTACACAGA 1483
Db      ||| 401 SerValPheLeuSerLeuAaGAsnLeuIleTyThrLeuAapIleSerIleThrArg 420
Qy      ||| 1484 GTTGCTTTCATAGGCATCTTCATAGGCTTGTCAGAGTCTCCAGAGCTTGAAAATGGCTGCC 1543
Db      ||| 421 ValAlaPheAaNglyIlePheAaNglyLeuSerSerLeuGlnValLeuLySMeAlaGly 440
Qy      ||| 1544 AATCTTTCAGAGAAACCTTCCTCCAGATATCTTCACAGAGCTGAGAACTTGACCTTC 1603
Db      ||| 441 AaSerPheGlnGlnAaPheLeuPheProAapIlePheThrGlnLeuAaGAsnLeuThrPhe 460
Qy      ||| 1604 CTGACCTCTCTCAGTGTCAACTGAGAGAGTTGTCTCCAAACAGATTTAATCTCATCTCC 1663
Db      ||| 461 LeuAepLeuSerGlnCySGLIMetGlnLeuSerProThrAlaPheAaSerLeuSer 480
Qy      ||| 1664 AGTCTTCAGGATCTAAATATAGAGCAACAACATCTTTTATTTAGTAGACTTCTTAT 1723
Db      ||| 481 SerLeuGlnValLeuAaMetSerPheAaAaPhePheSerLeuAapThrPheProTy 500
Qy      ||| 1724 AAGGTCTGAACCTCCCTCAGAGGTTCTGATTAAGTCTCATCATCATTAATGACTTCCAA 1783
Db      ||| 501 LySGLIMetAaSerLeuGlnValLeuAapTySerLeuAaAaIleMetThrSerLyS 520
Qy      ||| 1784 AAACAGAACTACAGCAATTTTCAAGTAGTCTAGCTTTCTTAAATCTTACTCAGAAAGAC 1843
Db      ||| 521 LySGLIMetGlnLeuGlnIlePheProSerSerLeuAlaPheLeuAaAaLeuThrGlnAaAaP 540
Qy      ||| 1844 TTTCCTTGTAATCTTTGAAACACAGAGTTTCTGCAATGAGTACAGACAGACAGAGCTC 1903
Db      ||| 541 PheAlaCySerThrCySGLIMetAaSerPheLeuGlnThrIleLeuGlyValSerValLeuSer 560
Qy      ||| 1904 TTGAGTGAAGTGAAGCAATGAATGTGCAACATCTTCAGATTAAGAGGAGGAGCTGTG 1963
Db      ||| 561 LeuValGlnValGlnAaGMeGlnCyAlaAlaThrProSerAapLySGLIMetProVal 580
Qy      ||| 1964 CTGAGTTGAATATCACCTGTCAAGATGAATAAGACCATCATGTGTGTGCTCTCAGT 2023
Db      ||| 581 LeuSerLeuAaAaIleThrCySGLIMetAaAaLySThrIleLeuGlyValSerValLeuSer 600
Qy      ||| 2024 GTGCTTGTAATATCTGTGTGAGCAGTTTGTGCTATTAAGTTCTATTTACACTGATGTT 2083
Db      ||| 601 ValLeuValValSerValValAlaValLeuValTyTySProTyPheAlaIleMetLeu 620
Qy      ||| 2084 CTGCTGGCTGCTAAGATAGTAGAGGTAAGAAACATCTATGATGCTTGTATATCATC 2143
Db      ||| 621 LeuAlaGlyCySGLIMetTyGlyArgGlyValLeuAaIleTyTyAaPheValAlaIleTy 640
Qy      ||| 2144 TCAAGCAGATAGAGACTGGGTGAAGATAGATGATGAAGATTAAGAAAGGGGTG 2203
Db      ||| 641 SerSerGlnAaPheGlnAaPheTyValArgAaNglyLeuValTyAaAaLeuGlnGlyVal 660
Qy      ||| 2204 CTTCAATTCAGCTCTGCTTCATACAGAGACTTATTCCTGGGTGGCCATGCTGCC 2263
Db      ||| 661 ProProPheGlnLeuCySGLIMetIleTyTyArgAaPheIleProGlyValAlaIleAla 680
Qy      ||| 2264 AACATCATCATGAAGTTTCATTAAGCCGAAAGGATGTTGTTGGTGTCCAGAC 2323
Db      ||| 681 AaAaIleIleHISGlnGlyPheHISLySerAaTyValIleValValValSerGlnHIS 700
Qy      ||| 2324 TTCAATCCAGACCGGTGTATCTTTGAATATGATGTGCTCAGACCTGCGAGTTTCTG 2383

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Db      ||| 701 PheIleGlnSerArgTrpCySGLIMetGluTyGlnIleAlaGlnThrTrpGlnPheLeu 720
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Db      ||| 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnIleValGlnIleTyThrLeuAaArg 740
Qy      ||| 2444 CAGCAGGTGAGAGCTGTACCGCTTCTCAGAGAGAACATTAATCTGAGTGGAGAGCAGT 2503
Db      ||| 741 GlnGlnValGlnLeuTyTyArgLeuLeuSerArgAaThrTyThrLeuGlnTyTyGlnAaPheSer 760
Qy      ||| 2504 GTCTGGGGCGGCACATCTTCTGAGACGACTCAGAAAGCCCTGCTGATGTGAATCA 2563
Db      ||| 761 ValLeuGlyArgHISIlePheTrpArgArgLeuArgValAlaLeuAaAaPheGlyLySer 780
Qy      ||| 2564 TGGATCCAGAAAGAACAGTGGGTACAGATGCAATTGGCAGGAAAGCAATCATCTATC 2620
Db      ||| 781 TrpAaProGlnGlyThrValGlyThrGlyCyAaAaThrProGlnGlnAlaThrSerIle 799

RESULT 6
US-10-038-854-135
: Sequence 135, Application US/10038854
: Publication No. US20040022781A1
: GENERAL INFORMATION:
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Li, Li
: APPLICANT: Wolenc, Adam R
: APPLICANT: Verne, Corine
: APPLICANT: Bisen, Andrew J
: APPLICANT: Liu, Xiaohong
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Shinkets, Richard A
: APPLICANT: Tchernev, Velizar
: APPLICANT: Spaderna, Steven K
: APPLICANT: Gorman, Linda
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Patlurajan, Meera
: APPLICANT: Gusev, Vladimyr
: APPLICANT: Gangolli, Esha A
: APPLICANT: Guo, Xiaojia S
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Raetelli, Luca
: APPLICANT: Caeman, Stacie J
: APPLICANT: Boldog, Ferenc
: APPLICANT: Burgess, Catherine E
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Ellerman, Karen
: APPLICANT: Gunther, Erik
: APPLICANT: Smithson, Glenda
: APPLICANT: Millet, Isabelle
: APPLICANT: MacDougall, John R
: TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21402-230
: CURRENT APPLICATION NUMBER: US/10/038, 854
: PRIOR FILING DATE: 2003-01-22
: PRIOR APPLICATION NUMBER: 60/258,928
: PRIOR FILING DATE: 2000-12-29
: PRIOR APPLICATION NUMBER: 60/259,415
: PRIOR FILING DATE: 2001-01-02
: PRIOR APPLICATION NUMBER: 60/259,785
: PRIOR FILING DATE: 2001-01-04
: PRIOR APPLICATION NUMBER: 60/269,814
: PRIOR FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/279,832
: PRIOR FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/279,833
: PRIOR FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/279,863
: PRIOR FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/283,889
: PRIOR FILING DATE: 2001-04-13
: PRIOR APPLICATION NUMBER: 60/284,447
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: 60/286,683

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PRIOR FILING DATE: 2001-04-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 411
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 135
 LENGTH: 661
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-038-854-135

Alignment Scores:
 Pred. No.: 1,11e-54 Length: 661
 Score: 663.00 Matches: 196
 Percent Similarity: 45.68% Conservative: 116
 Best Local Similarity: 28.70% Mismatches: 289
 Query Match: 7.73% Indels: 82
 DB: Gaps: 16

US-09-396-985B-1 (1-4868) x US-10-038-854-135 (1-661)

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QY 200 GTTCTTAATATTACTTATCAATGAGCTGGAATTTCTACAAATCCCGAGAACCTC 259
DB 32 GluValAsnLysThrTyAsnCyGlnAsnLeuGlyLeuAsnGlnLysLeuProGlyThrLeu 51
QY 260 CCCTTCTCAACCAAGAACTGAGCCTGAGCTTAAATCCCTGAGGATTTAGGAGCTAT 319
DB 52 ProAsnSerThrGluCyLeuGluPheSerPheAsnValLeuProThrIleGlnAsnThr 71
QY 320 AGCTTCTTCACTTCCAGAACTGAGCTGCTGATTTATCCAGGTGGAATTCAGACA 379
DB 72 ThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCyGlnLysLeuTyrTrp 91
QY 380 ATTGAAGATGGGAGCATATCAGAGCTAAGCCACTCTCTACCTTAATATTGACAGAAAC 439
DB 92 IleIleGluAspThrPheGlnSerGlnIleAspLeuAspThrLeuValLeuThrAlaAsn 111
QY 440 CCCATCCAGAGTTAGCCCTGGAGCCCTTTTCTGAGCTATCAAGATTAAACAGAGCTGTG 499
DB 112 ProLeuIlePheMetAlaGluThrAlaLeuSerGlyProLysAlaLeuLysIleLeuPhe 131
QY 500 GCTGTGAGAGCAATCTAGACTCTCTAGAGAACTTCCCATTTGAGCATCTGAAAACCTTG 559
DB 132 PheIleGlnThrGlyIleSerSerIleAspPheIleProLeuIleAsnGlnLysThrLeu 151
QY 560 AAAAGACTTATGNGGCTCAATCTTATCCATCTTCAATCTTCAATTAACCTGATTTTCT 619
DB 152 GluSerLeuTyrlLeuGlySerAsnIleIleSerSerIleLysLeuProLysGlyPhePro 171
QY 620 AATTCAGCAATCTAGAGCACTTGACCTTCCAGACAAGATTCAAGATTAAATTTATTCG 679
DB 172 Thr---GluLysLeuLysValLeuAspPheGlnAsnAsnAlaIleHisTyLeuSerLys 190
QY 680 ACAGACTGGCGGGTCTACATCAATGCCCTACTCAATCTCTCTTTAGACTGTCCCTG 739
DB 191 GluAspMetSerSerLeuGlnGln-----AlaThrIleLeuSerLeuAsnLeuAsnLys 208
QY 740 AATCTTATGAATTTATTCACCAAGGTCATTTAAAGAAATTAAGGCTTCATTAAGTACT 799
DB 209 AsnAspIleAlaGlyIleGlnProGlyAlaPheAspSerAlaValPheGlnSerLeu--- 227
QY 800 TTAAAGATATATTTGATAGTTTAAATGTAATGAAGAACTTGATTCAGGCTGCTGGT 859
DB 228 -----AsnPheGlyGlyThrGlnAsnLeuLeuValIlePheLysGlyLeuLysAsn 244
QY 860 TTAAAGATCATCGTTGGTCTGCGAGAAATTGAAGAAATGAAGAACTTGAAAAGTTT 919
DB 245 SerThrIleGlnSerLeuThrProLysGlyThrPheGlnAspMetAspAsp---GluAspIle 263
QY 920 GACAAATGTGCTTAGAGGGCTGTGCAATTGACATTTGAAGAAATTCGATTTAGCATAC 979
  
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DB 264 SerProAlaValPheGlnGlyLeuCyGlnMetSerValGlnSerIleAsnLeu---Gln 282
QY 980 TTAGACTTACTACCTCCAGATGATATATTGACTTATTTATTTGATGACAAATGTTCTTCA 1039
DB 283 LysHisTyrlPhePheAsnIleSerSerAsnThrPheHisCyPheSer----- 298
QY 1040 TTTTCCCTGGAGTGTGACTATTTGAAGGGTAAAGACTTTCTTAATTTGCGATGG 1099
DB 299 -----GlyLeu 300
QY 1100 CAACATTGAAGATTGTAATCTGTAATTTGACAGTTTCCGACA-----TTGAAATCTC 1153
DB 301 GlnIleuLeuAspLeuThrAlaThrHisLeuSerGluLeuProSerGlyLeuValGlyLeu 320
QY 1154 AATCTCTCAAGAGCTTACTTCTTCACTTCCACAAAGCTGGGAAT-----GCTTTTCA 1207
DB 321 SerThrLeuLysLysLeuValLeuSerAlaAsnLysPheGlnAsnLeuCyGlnLysIleSer 340
QY 1208 GAAGTGTATCTACCAAGCTTGAAGTT----- 1234
DB 341 AlaSerAsnPheProSerLeuThrHisLeuSerIleLysGlyAsnThrLysArgLeuGlu 360
QY 1235 -----CTGATCTCAGTAGAAT 1252
DB 361 LeuGlyThrGlyCyLysGluAsnLeuGlnAsnLeuArgLysLeuAspLeuSerHisAsp 380
QY 1253 GCGTTGAGTTTCAAGAGTGTGCTGTCTCAAGATGATTTGGGACACAGCCTTAAGTAT 1312
DB 381 AspIleGluThrSerAspSerCyAsnLeuGlnLeuArgAsnLeuSerHisIleGlnIleSer 400
QY 1313 TTATCTGAGCTTCATATGAGTGTATTAACATGAGTTCAAA-----TTCTGGGCTTGA 1369
DB 401 LeuAsnLeuSerTyrlAsnGluProLeuSerLeuLysThrGluAlaPheLysGlyCyPro 420
QY 1370 CAATGAGACATCTGAGATTTCAGACATTTCCAAATTTGAAACAAATGAGTAGTTTTCAGTA 1429
DB 421 GlnIleuLysLeuLeuAspLeuAlaPheThrArgLeuLysValLysAspAlaGlnSerPro 440
QY 1430 TTCTTACTACAGAAACCTCATTTACTTTCAGATTTCTCATCTACACAGCAAGTTGCT 1489
DB 441 PheGlnAsnLeuHisIleLeuLysValLeuAsnLeuSerHisSerLeuLeuAspIleSer 460
QY 1490 TTCAATGGACATCTCATATGCTGTGTCAGTCTGCAAGTCTTGAAGAGCTGGGCAATCT 1549
DB 461 SerGlnIleuPheAspGlyLeuProAlaLeuGlnIleAsnLeuGlnGlyAsnHis 480
QY 1550 TTCAGAGAAACCTTCTT-----CCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1603
DB 481 PheProLysGlyAsnIleGlnLysThrAsnSerLeuGlnThrLeuGlyArgLeuGluIle 500
QY 1604 CTGACCTCTCTCAGTCTCACTGAGCAGCTGTGTCACACAGATTTAACTCACTCTCC 1663
DB 501 LeuValLeuSerPheCyAspLeuSerSerIleAspGlnHisAlaPheThrSerLeuLys 520
QY 1664 AGCTTACAGTACTAAATATGAGCCACAACAACCTTCTTTCATTTGATGATACCTTTCCTAT 1723
DB 521 MetIleAsnHisValaLysPheSerHisAsnArg-----LeuThrSerSerIle 537
QY 1724 AAGTGTCAACTCCCTCCAG-----GTTCTTATTAACAGTCTCAATCATCATATGACT 1777
DB 538 GluAlaLeuSerHisLeuLysGlyIleTyrlLeuAsnLeuAlaSerAsnHisIleSerIle 557
QY 1778 TCCAAAAACAGAACTACAGCATTTTCCAGATGAGTCTAGCTTCTTA----- 1825
DB 558 Ile-----LeuProSerLeuLeuProIleLeuSerGlnIleArg 570
QY 1826 -----AATCTTACTCAGATGACTTGTGCTTGTGTAATCTGTAACACAGATTTCTGCA 1879
DB 571 ThrIleAsnLeuArgGlnAsnProLeuAspCyThrTySerSerAsnIleTyrlPheLeuGlu 590
QY 1880 TGATCAAGAGCAGAGAGCTCTTGTGTAAGTGAAGATGAGATGAGTGAACACCT 1939
  
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Db 591 TrpTyrIleGluAsnMetGlnLysLeuGluAspThrGluAspThrLeuCySGluAsnPro 610
Qy 1940 TCAGATAGCAGGCGATCGCTGCTGAGTTGAATATCACTTCAGATGAATAAACC 1999
Db 611 ProLeuLeuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaVal 630
Qy 2000 ATCATGTGTGTGCGCTCAGTGTCTGTAGTATCTGTGTGAGCAGATTCTGTCTAT 2059
Db 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
Qy 2060 AAGTCTCTAT 2068
Db 651 LysTyrPhe 653
RESULT 7
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchenev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Verneel, Corline A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-037-417-107
Alignment Scores:
Pred. No.: 1,11e-54 Length: 661
Score: 663.00 Matches: 196
Percent Similarity: 45.68% Conserved: 116
Best Local Similarity: 28.70% Mismatches: 289
Query Match: 7.73% Indels: 82
DB: 15 Gaps: 16
US-09-396-985b-1 (1-4868) x US-10-037-417-107 (1-661)
Qy 143 GCCATGGCCTTCCCTCTCTGCG--GTGAGACAGAAAGCTGGAGCCCTGCGAGCTG 199
Db 12 AlaLeuPheLeuAlaSerCyValArgAlaThrThrSerSerArgGlnIleGlyLeu 31
Qy 200 GTTCTGTAATTAATTATTAATCAATGATGAGACSTGAATTTTCAAAATCCCGACACTC 259
Db 32 GluValAsnLysThrTyraenCySGluValnLeuGlyLeuAsnGluIleProGlyThrLeu 51
Qy 260 CCCTTTCAGCAAGAAACCTGAGCCTGATTAATCCCTGAGGACATTAGGACGCTAT 319
Db 52 ProAsnSerThrGluCyLeuGluPheSerPheAsnValLeuProThrIleGlnAsnThr 71
Qy 320 AGCTTTCTTCAAGTTTCCAGAACTGCAAGTCTGATTTATTCAGTGTGAATTCAGACA 379
Db 72 ThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgGlyIleTyrr 91
Qy 380 ATTGAAGATGGGCGATATCAAGCCTTAAGCAGCAGCCTTCACTTAATATTGACAGAAAC 439
Db 92 IleIleGluAspThrThrPheGlnSerGlnIleArgLeuAspThrLeuValLeuThrAlaAsn 111
Qy 440 CCCATCCAGAGTTTAAAGCCCTGAGCAGCCTTTTCCGATATCAATGATTAAGCAAGCTGTG 499
Db 112 ProLeuIlePheLeuAlaGluThrAlaLeuSerIleProLysAlaLeuLysValnSlePhe 131
Qy 500 GCTGTGAGACAAATCTAGCATCTGATGAGAACTCCCAATGGACATCCAAACTTTTG 559
Db 132 PheIleGlnThrGlyIleSerSerIleAspPheIleProLeuIleAsnGlnLysThrLeu 151
Qy 560 AAAGAACTTAATGTGAGTCAATCAATCTTAATCAATCTTAATCAATCTTAATCTTCT 619
Db 152 GluSerLeuTyrrLeuGlySerAsnIleIleSerSerIleLysLeuProLysGlyPhePro 171
Qy 620 AATGTACCAATCTAGACAGCAGCAGCCTTCCAGCAAGAACTTCAAGATTTATGTC 679
Db 172 Thr--GluLysLeuValLeuAspPheGlnAsnAlaIleIleTyrrLeuSerLys 190
Qy 680 ACAGACTTGGGGGTTTCAATCAATGCAAAATGCCCCCTACTGATCTCTTTAGACCTGCTG 739
Db 191 GluAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeuAsnGly 208
Qy 740 AATCTTAATGAATTTATTCACACAGGTGCATTTAAAGAAATTAGGCTTCATAGCTACT 799
Db 209 AsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu--- 227
Qy 800 TTAAGAAATATTTTGAATGTTTAAATGTAAGAAACTGTATGCAAGGCTGCTGCT 859
Db 228 -----AsnPheGlyGlyThrGlnAsnLeuValIlePheLysGlyLeuLysAsn 244
Qy 860 TTAGAGTCCATCTTTGTTGTTCTGGAGAAATTTAGAAATGAGGAACTGGAAAAGTTT 919
Db 245 SerThrIleGlnSerLeuThrPheGlyIleThrPheGlnAspMetAspAsp---GluAspIle 263
Qy 920 GACAAATCTGCTTAAGAGGGCTGTGCAATTTGACATTTAGAGAAATTCGATGACATAC 979
Db 264 SerProAlaValPheGluGlyLeuCySGluMetSerValGlnSerIleAsnLeu---Gln 282
Qy 980 TTAGACTAATCACTCCGATGATATATGACTTATTAATGTTTGAAGAAAGTTTCTTCA 1039
Db 283 LysIleSTyrPhePheAsnIleSerSerAsnThrPheIleCysPheSer----- 298
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Db      143  IleProValHisLeuLeuGlnLeuLeuGlnSerLeuTyLeuGlnSerHisLeuSer 162
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Db      163  SerTLeuSerProValSerPhePro--AlaArgHisLeuValLeuSerPheGln 181
Qy      653  AGCAACAAGATTAAGATTAATTTATGACAGCACTTGCGGGGTCTTACATCAAAATGCCCTTA 712
Db      182  AsnHisAlaLeuHisTyTLeuSerArgGlnSerMetArgSerLeuGlnGln-----Ala 199
Qy      713  CTCGAATCTCTTGAAGCTGCTCCCTGAATCTTAAGCACTTATCCAAACAGGTGCAATTT 772
Db      200  IleAsnLeuSerLeuHisPheHisGlnGlnValHisValLeuGlnGlnGlnAlaPhe 219
Qy      773  AAAGAAATTAAGCTTCAAGTGAATTAAGAAATTAATTTGATAGTAAATGTAATG 832
Db      220  AspSerThrValPheGlnSerLeu-----AsnPheGlnGlnTyThrProAsnLeu 235
Qy      833  AAAACTGTATCAAGGCTGCTGCTGCTTGAAGTCCATGCTTGGTCTGAGCAATTT 892
Db      236  SerValIlePheHisGlnGlnLeuHisSerThrThrGlnSerLeuThrPhe 255
Qy      893  AGAATGAAGAACTTGAAGAAATTTGACAAATCTGCTTAAGAGGCTGTGCAATTTG 952
Db      256  GluAspIleAspAsp--GluAspIleSerSerAlaMetLeuGlnGlnGlnGlnMet 274
Qy      953  ACCATTAAGAAATTCGATTAAGCACTTAAGCACTTAAGTGAATTAATTTATTTGAC-- 1009
Db      275  SerValGlnSerLeuHisLeuGln-----GlnHisArgPheSerAspIleSerSerThr 292
Qy      1010  TTTATTAATTAATTTGACCAATGTTTCTTCAATTTCCCTGAGTGAAGTGAATGAAG 1069
Db      293  ThrPheGlnGlnSerPheThrGlnLeuGlnGlnLeuAspLeuThrAlaThrHisLeuGln 312
Qy      1070  GTAAAGCACTTTCTTAATTAATTTGAGTGAACATTTAGAAATTAAGTAAAC----- 1120
Db      313  LeuProSer-----GlyMetLeuGlnLeuAsnLeuLeuGlnGlnGlnGlnGlnVal 327
Qy      1121  -----TGTAATTT-----GGACAGTTTCCCAACTTG 1147
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Qy      1148  -----AACTCAAACTCTGCAAAAGGCTTACTTCACTTCCAAAC 1186
Db      348  ThrHisLeuTyTLeuArgGlnValValLeuHisLeuGlnGlnGlnGlnGlnGlnGln 367
Qy      1187  AAAGGTGAAGATGCTTTTTCAGAAATGATCTTACCAAGCTTGAAGTTTGAATGATCAGT 1246
Db      368  LeuLeuGlnGlnGln-----LeuGlnThrLeuAspLeuSer 378
Qy      1247  AGAAATGGCTTGAAGTTTCAAAAGTGTGCTTCTCAAAAGTATTTGGGACAAACAGCTTA 1306
Db      379  HisAsnAspIleGlnAlaSerAspCysCysSerLeuGlnLeuTyAsnLeuSerHisLeu 398
Qy      1307  AAGTATTTAATCTGAGCTTCAATGATGTTTATCACTAGATGAAC-----CTTGGGC 1363
Db      399  GlnThrLeuHisLeuSerHisAsnGlnProLeuGlnGlnGlnGlnGlnGlnGlnGln 418
Qy      1364  TTGAACAACATGAACATCTGGAATTTCCAG-----CAATCCAAATTTGAAACAA 1411
Db      419  CysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuHisLeuAsnAlaProGln 438
Qy      1412  ATGAGTGAAGTTTCA-----GTAATCTTCACTCAAGAAACCTCAATTTCA-----CTT 1459
Db      439  ---SerProPheGlnAsnLeuHisPheLeuGlnValLeuHisLeuThrTyTyrCysPheLeu 457
Qy      1460  GACATTTCTCTACTCAACACAGAGTGTCTTCAATGGCACTTCAATGGCTGTCCAGT 1519
Db      458  AspThrSerAsnGlnHis-----LeuLeuAlaGlnLeuProVal 470
Qy      1520  CTCGAAGCTTGAAGATGGCTGCAATTTCTTTCAGAGAAATTCCTT-----CCAGAT 1573
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Db      491  LeuLeuGlnThrValGlnSerLeuGlnValLeuIleLeuSerSerCysGlnLeuLeuSer 510
Qy      1634  TTGTCTCAACAGCATTTAATCACTCTCCAGTCTTCAAGTACTTAATATAGACCAAC 1693
Db      511  IleAspGlnGlnAlaPheHisSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 530
Qy      1694  AACTTCTTT-----TCATTGATTAAGTTCCTTAT-----AAG 1726
Db      531  SerLeuThrCysAspSerIleAspSerLeuSerHisLeuGlnGlnGlnGlnGlnGlnGln 550
Qy      1727  TGTCTGAACCTCCCTCCAGGCTTGTGAATTAAGTCACTCAATTAAGCACTTCAAAAAA 1786
Db      551  AlaAlaHisSerIleAsnIleIleSerProArgLeuLeuProIleLeu----- 566
Qy      1787  CAGAACTACAGCATTTTCCAAAGTACTTAAGTCTTCTTAATATTTACTCAAAATGACTTT 1846
Db      567  -----SerGlnGlnSerThrIleHisLeuSerHisAsnProLeu 579
Qy      1847  GCTTGATCTTGTGAACACAGAGTTTCTGCAATGATCAAGACCAAGACAGCTTTG 1906
Db      580  AspCysThrCysSerAsnIleHisPheLeuThrTyTyrGlnGlnLeuHisGlnGlnGln 599
Qy      1907  GTGGAAGTTGAACGATGAATGAATGCAACCTTCAGATGAAGCAGGCGATGCTGCTG 1966
Db      600  GlnGlnGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 619
Qy      1967  AGTTGAAATTAACCTGTCCAGATGAATTAAGACCAATGATGCTGCTGCTTCAAGTGTG 2026
Db      620  AspValLeuSerCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 637
Qy      2027  CTGTGATGATCTTGTGAAGATGCTTGTGCTAT 2059
Db      638  PheLeuLeu-----LeuLeuAlaIleLeuLeuPhe 647

RESULT 9
US-10-038-854-134
: Sequence 134, Application US/10038854
: Publication No. US20040022781A1
: GENERAL INFORMATION:
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Li, Li
: APPLICANT: Wolenc, Adam R
: APPLICANT: Verne, Corine
: APPLICANT: Eissen, Andrew J
: APPLICANT: Liu, Xiaohong
: APPLICANT: Malysankar, Uriel M
: APPLICANT: Shinkets, Richard A
: APPLICANT: Tchernen, Velizar
: APPLICANT: Spederna, Steven K
: APPLICANT: Gorman, Linda
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Patursajan, Meera
: APPLICANT: Gusev, Vladimir Y
: APPLICANT: Ganjoli, Raha A
: APPLICANT: Guo, Xiaojia S
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Rastelli, Luca
: APPLICANT: Casman, Stacie J
: APPLICANT: Boldog, Ferenc
: APPLICANT: Burgess, Catherine E
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Ellerman, Karen
: APPLICANT: Gunther, Erik
: APPLICANT: Smithson, Glenda
: APPLICANT: Millet, Isabelle
: APPLICANT: MacDougall, John R
: TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21402-230
: CURRENT APPLICATION NUMBER: US/10/038, 854
: CURRENT FILING DATE: 2003-01-22

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Qy 1235 CTGAATCTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTCT 1279
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Qy 1280 CAAGTGAATTTGGGACACAGCCTAAAGTATTTAGATCTGAGCTTCAATGAGTGTATT 1339
Db 383 -----GluAspAlaTyrProSerLeuGlnThrLeuIleuValGlnAsn----- 397
Qy 1340 ACCATGATTCAAACTTCTGGGCTTAGAACACTAGACATCTGATTTCCAGCATTC 1399
Db 398 -----HisLeu-----Ala 400
Qy 1400 AATTGAAACAATGAGTGAATTTTCAATATCTATCATCTCAGAAACCTCATTTACCTT 1459
Db 401 SerLeuGluLysThrGlu-----ThrLeuThrLeuLysAsnLeuThrAsnIle 418
Qy 1460 GACATTTCTCATCTCACACAGAGTTGCTTCAATGAGCATCTTCAATGGCTTGTCCAGT 1519
Db 419 AspIleSerLys----- 422
Qy 1520 CTCGAAGCTTGAAATGCGTGCATATCTTTCCAGAAACTTCCCTCAGATATCTTC 1579
Db 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
Qy 1580 ACAGAGCTGAGAACTTGACCTTCCGTGACCTCTTCACTGATGTCATCTGAGACAGTTGCT 1639
Db 433 GlnTrpProGluLysMetLysTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
Qy 1640 -----CCAAACAGCATTTAACTCACTCTCCAGTCTTCCAGGATCTTAAATAGACAC 1690
Db 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
Qy 1691 AAC-----AACTCTTTTCATGTGAT----- 1711
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Db 507 SerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---HisThrLeu 525
Qy 1817 GCTTTCTTAATCTTACTCAGAAATGACTTGTGTTGATCTTGGAACACAGAGTTTCTCTG 1876
Db 526 LysThrLeuGluAlaGlyLysAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
Qy 1877 CAATGATCAAGACACAGAGCAGCTCTTGTTGGAAGTT-----GAAACA 1921
Db 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 561
Qy 1922 ATGGAATGTGCAACACTTTCAGATBAGCAGGCGATGCTGCTGAGATTGAATATCAC 1981
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLysSer 581
Qy 1982 -----TGTCAGATGAATTAAGACATCTTGTTGGTGGTGGCTCCAGTGGCTGTA 2032
Db 582 ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysValAlaLeuPheLeuLeu 601
Qy 2033 GTATCTGTTTGAAGACTTGTGCTATAGTTTAT-----TTTCACCTGAGCTTCTT 2086
Db 602 IleLeuLeuThrGluValLeuLeuCysHisArgPheHisGlyLeuTyrTyrMetLysMetMet 621
Qy 2087 GCTGCTGCATTAAGTATGTA-----GGTGAACAATC---TAT 2135
Db 622 TrpAlaTrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysThr 641
Qy 2126 GATGCTTTGTTATCTACTCAAGCAGATGAGAGCTGGTGAAGGAATGACTGTGTAAG 2185

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Db 642 AspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGln 661
Qy 2186 AATTAGAAAGAGGGGCGCTCCATTTTCAGCTGCTGCTTCACTACAGACATTTATCCC 2245
Db 662 GluLeuGlnAsnPheAsnProProPheLysLeuCysLeuHisLysArgAspPheIlePro 681
Qy 2246 GGTGGCGCATTTGCTGCGCAACATCATCAATGAAGTTTCCATAAAGCCGAAAGTAT 2305
Db 682 GlyLysTrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrVal 700
Qy 2306 GTTGTGTGTCCAGACATTCATCCAGAGCGCGTGTATCTTTGAATATGAGATGCT 2365
Db 701 PheValLeuSerGluAsnPheValLysSerGluTyrCysLysTyrGluLeuAspPheSer 720
Qy 2366 CAGACCTGGCAGTTTCTGAGCAGTCGCTGCTGTATCATCTTCAATGCTCCAGAAAGT 2425
Db 721 HisPheArgLeuPheGluGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIle 740
Qy 2426 GAGAAAGCCGTGCTCAGACAGCAG---GTGAGCTGTACCGCTTCTCAGAGGAACT 2482
Db 741 GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy 2483 TACCTGAGTGGAGAGCAGATGTCCTGGGCGGACATCTTCTGAGACGATCAGAAA 2542
Db 761 TyrLeuGluTrpProMetAspGluAlaGlnArgGluGluPheTrpValAsnLeuArgAla 780
Qy 2543 GCCCTG 2548
Db 781 AlaIle 782

RESULT 11
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PR
; ORGANISM: Homo Sapiens
US-10-456-947-46

Alignment Scores:
Pred. No.: 7.54e-49 Length: 784
Score: 603.50 Matches: 233
Percent Similarity: 41.88% Conserved: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.03% Indels: 219
DB: 15 Gaps: 38

US-09-396-985b-1 (1-4868) x US-10-456-947-46 (1-784)
Qy 245 ATCCCGCAACAACGCCCCCTTCTCAACCAAGACCTGACCTTAAATCCCTGAGG 304
Db 46 IleProSerGlyLeuThrGluAlaValLysSerLeuAspLeuSerAsnAsnArgIleThr 65
Qy 305 CATTTAGCAGACTTATGACTTCTTCACTTCCAGAACTGAGAGGCTGTGATTTTCCAGG 364
Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValIleThrSer 85

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QY 365 TGCGAATCCAGACATTTGAAGATGGGACATATGACAGCCTTAAGCCACTTCTACCTTA 424
DB 86 AsnGly11IleasnThr11GluGluAspSerPheSerLeuGlySerLeuGluHisLeu 105
QY 425 ATATTGACAGAAACCCCATCCAGATTAGCCCTGGAGCCTTTCTGACATACAGT 484
DB 106 AspLeuSerYrAnnyrLeuSerAsnLeuSerSerThrPheLysProLeuSerSer 125
QY 485 TTACAGAACTG----- 508
DB 126 LeuThrPheLeuAsnLeuGlyAsnProYrLysThrLeuGlyLutThrSerLeuPhe 145
QY 509 ACAAAATGAGATCTCTAGAGAACTCCCATGGACATCTCAAAATC----- 556
DB 146 SerHisLeuThrLysLeuGluHisLeuAspGlyValGlyAsnMetAspThrPheThrLysIle 165
QY 557 -----TTGAAGAACTTAATGTGGCTCAACATCTT 586
DB 166 GluArgLysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAsp 185
QY 587 ATCCAAATCTTTCAAAATTAAGTATTTTCTATCTGACCAATCTAGAGCACTTGAC 646
DB 186 LeuGlnSerYrGlu-----ProLysSerLeuSerLysIleGlnAsnValSerHisLeuIle 204
QY 647 CTTTCCAGCAACAG-----ATTCAAGATAT 673
DB 205 LeuHisMetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerVal 224
QY 674 TATTGACAGACCTGGGTTCTACATCAATGCCCCACTCAATCTCTTTAGACCTG 733
DB 225 GluCysLeuGluLeuAsp-----AspThr 232
QY 734 TCCCTGAATCCTTAAGACTTT-----ATCCACAGAGTGCATTTAAAGAAATTAAGCTT 787
DB 233 AspLeuAspThrPheHisPheSerGluLeuSerThrGlyLutThrAsnSerLeu-----Ile 251
QY 788 CATAGAGTGAATTTAAGAAAT-----AATTTGATAGTTTA-----AATGATAGTAA 835
DB 252 LysLysPheThrPheHisGlnValLysIleThrAspGluSerLeuPheGlnValMetLys 271
QY 836 ACTGT-----ATTCAAGGTCTGGCTGGTTTGAAGTCAATCGTTGGTTCTG----- 883
DB 272 LeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGly 291
QY 884 ---GGAGATTTAGAATGAAGAACTTGAGAAAGTTTGCAAAATGCTGCTTGAGAGGC 940
DB 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu--- 310
QY 941 CTGAGCAATTTGACCATTTGAAGAAATCCGATTAGCA-----TACTTGAAGCTTACTG 994
DB 311 -----ThrLeuThrIleArgArgLeuHisIlePheAspPheThrLeuPheThr----- 326
QY 995 GATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1054
DB 327 ---AspLeuSerThrLeuThrSerLeuThrGluThrValLys-----Arg 340
QY 1055 GTGACTATTTGAAGGGTAAAGACTTTTCTTAATTAATTTGAGATGGCAACATTTAGAAATTA 1114
DB 341 IleThrValGluAsnSerLysValPhe-----Leu 350
QY 1115 GTTAACCTTAATTTGACAGATTCCCATTTGAAACTCAAAATCTCAAAAGGTTTACT 1174
DB 351 ValProCysLeuLeuSerGln----- 357
QY 1175 TTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACAAAGCTTGAGTTT 1234
DB 358 -----HisLeuLysSerLeuGluLutYr 364
QY 1235 CTAGATCTCAGTGAAT-----GGCTTGAAGTTTCAAAAGTTGCTGTTCT 1279
DB 365 LeuAspLeuSerGluAsnLeuMetValGluGluLutYrLeuLysAsnSerAlaCys----- 382

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QY 1280 CAAAGTGAATTTGGGCAACACAGCCTTAAGATTAATTAAGTCTGACCTTCAATGGTGTAT 1339
DB 383 -----GluAspAlaThrProSerLeuGlnThrLeuIleLeuAspGlnAsn----- 397
QY 1340 ACCATGATGTTCAAACTTTGGGCTTAAAGAACTTGAAACATTTGGATTTCCAGCATTC 1399
DB 398 -----HisLeu-----Ala 400
QY 1400 AATTTGAACAAATGAGTGAAGTTTCAGTATCTCTATCACTGAGAAACCTCATTTACCTT 1459
DB 401 SerLeuGluLutThrGlyLut-----ThrLeuThrLeuLysAsnLeuThrAsnIle 418
QY 1460 GACATTTCTCATCTGACACACAGAGTTGCTTCAATGGCAATCTTCAATGGCTTGCAGT 1519
DB 419 AspIleSerLys----- 422
QY 1520 CTGAAAGTCTTGAAAATGGCTGGCAATTTCTTTCCAGAAACCTTCTCCAGATATCTTC 1579
DB 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
QY 1580 ACAGAGCTGAGAAACTTGAACCTTCTGAGACCTCTCAGTGTCAAGTGGAGAGTTGCT 1639
DB 433 GluThrProGluLutMetLysYrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
QY 1640 -----CCAAAGCATTTAATGATCTCCAGTCTTTCAGGTACTTAATATGAGGCAC 1690
DB 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
QY 1691 AAC-----AAGTTCTTTTATTGAT----- 1711
DB 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGluLeuLysGluLeuYrIleSerArg 486
QY 1712 -----ACGTTTCT-----TATTAAGTGTGAATCCCTCCAGGTTTCTTGAATTAC 1756
DB 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValIleLysIle 506
QY 1757 AGTCTCAATGACATTAATGACTTCCAAAAAACAGAACTACAGCAATTTCCAAAGTACTTA 1816
DB 507 SerArgAsnAlaIleThrThrPheSerLysGluGluLeuAspPhePhe-----HisThrLeu 525
QY 1817 GCTTTCTTAATCTTACTGCAATGACTTGTGCTTGTACTTGTGAACCCAGAGTTTCTG 1876
DB 526 LysThrLeuGluLutAlaGlyLysAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
QY 1877 CAATGATCAAGACCCAGAGGAGCTCTGTGTGAAGTT-----GAACGA 1921
DB 546 Gln-----GluGlnGlnAlaLeuAlaLysValIleuIleAspThrProAlaAsn 561
QY 1922 ATGGAATGTCACACCTTCAAGATTAAGCAGGCAATGCTGTGCTGATTTGAATATCAC 1981
DB 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
QY 1982 -----TGTCAGATGAATTAAGACCATTTGTGTGTGTGCTGCTTCAAGTGTGCTGTA 2032
DB 582 ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
QY 2033 GTATCTGTGTAGAGAGTTCTGTGTATTAAGTTACT-----TTTCACTGATGCTTCTT 2086
DB 602 IleLeuLeuThrGlyValLeuCysHisArgPheHisIleGlyLeuThrPyrMetLysMetMet 621
QY 2087 GCTGGCTGCAATAAGTATGTGAG-----GGTGAACATC---TAT 2125
DB 622 ThrAlaThrLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysEyr 641
QY 2126 GATGCTTTGTTATCTACAGCAGGATGAGGACTGGGTAAAGAAATGAGCTTAAAGTAA 2185
DB 642 AspAlaPheValSerYrSerGluArgAspAlaYrThrValGluAsnLeuMetValGln 661
QY 2186 AATTTAAGAAAGGGGCTCCATTTCACTGCTGCTGCTTCACTACAGAGCTTAATTTCCC 2245
DB 662 GluLeuGluAsnPheAsnProProPheLysLeuLysLeuHisLysLysAspPheIlePro 681
QY 2246 GGTGTGCCATTGTGTGCCAACATCATCATGAAGGTTTCCATTAAGCCGAAAGGTGATT 2305

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Db 682 GlyIystrIlelleAspAsnIlelle---AsperIleGluIysSerHisIyethrVal 700
 QY 2306 GTTGAGGTGTCACACTTATCCAGACCGCGCTGCTACTTCTGATATGAGATTGCT 2365
 Db 701 pheValIeuSerGluAsnphValIysSerGluIyrCyIyGluLeuAspHeSer 720
 QY 2366 CAGACTGGCAGATTCTTGAGCAGTCGTGCTGATCATCTTCATGTCCTCAGAGGTG 2425
 Db 721 HispheArgIeuPheGluGluAsnAspAlaIleIleuIleLeuLeuGluProIle 740
 QY 2426 GAGAAGACCTGCTCAGCAGCAGCAG---GTGAGCTGTACCGCTTCTCAGACGAACT 2482
 Db 741 GluIyIyAlaIleProGluIArgPheCyIyIyLeuArgIyIleMetAsnThrIyethr 760
 QY 2483 TACTGAGGTGAGGAGCAGTGTCTGCGGGGAGCAGCATCTTCTGAGACGACTGAGAAA 2542
 Db 761 TyrIeuGluIyrProMetAspGluAlaGluIArgGluIyPheIyrValAsnLeuArgAla 780
 QY 2543 GCCCTG 2548
 Db 781 AlaIle 782

RESULT 12
 US-10-095-627-12
 ; Sequence 12, Application US/10095627
 ; Publication No. US20030027260A1
 GENERAL INFORMATION:
 APPLICANT: Goddard, Audrey
 Godowski, Paul J.
 Gurney, Austin
 Mark, Melanie
 Yang, Ruy-Bing
 TITLE OF INVENTION: Human Toll Homologues
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/095,627
 FILING DATE: 11-Mar-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,413A
 FILING DATE: 26-Jun-1998
 APPLICATION NUMBER: 60/083322
 FILING DATE: 28-Apr-1998
 APPLICATION NUMBER: 60/065311
 FILING DATE: 13-Nov-1997
 APPLICATION NUMBER: 60/062250
 FILING DATE: 17-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Marechang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1154-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 784 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-095-627-12
 Alignment Scores:
 Pred. No.: 9,44e-49 Length: 784
 Score: 602.50 Matches: 233
 Percent Similarity: 41.88% Conservative: 128
 Best Local Similarity: 27.03% Mismatches: 282
 Query Match: 7.02% Indels: 219
 DB: 14 Gaps: 38
 US-09-396-985b-1 (1-4866) x US-10-095-627-12 (1-784)
 QY 245 ATCCCGACACCTCCCTTCTCAACCAAGACCTGACCTTATATCCCTGAGG 304
 Db 46 IleProSerGluIeuThrGluAlaValIySerIeuAspSerAsnAsnArgIleThr 65
 QY 305 CATTTAGCAGCTATAGCTTCTTCAAGTTTCCAGAACTGCAAGTGTCTGATTTTCAAG 364
 Db 66 TyrIleSerAsnSerAspLeuGluIArgCyValAsnIeuGluAlaIleuValIeuThrSer 85
 QY 365 TGTGAATCCAGACATTTGAAGATGGGCAATTCAGACCTTACGCCCTCTACCTTA 424
 Db 86 AsnGlyIleAsnThrIleGluGluAspSerPheSerIeuGluIySerLeuGluHisIle 105
 QY 425 ATATTGACAGAAACCCCATCCAGAGTTTAGCCCTGGAGCCTTTCTGACTATCAAGT 484
 Db 106 AspIeuSerIyrAsnIyrIleuSerAsnIeuSerSerSerIrrPheIySproIeuSerSer 125
 QY 485 TTACAGAGCTG-----GTGGCTGTGAG 508
 Db 126 LeuThrPheIeuAsnLeuIeuGluIAsnProIyIySerIeuGluIyrIeuThrSerIeuPhe 145
 QY 509 ACAATCTAGCATCTCTAGAACTTCCCATTTGACATCTCAAAAT----- 556
 Db 146 SerHisIeuThrIyIeuGluIleIeuArgValGlyAsnIeuSerAsnIrrPheThrIyIle 165
 QY 557 -----TTGAAGAACTTATGTGGCTCACAATCTT 586
 Db 166 GluIArgIyAsnPheAlaGluIyLeuThrPheIeuGluIleuGluIleAspAlaSerAsp 185
 QY 587 ATCCATCTTTCAATTAATCTGAGTATTTTCTAATCTGACCAATCTAGACACTTGAAC 646
 Db 186 LeuGluIeuIyrGlu---ProIySerIeuIySerIleGluIeuValSerHisIeuIle 204
 QY 647 CTTTCCAGCAACAG-----ATTCAAAGTAT 673
 Db 205 LeuHisIeuIyGluHisIleIeuLeuIeuGluIlePheValAspValIrrSerSerVal 224
 QY 674 TATTGACAGACTTGGCGGTTTCAATCAATGCCCCCTACTCAATCTCTTTAGACCTG 733
 Db 225 GluCyIeuIeuIeuArg-----AspThr 232
 QY 734 TCCCTGAATCTTGAACCTT-----ATCCAACAGTGCATTTAAGAATTAGGCTT 787
 Db 233 AspIeuAspIrrPheHisPheSerGluIeuSerThrGlyIuIrrAsnSerIeu---Ile 251
 QY 788 CATTAAGCTACTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAA 835
 Db 252 IySerIeuPheThrPheArgAsnValIyIleIrrAspIuIeuSerIeuPheGluIeuValMetIyS 271
 QY 836 ACTTGT-----ATTCAGAGCTGTGGCTGTGAAGTCCATGCTGTGGTTCTG----- 883
 Db 272 LeuIeuAsnGluIleSerGlyLeuLeuGluIeuGluIeuPheAspSerCySthrIeuAsnGly 291
 QY 884 ---GGAGATTTGAAGAAATGAAGAACTTGAAGAAAGTTTGAACAATCTGCTTAGAGGCG 940
 Db 292 ValGlyIeuAsnPheArgIleSerAspAsnAspArgValIleAspProGlyIyValGlu--- 310
 QY 941 CTGTGCAATTTGACCAATGAAGAAATCCGATTAGCA-----TACTAGACTTACTACCTC 994
 Db 311 -----ThrIeuThrIleArgIeuHisIleProArgPheIyrIeuPheIyr----- 326
 QY 995 GATGATATTATTAATTAATTAATTTGACAAATGTTTCTTCAATTTCCCTGGTAGT 1054

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Db      327  ---AepLeuSerThrLeuTyrSerLeuThrGluValIys-----Arg 340
Qy      1055 GTGACTATGAAAGGATTAAGACTTTCTTATATTTGGATGCAACATTAGAAATTA 1114
Db      341  ILeuThrValGluAenSerIysValPhe-----Leu 350
Qy      1115 GTTAACTGTAATTAATTGGACATTTCCCATTTGAAACTCAAAATCTTCAAAAGGCTTACT 1174
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1175 TTCACTTCCAACAAAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTT 1234
Db      358  ----- 364
Qy      1235 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAAAGTTGCTGTCTTCT 1279
Db      365  LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuIysAaenSerAlaCys----- 382
Qy      1280 CAAGATGATTTGGGACAAACGAGCTTAAGATTTAGATCTGAGCTTCAATGATGTTATT 1339
Db      383  -----GluAspAlaATPrProSerLeuGlnThrLeuIleLeuArgGlnAaen----- 397
Qy      1340 ACCATGAGTTCAAACTTCTGGGCTTAGAACAACTAGAACATCTGATTTTCACAGATTCC 1399
Db      398  -----HisLeu-----Ala 400
Qy      1400 AATTGAAACAATAGATGATTTTTCAGTATTCCTATACCTCAGAAAACCTTATTAACCTT 1459
Db      401  SerLeuGluIysThrGlu-----ThrLeuLeuThrLeuIysAsnLeuThrAsnIle 418
Qy      1460 GACATTTCTCATACTCACCACAGAGTTGCTTTCATATGCGATCTTCAATGCTTGCCAGT 1519
Db      419  AspIleSerIys----- 422
Qy      1520 CTCGAAGCTTGAAAATGCTGGCAATTCCTTTCAGAGAAAACCTTCAGATATCTTC 1579
Db      423  -----AsnSerPheHisSer-----MetProGluThrCys 432
Qy      1580 ACAAGCTGAGAAAACCTTGACCTTCTCGACCTCTCTCAGTGTCACTGAGACAGTGTCT 1639
Db      433  GlnTrpProGluIysMetIysTyrLeuAaenLeuSerSerThrArgIleHisSerValThr 452
Qy      1640 -----CCAACGACATTTAACTCACTCTCCAGTCTTCAGTATCAATATATAGACAC 1690
Db      453  GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAaen 466
Qy      1691 AAC-----AACTCTTTTCATTGAT----- 1711
Db      467  AsnAaenLeuAaenLeuPheSerLeuAaenLeuProGlnLeuIysGluLeuTyrIleSerArg 486
Qy      1712 -----ACGTTTCCT---TATAAGTCTGGAACCTCCCTCCAGGCTTTGATTAC 1756
Db      487  AsnIysLeuMetTrpLeuProAspAlaSerLeuLeuProMetLeuValLeuIysIle 506
Qy      1757 AGTCTCAATCAATATGATGATCTCCAAAACAGAGAACTACAGACTTTTCCAAAGTATGCTA 1816
Db      507  SerArgAaenAlaIleThrThrPheSerIysGluGlnLeuAaenSerPhe---HisThrLeu 525
Qy      1817 GCTTTCTTAATCTTACTCAGATGACTTTCCTGCTGATCTTGTGAACACAGAGTTTCTCG 1876
Db      526  LysThrLeuGluAlaGlyIysAaenAaenPheIleCysSerIysGluPheLeuSerPheThr 545
Qy      1877 CAATGATCAAGACCAAGGCACTCTTGCGTAAGTT-----GAACGA 1921
Db      546  Gln-----GluGlnGlnAlaLeuAlaIysValLeuIleAspTrpProAlaAaen 561
Qy      1922 ATGGAATGTCAGACACTTTCAGATTAAGAGGCAATGCTGTCGAGTTTAATATATACAC 1981
Db      562  TyrLeuCysAaenSerProSerHisValArgGlyGlnGlnValGlnAaenValArgLeuSer 581
Qy      1982 -----TGTCAATGAATTAAGACATCATTTGTTGTGTGTGCTTCAGTGTGCTTGTGA 2032

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Db      582  ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeu 601
Qy      2033 GTATCTGTTTACACAGCTTCGTCGTCTATAGTTCTAT-----TTTCAACCGATGCTTCTT 2086
Db      602  IleLeuLeuThrGluIysAlaLeuCysHisArgPheHisGluLeuTyrIleMetIysMetMet 621
Qy      2087 GCTGAGCTGCAATAAGATAGTGTAGA-----GGTGAATAATC---TAT 2125
Db      622  TrpAlaTrpLeuGlnAlaIysArgIysProArgIysAlaProSerArgAaenIleCysTyr 641
Qy      2126 GATGCTTTTGTATCTTACTCAAGCCAGAGATGAGAGATCGGGTAAAGAAATGACTTAAAG 2185
Db      642  AspAlaPheValSerIysSerGluArgAspAlaTyrTrpValGluAaenLeuMetValGln 661
Qy      2186 AATTGAAAGAAGGGGCTTCATTTACGCTGCTGCTTCATTCATTCAGAGACTTATATCCC 2245
Db      662  GluLeuGluAaenPheAaenProProPheIysLeuCysLeuHisIysArgAaenPheIlePro 681
Qy      2246 GGTTGGCCATTTGCTGCGCAACATCATTCATGAAGTTTCCATTAAGCCGAAAGGTGATT 2305
Db      682  GlyIysTrpIleIleLeuAaenIleIle---AspSerIleGluIysSerHisIysThrVal 700
Qy      2306 GTTGTGCTGCCAGACATTCATTCAGAGCCGCTGGTGTATCTTTGAATATGAGATTCT 2365
Db      701  PheValLeuSerGluAaenPheValIysSerGluTrpCysIysTyrGluLeuAaenPheSer 720
Qy      2366 CAGACCTGAGATTTCTGACACATCGCTGCTGATCATCTTCACTTTCCTGCAAGAGCTG 2425
Db      721  HisPheArgLeuPheAspGluAaenAaenAspAlaAlaIleLeuLeuLeuGluProIle 740
Qy      2426 GAGAAACCTGCTGCTGACGACAGCAG--GTGAGCTGTACCGGCTTCCAGCAGAAACCT 2482
Db      741  GluIysIysAlaIleProGlnArgPheCysIysLeuArgIysIleMetAaenThrIysThr 760
Qy      2483 TACTGAGTGGAGAGACAGTGTCTGCGGCGGCACTCTTTCGAGACAGACTTCAGAAA 2542
Db      761  TyrLeuGluTrpProMetAaenGluAlaGlnArgGluIysIleThrPheValAaenLeuArgAla 780
Qy      2543 GCCCTG 2548
Db      781  AlaIle 782

RESULT 13
US-10-732-563-4
: Sequence 4, Application US/10732563
: Publication No. US20040132079A1
: GENERAL INFORMATION:
: APPLICANT: Gupta, Shalley K.
: APPLICANT: Ghosh, Tarun K.
: TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
: FILE REFERENCE: 58183W003
: CURRENT APPLICATION NUMBER: US/10/732,563
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 4
: LENGTH: 784
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-732-563-4

Alignment Scores:
Pred. No.: 9,44e-49 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.02% Indels: 219
DB: 16 Gaps: 38

US-09-396-985b-1 (1-4868) x US-10-732-563-4 (1-784)
Qy      245  ATCCCGACAACCTCCCTTCTCAACCAAGAACTTGACCTGAGCTTAAATCCCTGAGG 304

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Db      46  ILeProSerGlyLeuThrGluAlaValIleSerLeuAspLeuSerAsnAsnArgIleThr 65
Qy      305  CATTAGGACGCTAGCTTCTTCAGTTCCCGAAGCTGCGAGTGTGATTTATCCAGG 364
Db      66  TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
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Db      146  SerIleLeuThrIleGlyLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIle 165
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QY 2366 CAGACCTGGAGCTTTCAGACAGTCGTGCTGTATCTTCATTTGCTTCGACAAAGTGT 2425
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; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-796A-4

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 : Publication No. US20050026169A1
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 : APPLICANT: CARGILL, Michele et al.
 : TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 : FILE REFERENCE: CU001499
 : CURRENT APPLICATION NUMBER: US/10/741,600
 : NUMBER OF SEQ ID NOS: 73997
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 1390
 : LENGTH: 784
 : TYPE: PRF
 : ORGANISM: Homo sapiens
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Db 781 Alarie 782

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 153.708 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result *
Query

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	4315.5	64.2	837	10	US-09-950-041-26
2	4141	61.6	799	10	US-09-950-041-8
3	4141	61.6	799	10	US-10-128-166-7
4	4141	61.6	799	16	US-10-732-563-8
5	4141	61.6	799	16	US-10-732-796A-8
6	656.5	9.8	661	15	US-10-038-854-135
7	656.5	9.8	661	15	US-10-037-417-107
8	619.5	9.2	661	13	US-10-114-893-10
9	619.5	9.2	661	13	US-10-038-854-134
10	603.5	9.0	784	10	US-09-950-041-4
11	603.5	9.0	784	15	US-10-456-947-46
12	602.5	9.0	784	14	US-10-095-627-12
13	602.5	9.0	784	16	US-10-732-563-4
14	602.5	9.0	784	16	US-10-732-796A-4
15	602.5	9.0	784	17	US-10-741-600-1390
16	602.5	9.0	784	17	US-10-741-600-1391
17	599.5	8.9	784	13	US-10-145-014-23
18	580.5	8.6	1032	10	US-09-954-987B-192
19	580.5	8.6	1032	14	US-10-272-502A-31
20	580.5	8.6	1032	15	US-10-407-952-32
21	567	8.4	1050	10	US-09-954-987B-175
22	567	8.4	1050	14	US-10-272-502A-22
23	567	8.4	1050	15	US-10-407-952-26
24	533	7.9	1032	10	US-09-950-041-37
25	533	7.9	1040	9	US-09-864-761-38325
26	533	7.9	1041	9	US-09-168-978-3
27	533	7.9	1041	9	US-09-978-295A-498
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43	533	7.9	1041	10	US-09-978-193A-498
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45	533	7.9	1041	10	US-09-978-757A-498

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DK0724X1
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/09/950,041
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

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; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-950-041-26

Alignment Scores:
Score: 0 Length: 837
Percent Similarity: 4315.50 Matches: 837
Best Local Similarity: 95.33% Conservative: 0
Query Match: 64.18% Indels: 41
DB: 10 Gaps: 1

US-09-396-985b-3 (1-3811) x US-09-950-041-26 (1-837)

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QY 108 AGACCAAGAACTGGAGACCTCGGCTGGAGACTTGGCCCTTAACCAACAGAAAGCTGG 167
DB 21 ArgProGluSerThrPgluProCysValGlu----- 30
QY 168 CATGAACCCAGAGCTTCAGACGCCGAGCCTCAGCCCTTCACCCCGATTCCATTGCTT 227
DB 30 ----- 30
QY 228 CTTCGTAATGCTGCGCTTTTATCATCAGGAGGCGTTCCTAATATTACTTATCAATGCA 287
DB 31 -----ValProAlaIleThrTyrGlnCysMet 39
QY 288 GAGCTGAATTTCTCAAAATCCCGACCAACTCCCTCTTCAACCAAGAACTGGAGCTG 347
DB 40 GluLeuAlaSerPheTyrIleProAspAsnLeuProPheSerThrTyrAsnLeuAspLeu 59
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QY 408 GTGCTGATTTATCCAGGTGTGAATCCAGACAATTTGAAGATGGGCAATATCAGAGCCTA 467
DB 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeu 99
QY 468 AGCCACCTCTCTACTTAATATTGACAGAGAAACCCATCCAGATTTAGCCCTGGAGACC 527
DB 100 SerHisIleuSerThrLeuIleIleuThrGlyAsnProIleGlnSerLeuAlaIleuGlyAla 119
QY 528 TTTTCTGACATATCAAGTTTACAGAGCTGGGTGCTGAGAGCAAACTAGCATCTCTA 587
DB 120 PheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuAlaSerLeu 139
QY 588 GAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAATGTTGAGCTCACATCTT 647
DB 140 GluAlaSerPheProIleGlyHisIleuSerThrLeuSerGluLeuAlaValHisIleuLeu 159
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QY 708 CTTCACAGAACCAATTTCAAGTATTTATTGACACAGACTTGGCGGCTTCAATCAATG 767
DB 180 LeuSerSerAsnTyrIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
QY 768 CCCCTACTCAATCTCTCTTATAGACCTGTCCCGAAGCCCTATGAACCTTTATCCAAACGAGT 827

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DB 220 AlaPheLeuGlnIleArgLeuHisTyrLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
QY 888 GATATGAAAACCTGTATTCAAGGTCTGGCTGTGTTTGAAGTCCATGCTTTGTTCTGGGA 947
DB 240 ValMetTyrThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly 259
QY 948 GAATTTGAAATGAGGAAACTTGGAAAAGTTTGACAAATCTGCTCTAGAGGCGCTGTGC 1007
DB 260 GluPheArgAsnGlnGlyAsnLeuGlnTyrPheAspTyrSerAlaLeuGlnGlyLeuCys 279
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DB 420 GlnGlnLeuGlnHisIleuAspPheGlnHisSerAsnLeuSerGlnMetSerGluPheSer 439
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DB 540 CysLeuAsnSerLeuGlnValIleuAspTyrSerLeuAsnHisIleMetThrSerTyrLeu 559
QY 1848 CAGGAATCAAGCAATTTTCCAAAGTAGTCTAGCTTTCTTAAATCTTCAATGAGTACTTT 1907
DB 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579

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QY 1908 GCTTGTACTGTGAACACAGAGTTCTCGATGATCAAGACAGAGCAGCTCTTG 1967
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Db 600 ValGluValGluArgMetGluCysAlaThrProSerApySgInGlyMetProValLeu 619
QY 2028 AGTTGAATATCCCTCGATGATGAATGAACCACTATGCTGCTGCTGCTGCTGCTG 2087
Db 620 SerLeuasnIleThrCysGlnMetCasnLysThrIleLeGlyValSerValLeuSerVal 639
QY 2088 CTGTAGATATCTGTGTAGAGAGTTCTGATCTAATAGTTATTTTACCTGATCTCTT 2147
Db 640 LeuValValSerValValAlaValLeuValTyrIlySpherPheHsleuMetLeuLeu 659
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QY 2568 CTGGGGGGGACATCTTCTGAGACGACTCAAGAAAGCCCTGCTGATGTTAAATCAATGG 2627
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RESULT 2
US-09-950-041-8
: Sequence 8, Application US/09950041
: Publication No. US20030032090A1
: GENERAL INFORMATION:
: APPLICANT: Hardiman, Gerard T.
: APPLICANT: Rock, Fernando L.
: APPLICANT: Bazan, J. Fernando
: APPLICANT: Kastelehn, Robert A.
: APPLICANT: Ho, Stephen W.K.
: APPLICANT: Liu, Yong-Jun
: TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
: FILE REFERENCE: DX0724X1
: CURRENT APPLICATION NUMBER: US/09/950, 041
: PRIOR FILING DATE: 2002-05-06
: PRIOR APPLICATION NUMBER: 09/728,540
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: 60/207,558
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: 09/073,363

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: PRIOR FILING DATE: 1999-06-05
: PRIOR APPLICATION NUMBER: 60/044,293
: PRIOR FILING DATE: 1997-05-07
: PRIOR APPLICATION NUMBER: 60/072,212
: PRIOR FILING DATE: 1998-01-22
: PRIOR APPLICATION NUMBER: 60/076,947
: PRIOR FILING DATE: 1998-03-05
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8
: LENGTH: 799
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-950-041-8

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Alignment Scores:
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Score: 4141.00 Matches: 799
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.59% Indels: 0
DB: 10 Gaps: 0

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US-09-396-985b-3 (1-3811) x US-09-950-041-8 (1-799)

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QY 345 CTAGACTTATATCCCTGAGGCAATTAAGCAGCTATAGCTTCTTCACTTCCAGAACTG 404
Db 21 LeuSerPheasnProLeuArgHsIleuGlySerTyrSerPhePheSerPheProGluLeu 40
QY 405 CAGCTGTGATTTATCCAGGTGTGAATATCAACAATTAAGATGGGCAATATCAGACC 464
Db 41 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
QY 465 CTAGACCACTCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTTACGCTGGA 524
Db 61 LeuSerHsIleuSerThrLeuIleuHsIleuHsIleuHsIleuHsIleuHsIleuHsIleu 80
QY 525 GCCTTTCTGACATATCAAGTTTACAGAAAGCTGTGTGCTGTGAGACAAATCTAGCATCT 584
Db 81 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 100
QY 585 CTAGAAACTTCCCATTTGACATCTCAAACTTTGAAGAATTATGTCCTCACAAT 644
Db 101 LeuGluAsnPheProIleGlyHsIleuLysThrLeuLysGluLeuAsnValAlaHsIleu 120
QY 645 CTATATCAATCTTCAAAATTAAGTGAATTTTCTTAATCTGACCAATCTAGAGCACTTG 704
Db 121 LeuIleGlnSerPheHsIleuProGluTyrPheSerAsnLeuThrAsnLeuGluHsIleu 140
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Db 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHsIleu 160
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QY 825 GGTCGATTTAAAGAAATTTGGCTTCAATAGCTGATCTTAAGAAATTAATTTGATAGTTA 884
Db 181 GlyAlaPheHsIleuIleArgLeuHsIlySleuThrLeuArgAsnAsnPheAspSerLeu 200
QY 885 AATGTAATGAACCTGTATTCAGGCTGCGCTGTTTGAAGTCCATCGTTGGTCTG 944
Db 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHsIleArgLeuValLeu 220
QY 945 GGAAGATTTGAAGAAAGAACTTGAAAGAACTTTGACAAATCTGCTTGAAGGCGCTG 1004
Db 221 GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 240

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 QY 1065 ATTGACTTATTTAATGTTTGAACAATGTTTCTTCATTTTCCGTGAGTGTGACTATT 1124
 Db 261 IleAspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
 QY 1125 GAAAGGTAAAGACTTTCTTAAATTTGGATGGACATTTAGAAATTAAGTTAACTGT 1184
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 QY 1185 AAATTTGACAGTTTCCACATGTAAGAACTCAATCTCTCAAAAGGCTTACTTCACTTCC 1244
 Db 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 QY 1245 AACAAAGTGGAAATGCTTTTTCAGAAAGTTGATTCACAAAGCTTGAGTTCTAGATCTC 1304
 Db 321 AsnLysGlyGlnAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
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 Db 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
 QY 1365 CTAAAGATTTAGATCTGAGCTTCAATGAGTGTGTTATTAACATGAGTTCAAACTTGGGC 1424
 Db 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
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 QY 1485 TCGATATTCCTATACCTCAAGAACTCATTTACCTTGAACATTTCTCATCTCACACAGA 1544
 Db 401 SerValPheLeuSerLeuAsnGlnLeuIleTyrLeuAspIleSerIleThrIleSerIle 420
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 Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
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 QY 1725 AGTCTCAGACTAATAATATGAGCCACAACAATCTTTTCATTTGATGATCGTTCTTAT 1784
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 QY 1845 AAAAGAGAACACAGCAATTTTCCAGATGACTACTTCTTAAATCTTAACTCAAGAAATGAC 1904
 Db 521 LysGlnGluLeuGlnIleAsnPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 QY 1905 TTGCTTGTATCTTGAACACCAAGTTTCTGCAATGATCAAGACCAAGGACAGCTC 1964
 Db 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 560
 QY 1965 TTGCTGAAAGTTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGAGGACTGTG 2024
 Db 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
 QY 2025 CTGAGTTTGATATCACTGTCAAGATGAATAAGCAATCATTTGGTGTGCTGCTCACT 2084
 Db 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
 QY 2085 GTGCTTGATATCTGTTGTAGCAGTTCTGCTATAAGTTCTATTTTCACCTGATGCTT 2144

Db 601 ValLeuValIleSerValValAlaValLeuValIleTyrLysPheTyrPheHisLeuMetLeu 620
 QY 2145 CTGCTGCTGCTGCAATAAGATGTGTAGAGGTGAAGAAATCAATCAATGCCCTTTGATCTAC 2204
 Db 621 LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 640
 QY 2205 TCAGGCAGAGATGAGACTGGGTGAAGATGAGCTGTAAAGAAATTTAGAAAGGAGGTG 2264
 Db 641 SerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGluVal 660
 QY 2265 CCTGCATTTCAAGCTGTGCTTCACTACAGAGACTTTATTTCCGTGTCATGCTGCC 2324
 Db 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaIle 680
 QY 2325 AACATATCCATGAAGTTTCCATAAAGCCCAAGAGTATGTGTGGTGTCCAGCAC 2384
 Db 681 AsnIleIleHisGluGlyPheHisLysSerArgLysValIleValValValSerGlnHis 700
 QY 2385 TTCATCCAGAGCCGTGTGTATCTTGAATATGATGATGCTGAGACTGTGAGTTCG 2444
 Db 701 PheIleGlnSerArgTrpCysIlePheGluTyrGluIleAlaGlnThrTrpGlnPheLeu 720
 QY 2445 AGCAGTGTGCTGTATCATCTTCAATGCTTGTGTCAGAGGTGAGAGACCTGTCAAG 2504
 Db 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLysArg 740
 QY 2505 CACGAGGTGAGCTGTACCGCTTCTCAGACAGAAACATTAACCTGGAGTGGAGACACT 2564
 Db 741 GlnGlnValGluLeuTyrGlnLeuLeuSerArgAsnThrTyrLeuGluTyrTrpGluAspSer 760
 QY 2565 GTCCTGGGGCGGACATCTTCTGAGACGACTCAGAAAAGCCTGTGATGTGTAATCA 2624
 Db 761 ValLeuGlyArgHisIlePheTrpArgGlnArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
 QY 2625 TGGAAATCCAGAAAGAACAGTGGGTACAGATGCAATTTGCAGGAGCAACATCTATC 2681
 Db 781 TrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 799

 RESULT 3
 US-10-128-166-7
 ; Sequence 7, Application US/10128166
 ; Publication No. US20030077279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ARDITI, MOSHE
 ; APPLICANT: RAJAVASHISTH, TRIPATHI
 ; APPLICANT: SHAH, PREDIMAN K.
 ; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
 ; FILE REFERENCE: 81476-0255398
 ; CURRENT APPLICATION NUMBER: US/10/128,166
 ; CURRENT FILING DATE: 2002-04-23
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 799
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; US-10-128-166-7

 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 4141.00 Matches: 799
 Percent Similarity: 100.008
 Best Local Similarity: 100.008
 Query Match: 61.59% Mismatches: 0
 DB: 14 Gaps: 0

 US-09-396-985B-3 (1-3811) x US-10-128-166-7 (1-799)
 QY 285 ATGAGCTGAATTTTCAAAATCCCGACACCTCCCTTTCACAAAGAACTGGAC 344
 Db 1 MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20

QY 345 CTGAGCTTTAATCCCTGAGGCAATTTAGGCACTATAGCTTCTCAGTTTCCAGAACTG 404
 DB 21 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
 QY 405 CAGGTGTGGAATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATATCAGAGC 464
 DB 41 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
 QY 465 CTAAAGCCACTCTTACCTTAATATTGACAGAAACCCCATCCAGATTTAGCCCTGGGA 524
 DB 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
 QY 525 GCCCTTCTGGACATATGAGTTTACAGAGCTGGGTGGTGGAGCAAACTGACATCT 584
 DB 81 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 100
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAATTTATGTGGCTCAGCAAT 644
 DB 101 LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
 QY 645 CTATTCGAATTTCAATTAATCTGAGTATTTTCTAATCTGACCAATCTTGAGCACTTG 704
 DB 121 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 140
 QY 705 GACCTTCCAGCAACAAGATTCAAGTATTTATGACAGACTGGGGTTCTACATCAA 764
 DB 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuAspValLeuHisGln 160
 QY 765 ATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTTATGAATTTATTCACAA 824
 DB 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
 QY 825 GGTGCATTTTAAAGAAATTTAGGCTTCATAGCTGACTTGAAGAAATTTATTTGATAGTTTA 884
 DB 181 GlyValaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
 QY 885 AATGTATATGAAACTTTGATTTCAAGGTCTGGCTGTTTAGAAGTCCACCTGTGGTCTG 944
 DB 201 AsnValaLeuLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspLeuValLeu 220
 QY 945 GGAAGATTTTGAAGATGAAGAACTTGAAGAAATTTGAACAATCTGCTAGAGAGCTG 1004
 DB 221 GlyIuIuPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 240
 QY 1005 TGCATTTTGAACATTTGAAGAAATTCGATTAGCATTTAGACTAATCTCGATGATATT 1064
 DB 241 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 260
 QY 1065 ATTGACTTATTTATTTGTTGGAACAATGTTTCTTCAATTTCCCGGTGAGGTGATCTATT 1124
 DB 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
 QY 1125 GAAAGGTTAAAGAATTTTCTTATTAATTTCCGATGGCAACATTTAGATTAAGTACTGT 1184
 DB 281 GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGluLeuValAsnCys 300
 QY 1185 AAATTTGACAGTTTCCCACTGAAACTCAATCTCTCAAAAGCTTACTTTCACTTCC 1244
 DB 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 QY 1245 AACCAAGTGGGAGATGCTTTTTCAGAGTTGATATACCAAGCTTGAAGTTTCTGATCTC 1304
 DB 321 AsnLysGlyGlyAsnAlaPheSerGluValaAspLeuProSerLeuGluPheLeuAspLeu 340
 QY 1305 AGTGAATGAGCTTGAAGTTTCAAAAGTGTGCTCTCAAAAGTATTTGGGCAACACGAGC 1364
 DB 341 SerThrAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
 QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGCTGTATTAACATGAGTCAAACTTCTTGAGC 1424
 DB 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380

QY 1425 TTGAACAATGAAACATCTGATTTTCCAGCATTTCCAAATTTGAAACAATAGTAGTTT 1484
 DB 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
 QY 1485 TCAATATCTTATCACTCAGAAAATCTCATTTTACCTTTGACATTTTCTCATCTCACACAGA 1544
 DB 401 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisArg 420
 QY 1545 GTTGCTTTTGAATGGCAATCTTCAATGGCTTGTCCAGTCCGAAAGCTTGAAGAAATGGCTGGC 1604
 DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
 QY 1605 AATTTCTTCCAGAAAATCTCTTCCAGATATTTTCAAGAGCTGAGAAAATTTGACCTTC 1664
 DB 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuAsnLeuThrPhe 460
 QY 1665 CTGACCTCTCTCAGTGTCAACTGAGACAGTGTGTCCAAACAGATTTAACTCATCTCC 1724
 DB 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGCTTCAGGTACTTAAATATAGCCCAACAACATCTCTTTCATTTGATAGTTTCTTAT 1784
 DB 481 SerLeuGlnValLeuLeuMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
 QY 1785 AAGTGTGAACTCCCTCAGTCTTGTGATTAAGTCTCAATGACATTAATGACTTCCAAA 1844
 DB 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
 QY 1845 AAAACAGAACTACAGCAATTTTCCAAAGTACTAGCTTTCTTAAATCTTACTCAGAAATGAC 1904
 DB 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 QY 1905 TTGCTGTGATCTTGTGAACACCAAGTTCCTGCAATGATTCAGAGCAACAGAGCACTC 1964
 DB 541 PheAlaCysThrCysGluHisGlnSerPheLeuGlnIleThrLysAspGlnAspGlnLeu 560
 QY 1965 TTGTTGGAATTTGAACGAATGGAATGGAATGCAACCTTCAGATTAAGCGGCACTGCTGTG 2024
 DB 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnLysMetProVal 580
 QY 2025 CTGAGTTTGAATATCACTCTGTCAGATGAATTAAGCAATCTTGCTGTGCTGCTCAGT 2084
 DB 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLeuSer 600
 QY 2085 GTGCTGTGATATCTGTGTGAGCAAGTTCGTGTCATTAAGTTCATTTTCACTGATGCTT 2144
 DB 601 ValLeuValValSerValValaValaValaValaLysPheTyrPheHisLeuMetLeu 620
 QY 2145 CTGCTGGCTGCAATTAAGTATGTAAGGTGAAGAACTCATATGCTTGTGTTATGATAC 2204
 DB 621 LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 640
 QY 2205 TCAAGCAGAGTGAAGCATGGGGTAAAGATGAGCTAGTAAGATTAAGATTTGAAGAAAGGGTG 2264
 DB 641 SerSerGlnAspGluAspIlePValArgAsnGluLeuValLysAsnLeuGluGluGlyVal 660
 QY 2265 CTTCCATTTAGCTGTGCTTCACTACAGAGACTTATTTCCCGGTGGGCAATGCTGCC 2324
 DB 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 680
 QY 2325 AACATCATCATGAAGTTTCCATTAAGCCGAAAGGATGATTTGTGGGTGCTCCACAGAC 2384
 DB 681 AsnIleIleHisGluGluPheHisLysSerAspLysValIleValaValaValaSerGlnHis 700
 QY 2385 TTGATCCAGACCGCTGTGTATCTTTGAATAGATTTGCTCAGACTGGAGTTTCTG 2444
 DB 701 PheIleGlnSerArgTyrCysIlePheGluTyrGluIleAlaGlnThrTyrGlnPheLeu 720
 QY 2445 AGCAGTGTGCTGTATCATCTTCAATTTGCTGCAAGAGGTGAGAAAGACCTGCTCAGG 2504
 DB 721 SerSerArgAlaGlyIleIlePheIleValaLeuGlnLysValaGluLysThrLeuLeuArg 740
 QY 2505 CACGAGGTGAGCTGATACGCTTCTCAGAGAGAACTTAACCTGGAGTGGAGAGACT 2564

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Db      741 GlnGlnValGluLeuVrArGLeuLeuSerArGsnHrYrLeuGluTrpGluAaspSer 760
QY      2565 GTCTGGGGGGGGCACTCTTGGAGACGACTCAAAAAGCCCTGCTGATGTGTAATCA 2624
Db      761 ValLeuGluYrGHisIlePheTrpArGArGLeuArGlysAlaLeuAaspGlyLysSer 780
QY      2625 TGGAAATCCAGAAAGACAGTGGGTACAGATGCAATTGGCAGAGCAACACTATC 2681
Db      781 TrpAsnProGluGlyInrValGlyTrpGlyCyAsnTrpGlnGluAlaInrSerIle 799

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RESULT 4

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US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732,563
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

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Alignment Scores:

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Pred. No.: 0 Length: 799
Score: 4141.00 Matches: 799
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.59% Indels: 0
Gaps: 0

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US-09-396-985B-3 (1-3811) X US-10-732-563-8 (1-799)

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QY      285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACCAAGAACCTGAGC 344
Db      1 MetGluLeuAsnPheTrpYrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
QY      345 CTGAGCTTTAATCCCTCGAGGCAATTTAGGCGACTATAGCTTTCTTCAAGTTTCCCAAGCTG 404
Db      21 LeuSerPheAsnProLeuArGHisIleuGlySerTyRserPhePheSerPheProGluLeu 40
QY      405 CAGGTGCTGATTTATCCAGGTGTAATCCAGACAAATTGAAAGTGGGGCATATCAGAGC 464
Db      41 GlnValLeuAaspLeuSerArGysGluIleGlnThrIleGluAaspGlyAlaTyRGlInSer 60
QY      465 CTAAAGCACTCTCTACCTTAATAATTGACAGAAACCCCATCCAGAGTTTACCCCTGGGA 524
Db      61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY      525 GCCTTTTCTGACATATCAAGTTTACAGAAAGCTGGTGGTGGAGACAAATCTTAGCATCT 584
Db      81 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 100
QY      585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAAATGTGGCTCACAAAT 644
Db      101 LeuGluAsnPheProIleGlyHisIleuLysThrLeuLysGluLeuAsnValAlaHisIAsn 120
QY      645 CTATTCGAATCTTTCAAATTAAGTGAATATTTCTAATCTGACCAATCTAGACACTTG 704
Db      121 LeuIleGlnSerPheLysLeuProGluTrpPheSerAsnLeuThrAsnLeuGluHisIleu 140
QY      705 GACCTTTTCAGACAAACAGATTCAAAATTTTATTGACAGACCTTGCGGGTTCTACATCAA 764
Db      141 AspLeuSerSerAsnLysIleGlnSerIleTyRcysThrAspLeuArGValLeuHisGln 160

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QY      765 ATGCCCCCTACTCAATCTCTTTAGACCTGTGCCCTGAACCTTATGAACTTATCCAGCA 824
Db      161 MetProLeuLeuAsnLeuSerLeuAaspLeuSerLeuAsnProMetAsnHelleGlnPro 180
QY      825 GGTGCAATTTAAAGAAATTAGGCTTCAATTAAGCTGACTTTTAAAGAAATATTTGATGTTA 884
Db      181 GlyAlaPheLysGluIleArGLeuHisIlySerLeuThrLeuArGAsnAsnPheAaspSerLeu 200
QY      885 AATGTAATGAAAATCTGTATTTCAAGGTCGGCGGTTTGAAGTCCATGTTGGTTGCTG 944
Db      201 AsnValMetLysThrCySileGlnGlyLeuAlaGlyLeuGluValHisIAsrGLeuValLeu 220
QY      945 GAGAAATTTTGAATGAGAAACCTTGAGAAAGTTTGAACAAATCTGCTCTAGAGGCTTG 1004
Db      221 GlyGluPheArGAsnGluGlyAsnLeuGluLysPheAaspLysSerAlaLeuGluGlyLeu 240
QY      1005 TGCATTTTGAACATTGAGAAATTCGATTAAGCATCTTGAAGTACTTACCTCGATGATATT 1064
Db      241 CyAsnLeuThrIleGluGluPheArGLeuAlaTyRLeuAaspTyRtyrLeuAaspArIle 260
QY      1065 ATTGACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGGGTGAGTGAATTT 1124
Db      261 IleAaspLeuPheAsnCySLeuThrAsnValSerSerPheSerLeuValSerValInrIle 280
QY      1125 GAAAGGTAAAGACTTTTCTTATTAATTCGATGCGAACATTTAGAAATTAAGTTAACTGT 1184
Db      281 GluArGValLysAaspPheSerTyRAsnPheGlyTrpGlnHisIleuGluLeuValAsnCyS 300
QY      1185 AAATTTGAGACGTTTCCACATTTGAAATCTCAAAATCTTCAAAAGCTTACTTCACTTCC 1244
Db      301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArGLeuThrPheThrSer 320
QY      1245 AACAAAGGTGGGAATGCTTTTTCAGAAAGTTGATCTCAACAGCTTGAGTTTCTAGATCTC 1304
Db      321 AsnLysGlyGlyAsnHisAaspSerGluValAaspLeuProSerLeuGluPheLeuAaspLeu 340
QY      1305 AGTAGAAATGGCTGAGTTTCAAGAGGTGCTGTTCTCAAAAGTAAATTTGGGACAAACAGC 1364
Db      341 SerThrAsnGlyLeuSerPheLysGlyCySArGSerGlnSerAaspPheGlyThrThrSer 360
QY      1365 CTAAAGTATTTAGATCTGAGCTTCAATGCTGTTATTTACATGATGTTCAAACTTCTTGGGC 1424
Db      361 LeuLysTyRLeuAaspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
QY      1425 TTGAACAATTAAGCAATCTCGAATTTCCAGCAATTTCAATTTGAAACAAATGAGTGAAGTT 1484
Db      381 LeuGluGlnLeuGluHisIleuAaspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
QY      1485 TCAGTATTCCTATCACTCAGAAACCTCAATTTACCTTGACATTTCTGATACTCACACAGA 1544
Db      401 SerValPheLeuSerLeuAsnGluLeuIleTyRLeuAaspIleSerHisIleThrHisIleTrpArG 420
QY      1545 GTTGCTTTCAATGCAATCTTCAATGCTGTGTCAGATCTGGAAGTCTTGAATAATGCTGGC 1604
Db      421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
QY      1605 AATTTCTTCCAGGAAACCTTCTTCCAGATATCTTCAAGAGCTGGAAGAACTTGACCTTC 1664
Db      441 AsnSerPheGlnGluAsnPheLeuProAaspIlePheThrGluLeuArGAsnLeuThrPhe 460
QY      1665 CTGAGACTCTCTCAGTGTCAACTGAGACAGTTGTCTTCAACAGACATTTAACTCACTCTCC 1724
Db      461 LeuAaspLeuSerGlnCySglnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
QY      1725 AGTCTTCAAGTAAATATAGCCCAACAACTTCTTTTCATTTGATGATACGTTTCTTAT 1784
Db      481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAaspTrpPheProTyR 500
QY      1785 AAGTGTCTGAACCTCCCTCCAGGTTCTTGGATTAAGTCTCAATCAATTAAGACTTCCAAA 1844
Db      501 LysCySLeuAsnSerLeuGlnValLeuAaspTyRSerLeuAsnHisIleMetThrSerLys 520
QY      1845 AAACAGAACTACAGACATTTTCAAGTAGTCTAGCTTCTTAAATCTTACTCAGAAATGAC 1904

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Db	521	LySGInGInLuleGInLInHiePheProSeSerLeuAlaPheLeuAsnLeuThrGlnMnAsp	540
Qy	1905	TTTGCTTGTACTGTGAAcACCAAGATTTCCTGCAATGATCAAGACAGGACGCTC	1964
Db	541	PheAlaCyStrnCysGluNHISolInSerPheLeuGInTrpLleYAspGlnAArgGInLeu	560
Qy	1965	TTGGTGGAAgTTGAAcGAATGGAAATGTGCACACCTTCAGATAGACAGGCAATGCCCTGTG	2024
Db	561	LeuValGInuValGInuArgMetGluCysAlaThrProSerAspYSGInGlyMetProVal	580
Qy	2025	CTGAGTTTGAATATACCGGTGCAGATGAATTAAGACATCATTTGGTGTGGTCCCTCAgT	2084
Db	561	LeuSerLysuAsnLleThrCysGlnMetAsnYStrNHleIGlyValSerValLeuSer	600
Qy	2085	GTGCTTGTAGATATCTGTGTAGACAGTTCGGCTTAAGTTCATTTTCACCTGATGCTT	2144
Db	601	ValLeuValValSerValValAlaValLeuValTrpLysPheTrYPheHISleuMetLeu	620
Qy	2145	CTTGCTGGCTGCATAAAGATAGTGAAGGTGAAAATCATCTATGATGCTTGTGTATCTAC	2204
Db	621	LeuAlaGlyCysLleYStrGlyArgGlyuAsnLleYTrpAspAlaPheValIleYTr	640
Qy	2205	TCAAGCCAGATGAGGAGCTGGGTAGAGATAGCTAGTAAAGAAATTTGAAAGAGGGGTG	2264
Db	641	SerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGlnGluVal	660
Qy	2265	CCTCCATTTAGACTGTGCCTTCACACTACAGAGACTTATTCGCCGGGTGGCCATTGCTGCC	2324
Db	661	ProProPheGlnPheCysLeuNHIStryTrpAspPheIleProGlyValAlaIleAla	680
Qy	2325	AACATCATTCATGAAGGTTTCATTAAGAACCGGAAGGTGATTTGTTGTGTGTCCAGCAC	2384
Db	681	AsnIleIleHISGlnGluYPheHISLysSerArgLysValIleValValSerGlnHIS	700
Qy	2385	TTTCATCCAGACCCGTGGTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTTTGTG	2444
Db	701	PheIleGlnSerArgTrpCysAllePheGlnTrpGluIleAlaGlnThrTTPGlnPheLeu	720
Qy	2445	AGCAGTCCGTGTGGTATCATCTTCATTTCTCCGAGAGAGGTGGAGAAACCTGTCCAGG	2504
Db	721	SerSerArgAlaGlyLleIlePheIleValLeuGlnLysValGlnLysTrpLeuLeuArg	740
Qy	2505	CAGCAGGTGAAGCTGTACCGCTTTCAGCAGAAcATTACCTGAGGTGAGAGACAGT	2564
Db	741	GlnGlnValGluLeuTrpArgLeuLeuSerArgAsnThrTrpLeuGluTrpGlnAspSer	760
Qy	2565	GTCTGTGGGGCGGCACATCTTCTGAGAGACGACTCAGAAAAGCCCTGTGATGTGTAATCA	2624
Db	761	ValLeuGlyArgHISIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSer	780
Qy	2625	TGGAAATCCAGAGGAACAGTGGGTACAGAGAGCAATTGGCAGGAAGCAACATCTATC	2681
Db	781	TrpAsnProGlnGlyThrValGlyTrpTrpLysAsnTrpGlnGlnAlaThrSerIle	799

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RESULT 5
US-10-732-796A-8
: Sequence 8, Application US/10732796A
: Publication No. US20040197865A1
GENERAL INFORMATION:
: APPLICANT: Gupta, Shalley K.
: APPLICANT: Ghosh, Tarun K.
: APPLICANT: Fink, Jason R.
: TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
: FILE REFERENCE: 58182US004
: CURRENT APPLICATION NUMBER: US/10/732,796A
: CURRENT FILING DATE: 2003-12-10
: NUMBER OF SEQ. ID NOS: 23
: SOFTWARE: PatentIn version 3.2
: SEQ. ID NO. 8
LENGTH: 799
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens

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US-10-732-796A-8	
Alignment Scores:	
Pred. No.:	0
Score:	4141.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	61.59%
DB:	16
US-09-396-985B-3 (1-3811) x US-10-732-796A-8 (1-799)	
Length:	799
Matches:	799
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

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Db	1	MetGluLeuAnpHeuPheYrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp	20
QY	345	CTGAGCTTAAATCCCGTAGGCACTTTAGGCACTATAGCTTCTTCAGTTTCCAGAACTG	404
Db	21	LeuSerPheAnpProLeuArgHisLeuLysIleYrSerPhePheSerPheProGluLeu	40
QY	405	CAGGTGCTGAATTTATCCAGGTGTGAATTCAGACAAATTGAAGATGGGGCATATCAAGC	464
Db	41	GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGluAspGlyAlaIleYrGlnSer	60
QY	465	CTAAGGCCACCTCTCAACCTTAATATATGACAGAAACCCCATCCAGATTACCCCGGCA	524
Db	61	LeuSerHisIleLeuSerThrLeuLileuThrGlyAsnProIleGlnSerLeuAlaGluGly	80
QY	525	GCCCTTTTCTGACATATCAAGTTTACAGAAAGCTGGGTGGCTGTGGAGACAAATCTAGCATCT	584
Db	81	AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer	100
QY	585	CTAGAGAACTTCCCACATTGGACATCTCAAACTTTGAAAGAACTTAATGTGGCTCACAAT	644
Db	101	LeuGluAnpHeProIleGlyHisIleLeuYrThrLeuLysGluLeuAsnValAlaHisAn	120
QY	645	CTTATCCCAACTTTCAAAATTAACAGATTTTCTATCTGACCAACTGTAGAGCACTTG	704
Db	121	LeuIleGlnSerPheLysLeuProGluYrPheSerAnpLeuThrAsnLeuGlnHisLeu	140
QY	705	GACCTTTCCACACAAGAACTTCAAGATTTATATGACAAGACTTCGGGGTTTTCATCAAA	764
Db	141	AspLeuSerSerAnpLysIleGlnSerIleYrCysThrAspLeuArgValLeuHisGln	160
QY	765	ATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAAACCTATGAACTTTATCCACCA	824
Db	161	MetProLeuAnpAnpLeuSerLeuAspSerLeuAnpProMetAnpPheIleGlnPro	180
QY	825	GGTGCAATTTAAGAAATTTAGGCTTCATAGCTGACTTTAAGAAATATTTTGATAGTTTA	884
Db	181	GlyAlaPheLysGluIleArgLeuHisIleYsLeuThrLeuAlaGlnAnpAnpPheAspSerLeu	200
QY	885	AAATTAATGAAAACTTGATATCAAGCTCTGGCTGGTTTGAAGATCCATCGTTTGGTTCTG	944
Db	201	AsnAlaMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu	220
QY	945	GGAATATTTGAATGAAGAACTTGGGAAAGTTTGAACAATCTGCTAGAGGGCTGTG	1004
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QY	1005	TGCAATTTGACCATGGAAGAAATTCGATTTAGCATACTTGACTATCACTACCTCGATGATAT	1066
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QY	1065	ATTGACTTATTTAATTTGTTGACAAATGTTTCTTCATTTTCCCTGGTGAAGTGTGACTAT	1122
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QY	1125	GAAAGGGTAAAGACTTTTCTTATATATTTGGATGGCAACTTTAAGATTTAGTTAACTGT	1186
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RESULT 6
US-10-038-854-135
Sequence 135, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vermet, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shinkets, Richard A
APPLICANT: Tobernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoli, Baha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Caeman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Mallet, Isabelle
APPLICANT: Macdougall, John R
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038, 854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258, 928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259, 415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259, 785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269, 814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279, 832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279, 833


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; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 135
; LENGTH: 661
; TYPE: PRF
; ORGANISM: Mus musculus
; US-10-038-854-135

Alignment Scores:
Pred. No.: 1,49e-53      Length: 661
Score: 656.50           Matches: 199
Percent Similarity: 45.31%      Conservative: 115
Best Local Similarity: 28.72%    Mismatches: 290
Query Match: 9.76%           Indels: 89
DB: 15                     Gaps: 17

US-09-396-985B-3 (1-3811) x US-10-038-854-135 (1-661)

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QY 291 CTGAATTTCTCAAAATCCCGACCACTCCCTTCTCAACCAAGACTGAGCTGAGC 350
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QY 351 TTTAATCCCTGAGGACTTTGAGCACTATAGCTTCTTCACTTCCAGAACTGCAAGTG 410
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QY 411 CTGATTTATTCAGGTGGAATCCAGACATTCGAATGAGGAGATTCAGAGCTTAAGC 470
DB 82 LeuAspLeuThrAargCysGlnIleTyrTrpIleHisgluAserThrPheGlnSerGlnHis 101
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QY 531 TCTGCACTATCAAGTTTACAGAGCTGCTGCTGAGACAAATCTAGCATCTCTAGAG 590
DB 122 SerIlyProLysAlaLeuLysHisIleuPhePheIleGlnThrGlyIleSerSerIleAsp 141
QY 591 AACTCCCATGGACATCTCAAAACCTTGAAGAATTATGAGGCTCAACAATCTATTC 650
DB 142 PheIleProLeuHisAsnGlnLysThrLeuGlnSerLeuTyrLeuGlySerAsnHisIle 161
QY 651 CAATCTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGACTGAGCTT 710
DB 162 SerSerIleLysLeuProLysGlyPheProThr---GluLysLeuLysValLeuAspPhe 180
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RESULT 7
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tcherenev, Vellizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
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APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Perenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10

QY PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-107
Alignment Scores:
Pred. No.: 1,49e-53 Length: 661
Score: 656.50 Matches: 199
Percent Similarity: 45.31% Conservative: 115
Best Local Similarity: 28.72% Mismatches: 290
Query Match: 9.76% Indels: 89
DB: 15 Gaps: 17
US-09-396-985b-3 (1-3811) x US-10-037-417-107 (1-661)
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Db      491 SerLeuGlnThrLeuGlnArgLeuGlnIleLeuValLeuSerPheCysAspLeuSerSer 510
Qy      1695 TTGCTCCACACAGATTAACTCACTCTCCAGTTCTCAGTACGATCAATATGACCAAC 1754
Db      511 IleAspGlnHisAlaPheThrSerLeuLysMetLeuAsnHisValAspLeuSerHisAsn 530
Qy      1755 AACTTCTTTTCAATGATGATCTTCTTATTAAGTGTGAAGCTCCCTCCAG-----GTT 1808
Db      531 Arg-----LeuThrSerSerSerIleGluAlaLeuSerHisLeuLysGlyIleTyr 547
Qy      1809 CTTGATTACAGCTCTCAATCACAATATGATGATCCAAAAACAGAACTACAGCACTTTTCCA 1868
Db      548 LeuAsnLeuHisAspAsnHisAlaLeuSerIleLeu-----LeuPro 560
Qy      1869 AGTAGCTAGCTTTCTTA-----AATCTTACTCAGAAATGACTTTGCT 1910
Db      561 SerLeuLeuProIleLeuSerGlnGlnArgThrIleAsnLeuArgGlnAsnProLeuAsp 580
Qy      1911 TGTACTGTGAACACAGAGTTTCTCTCAATGATGATCAAGACAGAGCACTTGTGTG 1970

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Db      581 CysThrCysSerAsnIleTyrPheLeuGluTyrTyrLysGluAsnMetGlnLysLeuGlu 600
Qy      1971 GAAGTTAACGAATGGAATGTGCAACACTTTCAGATTAAGAGGAGCATGCTGTGCTGAGT 2030
Db      601 AspThrGlnAspThrLeuLysGlnAsnProProLeuLeuArgGlyValAlaGlyLeuSerAsp 620
Qy      2031 TTGAATATCACCTGTGAGATGAATTAAGACATCATGTTGTTGTGCTGCTCACTGTTCTT 2090
Db      621 ValThrLeuSerCysSerMetAlaAlaValGlyIlePhePheLeuIleValPheLeuLeu 640
Qy      2091 GTAGTATCTGTTGATGACATTTGCTGTGCTTAATGTTCTAT 2129
Db      641 ValPheAlaIleLeuLeuIlePheAlaValIleTyrPhe 653

RESULT 8
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalley, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: CI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Alignment Scores:
Pred. No.: 5,51e-50 Length: 661
Score: 619.50 Matches: 200
Percent Similarity: 45.45% Conservative: 110
Best Local Similarity: 29.33% Mismatches: 277
Query Match: 9.21% Indels: 95
DB: 13 Gaps: 24

US-09-396-985B-3 (1-3811) x US-10-114-893-10 (1-661)
Qy      222 TTGCTTCTGCTAAATGCGCCGCTTTATACG-----GAGGTG 260
Db      12 ValLeuPheSerLysIleGlyCysLysValIleThrSerTyrAspGlnMetCysIleGluLys 31
Qy      261 GTTCTTAATTTTCTTATCATGATGATGAGATTAATTTTCAACAAATCCCGCAACCTC 320
Db      32 GluAlaAsnLysThrTyrAsnLysGluAsnLeuGlyLeuSerGluIleProAspThrLeu 51
Qy      321 CCCTTTCACCAAGAACTGACCTGAGCTTTAATCCCTGAGGCACTTATGAGCACTAT 380
Db      52 ProAsnThrThrGlnPheLeuGluPheSerPheAsnPheLeuProThrIleHisAsnArg 71
Qy      381 AGCTTCTTCAGTTTCCAGAACTGACAGTGTGAGATTATTCAGGTGTAATCCAGACA 440
Db      72 ThrPheSerArgLeuMetAsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTyr 91
Qy      441 ATTGAAGATGGGACATATCAGACCTTAAGCACTCTTAACTTAAATATGACAGAAAC 500

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Db      92  ILeuIsgluAerThrPheGlnSerHisIleGlnLeuSerThrLeuValLeuThrGlyAsn 111
Qy      501  CCCATCCAGAGTTTAAAGCCCTGGAGCCCTTTCTGACATATCAAACTTTACAGAACTGTG 560
Db      112  ProLeuIlePheMetAlaGluThrSerLeuAsnGlyProIysSerLeuValLeuPhe 131
Qy      561  GCTTGTGAGAACAAATGACATCTCTAGAGAACTTCCCAATGGACATCTCAAAACTTTG 620
Db      132  LeuIleGlnThrGlyIleSerAsnLeuGluPheIleProValHisAsnLeuGluAsnLeu 151
Qy      621  AAGAATTAATGTGGCTCACAATCTTATCCAAATCTTTCAAAATTAAGCTGAGTATTTTCT 680
Db      152  GluSerLeuTyrlLeuGlySerAsnHisIleSerSerIleIysPheProIysAspPhePro 171
Qy      681  AATGTACCAATCTAGACATTTGGACCTTTCCAGCAACAAGATTCAAAGATTATATTC 740
Db      172  ---AlaArgAsnLeuValLeuAspPheGlnAsnAlaIleHisTyrlIleSerArg 190
Qy      741  ACAGACTTGGGGTTCTACATCAATGCCCCCTACTCAATCTCTTTAGACCTGTCCCTG 800
Db      191  GluAspMetArgSerLeuGln-----AlaIleAsnLeuSerLeuAsnPheAsnGly 208
Qy      801  AACCTATGAATTTATTCACAACAGGTGATTTAAAGAAATTAAGCTTCATTAAGCTGACT 860
Db      209  AsnAsnValIysGlyIleGluLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
Qy      861  TTAAGAAATATTTTGATAGTTTAAATGTAATGAAGAACTTGATTCAAAGCTGGCTGCT 920
Db      228  -----AsnPheGlyIleThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsn 244
Qy      921  TTAGAAGTCCATCGTTTGGTTCTGGAGAAATTTGAATGAAGAACTTGAAGAACTT 980
Db      245  SerThrThrGlnSerLeuThrLeuGlyIlePheGluAspIleAspArg---GluAspIle 263
Qy      981  GACAAATGCTGCTTAGAGGGCTGTGCATTTGACATTTGAAGAAATTCGATTCATAC 1040
Db      264  SerSerAlaMetLeuValLeuGlyLeuGlySerValGlnSerLeuAsnLeuGln--- 282
Qy      1041  TTAGACTACTACCTCGATGATATTAATGAC---TTATTAATGTGGTGAACAAGTTTCT 1097
Db      283  ---GluHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGln 301
Qy      1098  TCAATTTCCCTGATGATGTGACTATTTGAAGGGTAAAGAACTTTCTTATATATTTGCGA 1157
Db      302  GluLeuAspLeuThrAlaThrHisIleuValGlyLeuProSer-----Gly 316
Qy      1158  TGGCAACATTTAGATTAGTTAAC----- 1181
Db      317  MetIysGlyLeuAsnLeuLeuValLeuValLeuSerValAsnHisPheAspGlnLeu 336
Qy      1182  TGTAAATTT-----GACAGTTTCCCAATTTG-----AAATC 1214
Db      337  CysGlnIleSerAlaAlaAsnPheProSerLeuThrHisIleuTyrlLeuArgIleAsnVal 356
Qy      1215  AAATCTCTCAAAAGGCTTACTTCACTTCCAAAGGCTGGGAATGCTTTTCCAGAACTT 1274
Db      357  LysIleValLeuHisIleuGlyValGlyCysValLeuGlyValLeuAsn----- 371
Qy      1275  GATCTACCAAGCCTTGATTTTGAATGATTCAGTAGAAATTCGCTGAGTTTCAAGTTGC 1334
Db      372  -----LeuGlnThrLeuAspLeuSerHisAsnAspIleGluAlaSerAspArg 387
Qy      1335  TGTCTCAAGTGAATTTTGGGCAACAACAGCCTTAAGTATTGAATCTGAGCTCAATGCT 1394
Db      388  CysSerLeuGlnLeuValAsnLeuSerHisIleuGlnThrLeuAsnLeuSerHisAsnGlu 407
Qy      1395  GTTATTAACATGAGTTCAAC---TTCTGGCTTGAACAACATGAACATCTGAGTTTC 1451
Db      408  ProLeuGlyLeuGlnSerGlnAlaPheValGlyCysProGlnLeuGlnLeuLeuAspLeu 427
Qy      1452  CAG-----CATTCATTTGAACAACATGAGTGAAGTTTCA-----GATATC 1493
Db      428  AlaPheThrArgLeuHisIleAsnAlaProGln---SerProPheGlnAsnLeuHisPhe 446

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Qy      1494  CTATCACTCAAGAAACCTCATTTTAC-----CTTGACATTTTGCATCTACACAGAGTT 1547
Db      447  LeuGlnValLeuAsnLeuThrTyrlCysPheLeuAspThrSerAsnGlnHis----- 463
Qy      1548  GCTTTCAATGGCATCTTCAATGGCTTTGCCAGTCTCGAAAGCTTGAAGATGGCTGGCAAT 1607
Db      464  -----LeuValIleGlyLeuProValIleuArgHisIleuAsnLeuValGlyAsn 479
Qy      1608  TCTTTCCAGGAAACCTCTCT-----CCAGATATCTTCACAGAGCTGAGAACTTGACC 1661
Db      480  HisPheGlnAspGlyThrIleThrIleTyrlAsnLeuLeuGlnThrValGlySerLeuGlu 499
Qy      1662  TTCCTGACCTCTCTGACGTGCAATGTCAGACAGACAGTGTCTCCAAACGATTTAAGCTTC 1721
Db      500  ValLeuIleLeuSerCysGlyLeuLeuSerIleAspGlnAlaPheHisSerLeu 519
Qy      1722  TCCAGTCTTCAGGTAATTAATATATAGCCACACAACTTCTTT-----TCATTGATACG 1775
Db      520  GlyIleMetSerHisValAspLeuSerHisAsnSerIleThrCysAspSerIleAspSer 539
Qy      1776  TTTCTTTAT-----AAGTGTGAACCTCCCTCCAGTCTTTGAT 1814
Db      540  LeuSerHisIleuValGlyIleTyrlLeuAsnLeuAlaAlaAsnSerIleAsnIleIleSer 559
Qy      1815  TACAGTCTCAATGACATTAATGACTTCCAAAAAACAGAACTACAGCATTTTCCAGTAT 1874
Db      560  ProArgLeuLeuProIleLeu-----SerGln 568
Qy      1875  CTAGCTTTCTTAATCTTACTCAGAAATGACTTTGCTTGTAGTGAACACAGAGTTTC 1934
Db      569  GlnSerThrIleAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPhe 588
Qy      1935  CTGCAATGATCAAGACACAGAGCAGCTTGTGTGGAAGTTGAACGAATGCAATGCA 1994
Db      589  LeuThrTrpTyrlArgGluAsnLeuHisIleValLeuGlnGlySerGlnGluThrThrCysAla 608
Qy      1995  ACACCTTCAGATTAAGCAGGGCATGCGCTGCTGAGTTGAATTAACCTTGCAGATGAAT 2054
Db      609  AsnProProSerLeuArgIleValIysIleuSerAspValIysLeuSerCysGlyIle--- 627
Qy      2055  AAGACATCATGTGCTGTGCTGCTTCCAGTGTGCTGTGATATCTGTTGAGACAGTTCTG 2114
Db      628  ---ThrAlaIleGlyIlePhePheLeuIleValIlePheLeu---LeuValAlaIleLeu 645
Qy      2115  GTCTAT 2120
Db      646  LeuPhe 647

RESULT 9
US-10-038-854-134
Sequence 134, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Verneq, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shinkets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoili, Esha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Caeman, Stacie J

```



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QY 1548 GCTTCAATGACATCTCAATGGCTTGTCCAGTCTGCAAGTCTTGAAATGGCTGGCAAT 1607
Db 464 -----LeuLeuAlaGlyLeuProValLeuArgHisValLeuAlaGlyLeuAsn 479
QY 1608 TCTTCCAGGAAACCTTCCTT-----CAGATATCTTCAACAGCTGAGAACTTGACC 1661
Db 480 HisPheGlnArgGlyThrIleThrIleThrPheAsnLeuLeuGlnThrValGlySerLeuGlu 499
QY 1662 TTCTGCACTCTCTCACTGATCAATGAGACAGCTTGTCCACAGCATTTAACTCACTC 1721
Db 500 ValLeuIleLeuSerSerCysGlyLeuLeuSerIleArgGlnGlnIlePheHisSerLeu 519
QY 1722 TCCAGTCTGACGATCAATATATATAGCCACAACTTCCTT-----TCATTGATACG 1775
Db 520 GlyLeuMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSer 539
QY 1776 TTTCCTTAT-----AAGTGTCTGAATCCCTCCAGTTCTTGAT 1814
Db 540 LeuSerHisLeuGlyGlyIleTyrLeuAsnLeuAlaIleAsnSerIleAsnIleIleSer 559
QY 1815 TACAGTCTCAATCAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTACT 1874
Db 560 ProArgLeuLeuProIleLeu-----SerGln 568
QY 1875 CTAGCTTTCTTAATCTTACTCAGATGACTTGTGCTGTACTTGTGAACACAGAGTTTC 1934
Db 569 GlnSerThrIleAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPhe 588
QY 1935 CTGCAATGATCAAGACACAGGACAGCTTGTGTGAAGTTGAACAGATGATGCA 1994
Db 589 LeuThrTrpTyrGlyGlnAsnLeuHisValLeuLeuIleGlySerGlnGlnIleThrCysAla 608
QY 1995 ACACCTTCAAGTAAACAGGAGCATGCTGTGCTGAATTTGAATGACCTGTCAATGAAT 2054
Db 609 AsnProGlySerLeuArgGlyValIleLeuSerAspValIleLeuSerCysGlyIle--- 627
QY 2055 AAGCAATCAATGTGGTGTGGTGGTCTCAGTGTGCTGATGATGCTGTTGTAAGCTTCTG 2114
Db 628 ---ThrIleIleGlyIlePhePheLeuIleValIlePheLeu---LeuLeuAlaIleLeu 645
QY 2115 GTCTAT 2120
Db 646 LeuPhe 647

RESULT 10
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OR INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950, 041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-4

Alignment Scores:
Pred. No.: 2,096-48 Length: 784
Score: 603.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.98% Indels: 219
DB: 10 Gaps: 38

US-09-396-985b-3 (1-3811) x US-09-950-041-4 (1-784)
QY 306 ATCCCGACAACTCCCTCTTCAACCAAGAACTTGACCTTAATCCCTGAGG 365
Db 46 IleProSerGlyLeuThrGlnAlaValIleYSerLeuAspLeuSerAsnArgIleThr 65
QY 366 CATTTAGCAGCTATAGCTTCTTCACTTCCGAACTGAGGTGCTGATTTATCCAGG 425
Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValIleThrSer 85
QY 426 TGTGAATCCAGCAATTGAAGATGGGCAATACAGAGCTTAAGCCACTCTTACCTTA 485
Db 86 AsnGlyIleAsnThrIleGlnIleAspSerPheSerLeuGlySerLeuGlnHisLeu 105
QY 486 ATATTGACAGAAACCCCATCCAGAGTTTAAAGCCCTTGAGCTTATCAATGAT 545
Db 106 AspLeuSerGlyAsnTyrIleuSerAsnLeuSerSerTrpPheIlePProLeuSerSer 125
QY 546 TTTCAGAGCTG-----GTGCTGTGGAG 569
Db 126 LeuThrPheLeuAsnLeuLeuGlnIleAsnProTyrIleThrLeuGlnIleThrSerLeuPhe 145
QY 570 ACAATCTGACATCTGTGAGAACTCCCATGATGACATCTCAAACT----- 617
Db 146 SerHisLeuThrIleLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIle 165
QY 618 -----TTGAAGAACTTAATGTGCTCAAACTTT 647
Db 166 GlnArgIleAspPheAlaGlyLeuThrPheLeuGlnIleLeuGlnIleAspAlaSer 185
QY 648 ATCCAACTTTCAAACTTCTGAGTATTTTCAATCTGACCAATCTAAGACCTTGAGC 707
Db 186 LeuGlnSerTyrGln---ProIleSerLeuIleSerIleGlnAsnValSerHisLeuIle 204
QY 708 CTTTCCAGCAACAG-----ATTCAAAGTAT 734
Db 205 LeuHisMetCysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal 224
QY 735 TATTGACAGACTGGGGGTTTACATCAAAATGCCCTCAATCTCTTTAGACCTG 794
Db 225 GluCysLeuIleuLeuArg-----AspThr 232
QY 795 TCCCTGAACCTTGAACCTT-----ATCCAACAGTGCATTTAAGAAATTAAGCTT 848
Db 233 AspLeuAspThrPheHisPheSerGlnLeuSerThrGlyIleThrAsnSerLeu---Ile 251
QY 849 CATAGCTGACTTTAAGAAAT-----AATTTGATGTGTTA---AATGTAATGAA 896
Db 252 LysIlePheThrPheThrGlnAsnValIleThrAspIleuSerLeuPheGlnIleMetIle 271
QY 897 ACTTGT-----ATTCAAGCTGTGCTGTGTTGAAGTCCATCGTTTGCTTCTG----- 944
Db 272 LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleLeuGlnIleAspAspCysThrIleAsnGly 291
QY 945 ---GGAGATTTTGAATGAGAACTTGAAAGTTTGACAAATCTGCTTACAGAGGC 1001
Db 292 ValGlyAsnPheArgIleAspAspAsnAspArgValIleAspProGlyIleValGlu--- 310
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Qy 1002 CTGGCAATTGACCATTTGAAGAAATTCGATTAACA-----TACTTAGACTACTACTC 1055
Db      |||||
Qy 311 -----ThreuleuthrileargAspleuHisleProargPheTyrlseuPheTyr----- 326
Db      |||||
Qy 1056 GATGATATTATGACTTATTAAATGTTTGAACAAATGTTTCTTCAATTTTCCCTGGTGAGT 1115
Db      |||||
Qy 327 ---AspleuSerThreuleuTyrlseuSerleuThrgluArgValys-----Arg 340
Db      |||||
Qy 1116 GTGACTATTGAAGGGTAAAGACTTTCTTATATATTCGGATGGGCAACATTAGAAATTA 1175
Db      |||||
Qy 341 IlethrValGluAsnSerLysValPhe-----Leu 350
Db      |||||
Qy 1176 GTTACTGTAAATTTGACAGTTTCCCATGTAATCAATCTTCGAAAAGGCTTACT 1235
Db      |||||
Qy 351 ValProCysLeuLeuSerGln----- 357
Db      |||||
Qy 1236 TTCACCTTCAACAAAGGTGGAAATGCTTTTTCAGAAATTGATCTTCAAGCTTGAAGTT 1295
Db      |||||
Qy 358 -----HisLeuLysSerleuGluTyr 364
Db      |||||
Qy 1296 CTAGATCTCAGTAGAAT-----GGCTTGAATTCGAAGCTTGCTGCTCT 1340
Db      |||||
Qy 365 LeuAspleuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 382
Db      |||||
Qy 1341 CAAAGTAGATTTGGGACCAACGACCTTAAAGTATTAGATCTGAGCTTCAATGCTGTAT 1400
Db      |||||
Qy 383 -----GluAspAlaTTrProSerleuGlnThrleuIleLeuArgGlnAsn----- 397
Db      |||||
Qy 1401 ACCATGAGTCAAACTTCTGGGCTTAGAACAACTAGAACATTTGATTTCCAGCATTC 1460
Db      |||||
Qy 398 -----HisLeu-----Ala 400
Db      |||||
Qy 1461 AATTGAAACAATGAGTAGATTTTCAGTATTCCTATACACAGAAACCTGATTAAGTCT 1520
Db      |||||
Qy 401 SerleuGluLysThrGlu-----ThreuleuThrleuLysAsnLeuThrAsnIle 418
Db      |||||
Qy 1521 GACATTTCTCATCTACACACAGAGTCTTTCATGAGCATCTTCAATGCTTGCTCAGT 1580
Db      |||||
Qy 419 AsplleSerLys----- 422
Db      |||||
Qy 1581 CTCGAGTCTTGAANAATGGCTGGCAATCTTTCCAGGAAAATTCTCCAGATATCTTC 1640
Db      |||||
Qy 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
Db      |||||
Qy 1641 ACAGAGCTGAGAAACTTGACCTTCTCTGACCTCTCTGAGTCAACTGAGACAGTGTCT 1700
Db      |||||
Qy 433 GlnTrpProGluLysMetLysTyrlseuAsnLeuSerSerThrArgIleHisSerValThr 452
Db      |||||
Qy 1701 -----CCAAACGACATTTAACTCACTCTCCAGTCTTCAGTACTAATATGAGCCAC 1751
Db      |||||
Qy 453 GlyCysIlePro-----LysThrleuGluIleLeuAspValSerAsn 466
Db      |||||
Qy 1752 AAC-----AAGCTTTTTCATTTGAT----- 1772
Db      |||||
Qy 467 AsnAsnLeuAsnLeuPheSerleuAsnLeuProGlnleuLysGluLeuTyrIleSerArg 486
Db      |||||
Qy 1773 -----AGCTTTCCCT---TATAAGTGTCTGAAGCTCCCTCCAGGTTCTTGATTAC 1817
Db      |||||
Qy 487 AsnLysLeuMetThrleuProAspAlaSerleuLeuProMetleuLeuValleuLysIle 506
Db      |||||
Qy 1818 AGTGCATCATCATATGATGACTTCCAAAACAGAACTAGACAGATTTTCCAAAGTAGTCTA 1877
Db      |||||
Qy 507 SerArgAsnAlaIleThrThrPheSerLysGluGlnleuLeuAspSerPhe---HisThrleu 525
Db      |||||
Qy 1878 GCTTTCTTAAATCTTACTCAGATGACTTTCCTGACTTGTACTTGAACACAGAGTTTCTCG 1937
Db      |||||
Qy 526 LysThrleuGluAlaGluGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
Db      |||||
Qy 1938 CAATGATCAACAGACCAAGGAGCTTTGGTGAAGTT-----GAACGA 1982
Db      |||||
Qy 546 Gln-----GluGlnGlnAlaLeuAlaLysValleuLysAspTrpProAlaAsn 561
Db      |||||
Qy 1983 ATGGAATGTGAACACTTCAGATTAAGACAGGAGCATGCTGTGCTGAGTTGAATATACAC 2042

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Db      |||||
Qy 562 TyrlseuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
Db      |||||
Qy 2043 -----TGTCAATGAATTAAGACCATCATGCTGTGTGCGCTCCAGTGTCTGTA 2093
Db      |||||
Qy 582 ValSerGluCysHisArgThrAlaLeuValSerIleCysValAlaLeuPheLeu 601
Db      |||||
Qy 2094 GTATCTGTGTAGACAGTCTGTGTCTAATAGTTCTAT-----TTTCACTGATGCTTCT 2147
Db      |||||
Qy 602 IleleuLeuThrGlyValleuLeuCysHisArgPheHisIleTyrlseuTrpTyrMetLysMetMet 621
Db      |||||
Qy 2148 GCTGGCTGCAATTAAGTATGTAGA-----GGTGAACATC---TAT 2186
Db      |||||
Qy 622 TrpAlaTrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 641
Db      |||||
Qy 2187 GATGCTTTGTATCTATCTCAAGCCAGATGAGACCTGGGTGAAGATGAGCTGTAAAG 2246
Db      |||||
Qy 642 AspAlaPheValSerTyrlseuSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGln 661
Db      |||||
Qy 2247 AATTAGAAAGAGGGGTGCTCCATTTCAAGCTGTGCTTCACTACATGAGACTTATCCC 2306
Db      |||||
Qy 662 GluLeuGluAsnPheAsnProProPheLysleuCysLeuHisLysArgAspPheIlePro 681
Db      |||||
Qy 2307 GGTGTGGCAATGCTGTGCAACATCATCATGAAGTTTCCATAAAGCCGAAAGTAT 2366
Db      |||||
Qy 682 GlyLysTrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrVal 700
Db      |||||
Qy 2367 GTTGTGTGTCCACGACTTCATCCAGAGCCGCTGGTGTATCTTTGAATATGAGATTTCT 2426
Db      |||||
Qy 701 PheValleuSerGluAsnPheValLysSerGluTyrCysLysTyrlseuAspPheSer 720
Db      |||||
Qy 2427 CAGACCTGGAGTTCGTGAGAGTGTGCTGTATCTATCTTCAATGCTTCGACAGAGTGT 2486
Db      |||||
Qy 721 HisPheArgLeuPheGluGluAsnAsnAspAlaAlaIleleuIleleuLeuGluProIle 740
Db      |||||
Qy 2487 GAGAAAGCCCTGTCTCAGACAGACAG---GTGAGCTGTACCGCTTCTCAGACAGACACT 2543
Db      |||||
Qy 741 GluLysLysAlaIleProGlnArgPheCysLysleuLysIleMetAsnThrIleThr 760
Db      |||||
Qy 2544 TACTGTAGTGGAGAGACAGTGTCTGTGGGCGGACATCTTCTGAGACAGACTAGAAA 2603
Db      |||||
Qy 761 TyrlseuLysTrpProMetAspGluAlaGlnArgGluGluPheThrValAsnLeuArgAla 780
Db      |||||
Qy 2604 GCCCTG 2609
Db      |||||
Qy 781 AlaIle 782
Db      |||||

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RESULT 11
 US-10-456-947-46
 ; Sequence 46, Application US/10456947
 ; Publication No. US20040053841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kevin J. Tracey
 ; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
 ; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
 ; FILE REFERENCE: 3268.1001-007
 ; CURRENT APPLICATION NUMBER: US/10/456,947
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 10/147,447
 ; PRIOR FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: 60/291,034
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 46
 ; LENGTH: 784
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-456-947-46

Alignment Scores:

Pred. No.: 2.09e-48 Length: 784
Score: 603.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.98% Indels: 219
DB: 15 Gaps: 38
US-09-396-985B-3 (1-3811) x US-10-456-947-46 (1-784)
QY 306 ATCCCGGACAACTCCCTTCTCAACCAAGAACTGGACCTGAGCTTAAATCCCTGAGG 365
DB 46 ILeProSerGlyLeuThrGluAlaValIysSerLeuSerAspAsnArgIleThr 65
QY 366 CATTAGGACCTATAGCTTCTTCAAGTTCCAGAGCGGTGGATTTATCCAGG 425
DB 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
QY 426 TGTGAATCCAGCAATTTGAAGATGGGCAATATCAGACCTAGCCACTCTTACCTTA 485
DB 86 AsnGlyIleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGlnHisLeu 105
QY 486 ATATTGACAGAAACCCCAAGATTAGCCCTGGAGCCTTTTCTGACATCAACT 545
DB 106 AspLeuSerTyrAsnTyrLeuSerAsnLeuSerSerSerTyrPheIysProLeuSerSer 125
QY 546 TTACAGAAAGCTG-----GTGGCTGTGGAG 569
DB 126 LeuThrPheLeuAsnLeuLeuGlyAsnProTyrIlyThrLeuGlyGluThrSerLeuPhe 145
QY 570 ACAAACTTAGACATCTTAGAGAACTCCCACTTGACATCTCAAACT----- 617
DB 146 SerHisLeuThrIlyLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIlySer 165
QY 618 -----TTGAAGAAGCTTAATGGGCTCACAACTT 647
DB 166 GlnArgIlyAspPheAlaGlyLeuThrPheLeuGlnGluLeuGluIleAspAlaSerAsp 185
QY 648 ATCCCACTTTCAAAATTAAGATTTTCTAATGACCAATCTAGACAGCTTGAC 707
DB 186 LeuGlnSerTyrGlu---ProIySerLeuIySerIleGlnAsnValSerHisLeuIle 204
QY 708 CTTTCCAGCAACAG-----ATTCAAGTAT 734
DB 205 LeuHisMetIyGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerAl 224
QY 735 TATTGCACAGACTTCCGGGTTCTACATCAATGCCCTTACTCATCTCTTTAGACCTG 794
DB 225 GluCysLeuGluLeuArg-----AspThr 232
QY 795 TCCCGAAGCCGATGAACTT-----ATCCAACAGGATTTAAGAAATTAGGCTT 848
DB 233 AspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---Ile 251
QY 849 CATAGCTGACTTTAAGAAAT-----AATTGTAGATTTA---AATGTAATGAAA 896
DB 252 LysIlyPheThrPheArgAsnValIySerIleThrAspGlnSerLeuPheGlnValMetIys 271
QY 897 ACTGT-----ATCAAGCTGTGGCTGTTTGAAGTCATCGTTGGTCTG----- 944
DB 272 LeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGly 291
QY 945 ---GGAGAATTTGAAGATGAAGAACTTGGAAAAGTTTGACAAATCTGCTTAGAGGC 1001
DB 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIlyValGlu--- 310
QY 1002 CTGTCAATTTGACCATTTGAAGAAATTCGATTAGCA-----TACTTAGACTACTACCTC 1055
DB 311 -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
QY 1056 GATGATATTTAGCTATTTAATTGTTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGT 1115
DB 327 ---AspLeuSerThrLeuIySerLeuThrArgIuArgValIys-----Arg 340

QY 1116 GTGACTATTGAAGAGGTAAAGACTTTTCTTATATTTGGATGAGCAACATTTAGATTA 1175
DB 341 ILeThrValGluAsnSerIySValPhe-----Leu 350
QY 1176 GTTAACTGTAATTTGGACAGTTTCCACATGTAACATAATCTCAAAAGCGTTACT 1235
DB 351 ValProCysLeuLeuSerGln----- 357
QY 1236 TTGACTTCCAAAGAGTGGGAATGCTTTTTCAGAAAGTTGATCTCAAGCCTTGAGTT 1295
DB 358 -----HisLeuIySerLeuGluTyr 364
QY 1296 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAAAGGTGCTGTCT 1340
DB 365 LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuIyAsnSerAlaCys----- 382
QY 1341 CAAAGTATTTGGGACACACCGCTTAAGATTTAGATTGAGCTTCAATGGTGTATT 1400
DB 383 -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
QY 1401 ACCATGAGTTCAAACTTCTGGGCTTAGAACAACTGAAATGATGATTTCCAGCAATTC 1460
DB 398 -----HisLeu-----Ala 400
QY 1461 AATTGAAACAAATGAGTAGATTTCAGATTCCTATCTCACTGCAAACTCAATTACTT 1520
DB 401 SerLeuGluIySerThrGlyGlu-----ThrLeuLeuThrIleuIyAsnLeuThrAsnIle 418
QY 1521 GACATTTCTCATACTCACACCAAGTTGCTTTCAATGGCATCTTCAATGGCTGTCCAGT 1580
DB 419 AspIleSerIys----- 422
QY 1581 CTGAAAGTCTGAAAAATGCGTGGCAATCTTTCAGAGAAAACCTTCCTGAGATATCTTC 1640
DB 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
QY 1641 ACAAGCTGAGAAACTTGACCTTCTGAGACCTCTCTCAAGTCACTGAGACAGTGTCT 1700
DB 433 GlnThrProGluIyMetIyTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
QY 1701 -----CCAACGACATTTAACTCACTCTCAAGTCTTCAAGTACTTAATATGAGCCAC 1751
DB 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
QY 1752 AAC-----AAGTTCTTTGATTGGAT----- 1772
DB 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIySgluLeuTyrIleSerArg 486
QY 1773 -----ACGTTTCTT-----TATAGTGTCTGAATCCCTCCAGTTCCTTGATTAC 1817
DB 487 AsnIySgluMetThrIleuProAspAlaSerLeuLeuProMetLeuValIleuIySle 506
QY 1818 AGTCTCAATCACTATATGACTTCCAAAAACAGAACTACAGCATTTTCCAAAGTACTTA 1877
DB 507 SerArgAsnAlaIleThrThrPheSerIySgluGlnIleuAspSerPhe---HisThrLeu 525
QY 1878 GCTTTCAATCTTACTACGAATGACTTGTGCTTGTGTTGTTGTAACACAGAGTTTCTG 1937
DB 526 LysThrLeuGluAlaGlyIyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
QY 1938 CAATGATCAAGACACAGAGCAGCTTGTGAGAACTT-----GAAACA 1982
DB 546 Gln-----GluGlnGlnAlaLeuAlaIySValLeuIleAspTyrProAlaAsn 561
QY 1983 ATGGAATGTGCACACCTTGATAGATACAGAGGATGCTGTGCTGAGATTGAATATACAC 2042
DB 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnAlaGlnAspValArgLeuSer 581
QY 2043 -----TGTGAGATTAAGACATCATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2093
DB 582 ValSerGluCysHisArgThrAlaLeuValSerIyMetCysCysValAlaLeuPheLeu 601
QY 2094 GTATCTGTAGACAGTTTGTGCTATAGTTTAT-----TTTCACTGATGCTTCTT 2147


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Db 602 ILeuLeuThrGlyValIleuCyHieArgHieGlyLeuTrpYrMetIleuMet 621
Qy 2148 GCTGCGTCGCAAAAGTATGTAGA-----GGTGAAGAAATC---TAT 2186
Db 622 TrpAlaTrpLeuGlnAlaValArgIleProSerArgAsnIleCysThr 641
Qy 2187 GATGCTGTTGTTATCTCAAGCAGAGATGAGACTGGTGAAGAAATGAGCTGAAG 2246
Db 642 AspAlaPheValSerIleYrSerGlnArgAspAlaIleTrpValGluAsnIleValGln 661
Qy 2247 AATTGAAGAAGAGGGGCTCCATTCATTCAGCTGCTCCATTCAGAGACTTATTC 2306
Db 662 GluLeuGluAsnPheAsnProPheIleuCyHieValIleuValIlePro 681
Qy 2307 GGTGTGGCCATTGCTGCGCAATCATCTCATGAAGTTCCATAAAGCCGAAGTAT 2366
Db 682 GlyIleTrpIleIleAspAsnIleIle---AspSerIleGluIleValIleVal 700
Qy 2367 GTTGTGGTCCGACACTTCATCCAGAGCGCTGGTGTATCTTGAATATGATGTCT 2426
Db 701 PheValIleuSerGluAsnPheValIleSerGluTrpCysIleYrGluLeuAspPheSer 720
Qy 2427 CAGACTGGCAGTTTCTGAGCAGCTGCTGCTGATCATCTTCATTCATTCCTG 2486
Db 721 HisPheArgLeuPheGluGluAsnAspAlaIleIleuIleLeuGluProIle 740
Qy 2487 GAGAGACCTGCTCAGGACAGAG---GTGAGCTGTACCCCTTCAGAGAGAACT 2543
Db 741 GluIleValAlaIleProGlnArgPheCysIleuIleValIleMetAsnThrIleThr 760
Qy 2544 TACCTGGAGTGGAGGAGCAGTGTCTGGGGGAGCAGACTCTTCTGAGAGCAGT 2603
Db 761 TyrLeuGluTrpProMetAspGluAlaGlnArgGluIlePheTrpValAsnIleuArgAla 780
Qy 2604 GCCCTG 2609
Db 781 AlaIle 782

RESULT 12
US-10-095-627-12
; Sequence 12, Application US/10095627
; Publication No. US20030027260A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; Godowski, Paul J.
; Guirey, Austin
; Yang, Ruey-Bing
; Mark, Melanie
; TITLE OF INVENTION: Human Toll Homologues
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,627
; FILING DATE: 11-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,413A
; FILING DATE: 26-Jun-1998
; APPLICATION NUMBER: 60/083322
; FILING DATE: 28-Apr-1998
; APPLICATION NUMBER: 60/065311

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; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: 60/062250
; FILING DATE: 17-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marechany, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1154-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 784 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12

Alignment Scores:
Pred. No.: 2,61e-48 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.96% Indels: 219
DB: Gaps: 38

US-09-396-985B-3 (1-3811) x US-10-095-627-12 (1-784)
Qy 306 ATCCCGCAGACCTCCCTTCACACAGACCTGAGCTTAAATCCCTGAG 365
Db 46 IleProSerGlyLeuThrGlnAlaValIleSerLeuAspLeuSerAsnAsnArgIleThr 65
Qy 366 CATTGAGCAGCTATAGCTTCTTCAGTTTCCAGACTGAGGTGCGATTAATCCAG 425
Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnIleuGlnAlaIleuValIleuThrSer 85
Qy 426 TGTGAATCCAGCAATTTGAAGATGGGCAATACAGACCTTCACTTCACTTA 485
Db 86 AsnGlyIleAsnThrIleGluGluAspSerPheSerSerIleuGluIleuIleu 105
Qy 486 ATATTGACAGAAACCCCATCCAGAGTTTACCCTGGAGCTTTTCTGATATCAAGT 545
Db 106 AspLeuSerTyrAsnTyrIleuSerAsnIleuSerSerTrpPheIysProIleuSerSer 125
Qy 546 TTACAGAGCTG-----GTGGCTGTGGAG 569
Db 126 LeuThrPheLeuAsnIleuGluIleuAsnProTyrIleThrIleuGluIleuThrIleuPhe 145
Qy 570 ACAATCTAGCATCTCTAGAGAACTTCCCATGGACATCTCAAACT----- 617
Db 146 SerHisIleuThrIleuGluIleuIleuValGluValGluAsnMetAspThrPheThrIle 165
Qy 618 -----TTGAAGAACTTAATGTGCTCAAACTTT 647
Db 166 GluArgIleAspPheAlaGluIleuThrPheLeuGluIleuGluIleuAlaSerAsp 185
Qy 648 ATCAATCTTTCAATTAATCTGAGATTTTCAATCTGACCAATCAGACCTTGAC 707
Db 186 LeuGlnIleuTyrGlu---ProIleuSerLeuIleuSerIleuGlnIleuValSerHisIleu 204
Qy 708 CTTTCCAGCAAGAG-----ATTCAAGATTT 734
Db 205 LeuHisMetIleuGlnHisIleuLeuLeuGluIleuPheValAspValIleuSerVal 224
Qy 735 TATTGACAGACTGGGGTTTACATCAAAATGCCCTACTCAATCTCTTATAGACTG 794
Db 225 GluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 811
Qy 795 TCCCTGAACTTATGAAGTT-----ATCCACAGGTGATTAAGAATATGAGCTT 848
Db 233 AspLeuSerThrPheHisPheSerGluLeuSerThrIleuIleuThrAsnSerIleu---Ile 251
Qy 849 CATTAAGTGAAGTTAAGAAAT-----AATTTGATGTTTA---AATGTAATGAAA 896

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Db      252  LysLeuSerThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLys 271
Qy      897  ACTTGT-----ATTCAAGGTCTGGCTGGTTTAAAGTCCATCGTTGGTTCTG----- 944
Db      272  LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleuLeuPheAspSerCysThrLeuAsnGly 291
Qy      945  ---GGAAATTATGAAATGAAAGAACTTGGAAAGTTTGAACAATCTGCTAGAGGC 1001
Db      292  ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGln--- 310
Qy      1002  CTGTGCAATTTGACCAATTTGAAGAAATCCGATTAGCA-----TACTTAAGCTACTTACCTC 1055
Db      311  -----ThrLeuThrIleArgArgLeuHisIleProArgPheLeuPheLeuPheTy----- 326
Qy      1056  GATGATATTTATGCTATTATTAATTTGTTGACAAATGTTTCTCATTTTCCCTGGTAGT 1115
Db      327  ---AspLeuSerThrLeuTySerLeuThrGluArgValLys-----Arg 340
Qy      1116  GTGACATTTGAAAGGGTAAAGACTTTTCTATATTAATTCGGATGGCAACATTAGAAATTA 1175
Db      341  IleThrValGluAsnSerLysValPhe-----Leu 350
Qy      1176  GTTAACTGTAATTTGACAGCTTTCCACATTTGAACCTCAATCTCAAAAGGCTTACT 1235
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1236  TTCACTTCCAAAGGATGCGTTTTCAGAACTTGATCTTACCAAGCTTGAGTTT 1295
Db      358  -----HisLeuLysSerLeuGlnLys 364
Qy      1296  CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTCTT 1340
Db      365  LeuAspLeuSerGlnuLeuAsnMetValGluGluTyLeuLysAsnSerAlaCys----- 382
Qy      1341  CAAGATGATTTGGGACACCAAGCTTAAGTATTAGATCTGAGCTTCAATGCTGTTAATT 1400
Db      383  -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
Qy      1401  ACATGAGTTCAAACTTCTGGGCTTAGAACAACTGAGAACTTGAGTTTCCAGATTC 1460
Db      398  -----HisLeu-----Ala 400
Qy      1461  AATTGAAACAATAGAGTAGTTTTCAGTATCTCTATCACTCAGAACTCATTTACTT 1520
Db      401  SerLeuGluLysThrGlyGlu-----ThrLeuLeuThrLeuLysLeuThrAsnIle 418
Qy      1521  GACATTTCTCACTACTCACACCAAGTGTCTTCAATGCGCATCTTCAATGCTGTCCAGT 1580
Db      419  AspIleSerLys----- 422
Qy      1581  CTCGAAAGCTTGAATAGCGTGGCAATTCCTTCCAGGAAACTTCCTCCAGATATCTTC 1640
Db      423  -----AsnSerPheHisSer-----MetProGlnThrCys 432
Qy      1641  ACAGAGCTGAGAAATGACCTTCTGGACCTCTCTCAGTGTCAACGAGACAGTGTCT 1700
Db      433  GlnThrProGluLysMetLysTyLeuAsnLeuSerThrArgIleHisSerValThr 452
Qy      1701  -----CCAAAGCATTTTAACCTCACTCTCCAGTCTTCAGTACTAAATATAGGCAC 1751
Db      453  GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
Qy      1752  AAC-----AAGCTTTTTCATTGGAT----- 1772
Db      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyIleSerArg 486
Qy      1773  -----ACGTTTCTCT-----TATAAGTGTGGAAGCTCTCCAGGTTCTTGATTAC 1817
Db      487  AsnLysLeuMetThrIleuProAspAlaSerIleuLeuProMetLeuValLeuLysIle 506
Qy      1818  AGTCTCAATCAATATGACTTCCAAAACAGGAACTACAGCAATTTTCCAGTACTGCTA 1877

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Db      507  SerArgAsnAlaIleThrThrPheSerLysGlnIleuAspSerPhe---HisThrLeu 525
Qy      1878  GCTTCTTAAATCTTACTCAGAAATGACTTGTGTTACTTGTGTAACACCAAGTTTCTG 1937
Db      526  LysThrLeuGlnAlaGlyLysAsnPheIleCysSerCysGlnuLeuLeuSerPheThr 545
Qy      1938  CAATGATCAACGACCAAGGACGCTTGTGGAAAGTT-----GAACGA 1982
Db      546  Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 561
Qy      1983  ATGGAATGTGCAACACTTCAATTAAGCAGGATCCCTGTGTGATTTGAATATCACC 2042
Db      562  TyrLeuCysAspSerProSerHisValArgGlyGlnGlnAlaLysArgValLeuSer 581
Qy      2043  -----TGTCAATGATATAAGACCATCATTTGGTGTGGTGTGCTCCAGTGGCTTGA 2093
Db      582  ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
Qy      2094  GATCTGTGTGTAGACAGTTCTGTGCTTAAATTTCTA-----TTTCACTGATGCTTCTT 2147
Db      602  IleLeuLeuThrGlyValLeuLysCysHisArgPheHisGlyLeuThrTyMetLysMetMet 621
Qy      2148  GCTGGCTGCATTAAGTATGGTAGA-----GTTAAACATC---TAT 2186
Db      622  TyrAlaTyrLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTy 641
Qy      2187  GATGCTTTGTTATCTACTCAAGCCAGATGAGTGAAGTGGGTAAGATGAGTAAAG 2246
Db      642  AspAlaPheValSerTyrSerGlnuArgAspAlaTyTrpValGluAsnMetValGln 661
Qy      2247  AATTGAAAGAAAGGGTGCCTCCATTTCAAGCTTGCCTTCACTTAACAGACTTATTTCC 2306
Db      662  GluLeuGlnAsnPheAsnProForPheLysLeuCysLeuHisValArgAspPheIlePro 681
Qy      2307  GGTGTGCACTTCTGTGCCAATCATTCATGAAGTTTCCATTAAGCCGAAAGGTTGATT 2366
Db      682  GlyLysArgTrpIleLeuAsnIleIle---AspSerIleGluLysSerHisLysThrVal 700
Qy      2367  GTTGTGTGTGCCAGACTCATCATCAGAGCCGCTGGTGTATCTTGAATATGATGTGCT 2426
Db      701  PheValLeuSerGlnuAsnPheValLysSerGlnuTrpCysLysTyTrpGluLeuAspPheSer 720
Qy      2427  CAGACCTGGCAAGTTTCTGAGCACTCGTGTGTATCATTTCAATGCTCTGCAGAAAGTG 2486
Db      721  HisPheArgLeuPheAspGlnuAsnAspAlaIleIleuIleLeuLeuGluProIle 740
Qy      2487  GAGAAACCTGTCTCAGGACAGAG---GTGAGCTGTACCGCTTCTCAGACGAAACACT 2543
Db      741  GluLysLysAlaIleProGlnuArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy      2544  TACTGGAGTGGGAGGACAGTGTCTGTGGGCGGACATCTTCTGAGACGAGACTCAGAAA 2603
Db      761  TyrLeuGlnuTrpProMetAspGlnuAlaGlnuArgGluGlyPheThrValAsnLeuArgAla 780
Qy      2604  GCCCTG 2609
Db      781  AlaIle 782

RESULT 13
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 581830003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

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LENGTH: 784
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-732-563-4

Alignment Scores:

2.61e-48 Length: 784
 Score: 602.50 Matches: 233
 Percent Similarity: 41.88% Conservative: 128
 Best Local Similarity: 27.03% Mismatches: 282
 Query Match: 8.96% Indels: 219
 DB: 16 Gaps: 38

US-09-396-985B-3 (1-3811) x US-10-732-563-4 (1-784)

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QY 306 ATCCCGCAACCTCCCTTCACACCAAGACCTGACCTTATATCCCTGAG 365
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DB 46 lLeProSerGlyLeuThrGluAlaValSerLeuSerLeuSerLeuSerLeuThr 65
QY 366 CATTAGGACGCTATAGCTTCTTCAGTTCCAGAACGTCGAGTCTGATTTACAG 425
    : : : : :
DB 66 TyrlSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
QY 426 TGTGAATCCAGACATTTGAAGATGGGCATATACAGCCTTAAGCCACTTACCTTA 485
    |||||
DB 86 AsnGlyLeuAsnThrIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnHisLeu 105
QY 486 ATATTGACAGAAACCCATCCAGAGTTTACGCCCTGGAGCCTTTCTGACTATCAAGT 545
    |||||
DB 106 AspLeuSerTyrAsnTyrLeuSerAsnLeuSerSerTyrPheLysProLeuSerSer 125
QY 546 TTACAGAGCTG-----GTGGCTGTGGAG 569
    |||||
DB 126 LeuThrPheLeuAsnLeuLeuGlnLysAsnProTyrLysThrLeuGlnLysThrSerLeuPhe 145
QY 570 ACAATCTTACGACTCTTACAGAACTTCCCATTTGACATCTCAAAACT----- 617
    |||||
DB 146 SerHisLeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
QY 618 -----TTGAAGAACCTTAATGTGGCTCACATCTT 647
    |||||
DB 166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGlnLysLeuGlnIleAspAlaSerAsp 185
QY 648 ATCCATCTTTCACAAATTACTGATATTTTCTATCTGACCACTTACGACACTGAGC 707
    : : : : :
DB 186 LeuGlnSerTyrGln---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
QY 708 CTTTCCAGCAACAAG-----ATTCAAGATATT 734
    |||||
DB 205 LeuHisMetLysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal 224
QY 735 TATTGCACAGACTTCCGGGTTCTACATCAATGCCCTTACTCAATCTCTTTAGACCTG 794
    |||||
DB 225 GluCysLeuGlnLeuArg-----AspThr 232
QY 795 TCCCGAACCTTATGAACCTT-----ATCCACAGGTCGATTTAAGAATTAGGTT 848
    |||||
DB 233 AspLeuAspThrPheHisPheSerLeuSerThrGlyGlnThrAsnSerLeu---Ile 251
QY 849 CATTAAGCTGACTTTAAGAAAT-----AATTGTATAGTTA---AATGTAATGAA 896
    |||||
DB 252 LysLysPheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLys 271
QY 897 ACTTGT-----ATTCAAGTCTGCTGCTGTTAAGATCCATCGTTGGTCTTG----- 944
    |||||
DB 272 LeuLeuAsnGlnIleSerGlyLeuLeuGlnLysPheAspAspCysThrLeuAsnGly 291
QY 945 ---GGAGATTATTAAGAAATGAAACTTGAAAAAGTTGCAATCGCTCTAGAGGC 1001
    |||||
DB 292 ValGlyAsnPheArgLysAspAsnAspArgValIleAspProGlyLysValGln--- 310
QY 1002 CTGTGCAATTTGACCATTTGAAGAAATTCGATTAGCA-----TACTTAGACTTACTACTC 1055
    |||||

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DB 311 -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
QY 1056 GATGATATTTATTTACTTATTTAATTTGTTGACAAAGTTTCTTATTTCCCTGGTAGT 1115
    |||||
DB 327 ---AspLeuSerThrLeuTyrSerLeuThrGluArgValLys-----Arg 340
QY 1116 GTGACTATTTGAAGGTTAAAGACTTTTCTTAATTTGCGATGGACAACTTGAATTA 1175
    : : : : :
DB 341 IleThrValGlnAsnSerLysValPhe-----Leu 350
QY 1176 GTTAAGCTTAATTTGACAGCTTTCCACATTTGAACCTCAATCTTCAAAAGGCTTACT 1235
    |||||
DB 351 ValProCysLeuLeuSerGln----- 357
QY 1236 TTCACTTCCAAAGAGTGGGAATGCTTTTTCAGAACTGATCTACAGAGCTTAGATT 1295
    |||||
DB 358 -----HisLeuLysSerLeuGlnTyr 364
QY 1296 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTTCT 1340
    |||||
DB 365 LeuAspLeuSerGlnAsnLeuMetValGluGlnTyrLeuLysAsnSerAlaCys----- 382
QY 1341 CAAGTGATTTGGGACACACCGCTTAAGATTTAGATCTGAGCTTCAATGCTGTATT 1400
    : : : : :
DB 383 ---GluAspAlaTyrProSerLeuGlnThrLeuIleLeuArgLysAsn----- 397
QY 1401 ACATGAGTTCAAACTTCTGGGCTTAGAACAACTAACAATCGATTTCCAGATTCC 1460
    |||||
DB 398 -----HisLeu-----Ala 400
QY 1461 AATTGAAACAAATGAGTGAATTTTTCAGTATTTCTATCACTGACAAACTCATTTACTT 1520
    : : : : :
DB 401 SerLeuGlnLysThrGlyGln---ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 418
QY 1521 GACATTTTCATACTACACACAGATGCTTTCAATGCAATCTTCAATGCTGTCCAGT 1580
    |||||
DB 419 AspIleSerLys----- 422
QY 1581 CTGAAATCTTGAAGAAATGGCTGGCAATCTTCCAGAGAAACCTTCCAGATATCTTC 1640
    |||||
DB 423 -----AsnSerPheHisSer---MetProGlnThrCys 432
QY 1641 ACAGAGCTGAGAAACTGACCTTCTCGAGACTCTCTCAGTGTCAACGAGAGAGTGTCT 1700
    : : : : :
DB 433 GlnTyrProGlnLysMetLysTyrLeuAsnLeuSerThrArgIleHisSerValThr 452
QY 1701 -----CCAACAGCATTTAATCTCACTCTCAGTCTTCAAGTACTTAATATGAGCCAC 1751
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DB 453 GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
QY 1752 AAC-----AAGTCTTTTCATTGAT----- 1772
    |||||
DB 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArg 486
QY 1773 -----ACGTTTCT---TATAAGTGTGAACTCCCTCCAGGTTCTGATTAC 1817
    |||||
DB 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuLysIle 506
QY 1818 AGTCTCAATCAATATGACTTCCAAAACAGAGAACTACAGATTTTCCAGTAGTCTA 1877
    |||||
DB 507 SerArgAsnAlaIleThrThrPheSerLysGlnLeuAspPhe---HisThrLeu 525
QY 1878 GCTTTCTTAATCTTACTACGAATGACTTGTGCTTGTGTTGTAACACAGAGTTTCTG 1937
    |||||
DB 526 LysThrLeuGlnAlaGlyLysAsnAspPheIleCysSerCysGlnPheLeuSerPheThr 545
QY 1938 CAATGATCAAGACACGAGGACCTTCTGTGGTAAGTT-----GAACGA 1982
    |||||
DB 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuLeuIleAspTyrProAlaAsn 561
QY 1983 ATGGAATGTGCAACACTTCAGATTAAGACAGGAGATGCTGTGATTTGAATATCACC 2042
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DB 562 TyrlLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581

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QY 1236 TTCACCTTCCAAAGAGTGGAAATGCTTTTCAGAACTGATCTCAACAGCTTGAGTT 1295
Db 358 -----HisleuylsSerleuGluThr 364
QY 1296 CTAGATCTCAGTAGAAT-----GGCTTGAGCTTCAAGGTTGCTGTCT 1340
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluThrLeuLysAsnSerAlaCys----- 382
QY 1341 CAAGTGAATTTGGGACACAGCCTAAAGTATTAGATCTGAGCTTCAAGGTTAT 1400
Db 383 -----GluAspAlaTrpProSerleuGlnThrLeuIleLeuArgGlnAsn----- 397
QY 1401 ACCATGAGTTCAAACTTCTGGCTTAGAACAACATAGACATTTCCAGACTTC 1460
Db 398 -----Hisleu-----Ala 400
QY 1461 AATTGAAACAATGAGTAGAGTTTTCAGTATTCCTATCATCTCAAGAACTCATTTACCT 1520
Db 401 SerleuGluLysThrGlu-----ThrleuLeuThrLeuLysAsnLeuThrAsnIle 418
QY 1521 GACATTTCTCATCTACACACAGAGTTGCTTCAATGAGCATCTCAATGCTTCCAGT 1580
Db 419 AspIleSerLys----- 422
QY 1581 CTCGAACTTGAAATGGCTGGCAATCTTTCCAGAAACTTCCTCCAGATATCTTC 1640
Db 423 -----AsnSerPheHisSer-----MetProGlnThrCys 432
QY 1641 ACAGAGCTGAGAACTTGACCTTCCTGGACCTCTCTCAAGTCACTGGAGCACTGTCT 1700
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QY 1701 -----CGAAGACATTTAATCTCACTCTCCAGTCTTCAGGATCTTAATAAGCCAC 1751
Db 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
QY 1752 AAC-----AACTCTTTTCATTTGAT----- 1772
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QY 1878 GCTTTCTTAATCTTACTCAGATGACTTGTCTGATCTTGTAACCCAGAGTTTCTCTG 1937
Db 526 LysThrLeuGluAlaGlyLysAsnPheIleCysSerCysGluPheLeuSerPheThr 545
QY 1938 CAATGATCAAGACAGCAGGCACTTGTGTGAGATT-----GAACGA 1982
Db 546 Gln-----GluGlnGlnAlaLeuValLysValLeuIleAspTrpProAlaAsn 561
QY 1983 ATGGAATGTGCACACCTTCAGATAGAGGCACTGCTGCTGAGATTGATATACACC 2042
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
QY 2043 -----TGTGATGATTAAGACATCATGTTGGTGGTGGTGGTCCAGTGGCTTGTA 2093
Db 582 ValSerLeuCysHisArgThrAlaLeuValSerGlyMetCysCysValAlaLeuPheLeu 601
QY 2094 GTATCTGTGTAGAGAGTTGTGCTATTAAGTTAT-----TTTCACTGATCTTCT 2147
Db 602 IleLeuLeuThrGluValLeuLeuCysHisArgPheHisGlyLeuTrpGlyMetLysMetMet 621
QY 2148 GCTGGCTGATTAAGTATGTAGA-----GGTGAAGAAATC---TAT 2186
Db 622 TrpAlaTrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysLys 641

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QY 2247 AATTAAAGAAAGGGGCTCTCCATTTACAGTCTGCTTTCATCAACAGACTTATCCC 2306
Db 662 GluLeuGlnAsnPheAsnProPheLysLeuCysLeuHisLysArgAspPheIlePro 681
QY 2307 GGTTGGCATTGCTGTCCAATCATCATCAATGAGTTTCCATTAAGCCGAAAGGATT 2366
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QY 2367 GTTGTGTGTCCAGACATTCATCCAGAGCCGTGTGATCTTTGAATAGAGATTCT 2426
Db 701 PheValLeuSerGluAsnPheValLysSerGluTrpCysLysThrGluLeuAspPheSer 720
QY 2427 CAGACTGGCAGTTTCTGACAGACTGCTGTGATATCTTCATTTGCTTCGACAGAGT 2486
Db 721 HisPheArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIle 740
QY 2487 GAGAGACCCCTGCTCAGGACAGAG-----GTGGAGCTGTAACGCCCTTCACAGAGACT 2543
Db 741 GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
QY 2544 TACCTGAGTGGGAGAGACAGTGTCTGGGCGGACACATCTTTCGAGACGACTCAGAAA 2603
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QY 2604 GCCCTG 2609
Db 781 AlaIle 782

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; Publication No. US20050026169A1
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; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1390

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Query Match: 8.96% Indels: 219
DB: 17 Gaps: 38

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QY 366 CATTTAGGACATTAAGCTTCTCACTTCCAGAACTGCAAGGCTGTGATTTATCAGG 425
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QY 426 TGTGAATCCAGACATTTGAAGATGGGCAATATCAAGAGCTTAAGCACTCTTACCTTA 485
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QY	570	ACAATCTTACAGATCT	CTAGAGAACTTCCCATGTGCACATCTCAAAACT	-----	617	
Db	146	SerHisLeuThrTyrLeuGlnIle	LeuArgValGlyAsnMetAspThrPheThrLeuVal	165		
QY	618	-----	TTGAAGAATTAATGTGGCTCACAACTT	647		
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QY	708	CTTTCCAGCAACAAG	-----	ATTCAAAGTAT	734	
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QY	849	CATAAGCTGACTTAA	GAAT-----AATTTGATAGTTT--AATGTAATGAA	896		
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QY	897	ACTTGT-----ATTCAAGTCTGG	CTGGTTTACAACTCAATCGTTGGTCTG-----	944		
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QY	945	---GGAGAAATTAGAA	ATGAAAGAACTTGAAAGTTTGCAAAATCTGCTAGAGGCG	1002		
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QY	1002	CTGTGCAATTTGAC	CATTGAAAGAACTTCGATAGCA-----TACTTACATCACTCTC	1055		
Db	311	-----ThrLeuThrIleArg	ArgLeuHisIlePheAlaGlyPheTyrLeuPheTyr-----	326		
QY	1056	GATGATATTTAT	TGACTTATATGTTTGAACAAATGTTTCTTCAATTTCCCTGGTAGT	1115		
Db	327	---AspLeuSerThrLeuTyrSer	LeuThrGlyArgValLys-----Arg	340		
QY	1116	GTGACTATTTGAA	AGGTAAAGACTTTTCTATATTTCCGATGGCAACATTTAGAAATTA	1175		
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QY	1176	GTTTACTGTAAATTT	GACAGTTTCCACATGGAACSTCAAAAGGCTTACT	1235		
Db	351	ValProCysLeuLeuSerGln	-----	357		
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QY	1521	GACATTTCATCTACCTCACACAGAGTTGCTTTCAATGGCATCTTCAATGGCTGTCCAGT					1580
Db	419	AspIleSerIys-----	----				422
QY	1581	CTCGAAGCTTGAAAAAGCGTGGCAATCTTTCCAGAAAACCTTCCTCCAGATATCTTC					1640
Db	423	-----	AsnSerPheHisSer-----MetProGluThrCys	----			432
QY	1641	ACAGAGCTGAGAACTTGACCTTCTCGACCTCTCAGTGTCAAGTGCAGAGAGTTGCT					1700
Db	433	GlnThrProGluYstMetIysYstYrLeuAsnLeuSerThrArgIleHisSerValThr	----				452
QY	1701	-----CCACAGCAATTTAACTCACTCCAGTCTTCAGTCTCACTAAATATGAGCCAC					1751
Db	453	GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn	----				466
QY	1752	AAC-----AACTCTTTCACTGGAT-----					1772
Db	467	AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuYsgluLeuYrIleSerArg	----				486
QY	1773	-----ACGTTTCCT-----TATTAAGTGTGTAACCTCCGCGAGGTTCTGATTAAC					1817
Db	487	AsnIysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuYrIle	----				506
QY	1818	AGTCCATATCAATCATATGACTTCCAAAAACAGAACTACAGCAATTTCCAGATAGCTTA					1877
Db	507	SerArgAsnAlaIleThrThrPheSerIysGluInLeuAspSerPhe---HisThrLeu	----				525
QY	1878	GCTTTCTTAATCTTACTACAGAAAGACTTTTGACTTGTAACCTGTGTGAACACAGATTTCTG					1937
Db	526	LysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr	----				545
QY	1938	CAATGGATCAAGACACAGGCGACGCTGTGGTGGAATTT-----GAACGA					1982
Db	546	Gln-----GluGlnGlnAlaLeuAlaYsValLeuIleAspTrpProAlaAsn	----				561
QY	1983	ATGGAATGTGCACACCTTCAGATTAACAGGGCATGCGTGTGCTAGTTGAATATGACAC					2042
Db	562	TyrLeuCysAspSerProSerHisValArgGlyGlnGlnAlaGlnAspValArgLeuSer	----				581
QY	2043	-----TGTCAAGATGAATTAACCACTATGCTGTGTGCGTGTGCTCAAGTGTCTGTGA					2093
Db	582	ValSerGluCysHisArgThrAlaLeuValSerIleYMetCysCysValaLeuPheLeuLeu	----				601
QY	2094	GATCTGTGTGTGAAGAGTTCTGTGCTATGAAGTTAT-----TTTCACTGATGCTCTT					2147
Db	602	IleLeuLeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpYrMetLeuYsMetMet	----				621
QY	2148	GCTGGCTGCATAAAGTATGTAGTA-----GGTGAACATC-----TAT					2186
Db	622	TrpIatThrLeuGlnAlaYsArgLysProArgLysAlaProSerArgAsnIleCysTyr	----				641
QY	2187	GATGCTTTGTTATCTACTCAAGCGAGATGAGACTGGGTGAAGATGAGCTTAGTAAAG					2246
Db	642	AspAlaPheValSerYstSerGlnArgAspAlaTyrTrpValGluAsnLeuMetValGln	----				661
QY	2247	AATTTAGAAGAAGGGGTGCGCTCAATTTCAAGTGTGCTGCTCACTACAGACTTATATCC					2306
Db	662	GluLeuGluAsnPheAsnProProPheYsLeuCysHisValYsValAspPheIlePro	----				681
QY	2307	GATGTGGCCATGTGTGCGCAACATATCCATGAAGGTTTCCATTAAGCCGAAAGAGTAT					2366
Db	682	GlyYstTrpIleIleAspAsnIleIle---AspSerIleGlyYsSerHisIysThrVal	----				700
QY	2367	GTTGTGATGCCACACTTATCCAAAGCCGCTGGTGATCTTTGAATATGAGATTTGCT					2426

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Db      701 PheValIeuSerGluAsnPheValIysSerGluTrpCysLysTyrGluLeuAspPheSer 720
QY      2427 CAGACCTGGCAGTTTCTGAGCAGTGTGCTGTATCATCTTCATTGCTCGCAGAGGTG 2486
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QY      2604 GCCCTG 2609
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Job time : 224.708 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nbp model

Run on: March 30, 2005, 03:00:48 ; Search time 119.022 Seconds
(without alignments)
16418.453 Million cell updates/sec

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Sequence:

Scoring table: BLOSUM62
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Ygapop 6.0 , Ygapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 2814804

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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10: /cgnt2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgnt2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

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3	2675.5	51.7	799	16	US-10-128-166-7
4	2675.5	51.7	799	16	US-10-732-563-8
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6	579.5	11.2	661	13	US-10-114-893-10
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8	567.5	11.0	661	15	US-10-038-854-135
9	567.5	11.0	661	15	US-10-037-417-107
10	559	10.8	1032	10	US-09-954-987B-192
11	559	10.8	1032	14	US-10-272-502A-31
12	559	10.8	1032	15	US-10-407-952-32
13	546	10.5	1059	10	US-09-954-987B-187
14	546	10.5	1059	15	US-10-407-952-30
15	546	10.5	1059	17	US-10-753-267-30
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17	541	10.5	1041	9	US-09-978-295A-498
18	541	10.5	1041	9	US-09-978-697-498
19	541	10.5	1041	9	US-09-978-192A-498
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21	541	10.5	1041	10	US-09-978-189-498
22	541	10.5	1041	10	US-09-978-608A-498
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ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Kock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: EX0724XKI
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.1
SEQ ID NO 26
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-26

Alignment Scores:
Pred. No.: 1,966-269 Length: 837
Score: 2772.50 Matches: 554
Percent Similarity: 79.56% Conservative: 100
Best Local Similarity: 67.40% Mismatches: 162
Query Match: 53.55% Indel: 7
Gaps: 5

US-09-396-985b-46 (1-2951) x US-09-950-041-26 (1-837)

QY 226 CTGGCTAGGACTGTGATCATGCACTG---TTCTTCTCTGCTGACACACGAGAGCTTG 282
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QY 283 AATCCCTGCATAGAGGATGTTCTTAATTTACCTTACCAATGATGATGATGACAACTCAGC 342
DB 26 GluProCyValGlu--ValProAsnIleThyTrpGlnCyMetGluLeuAsnPhetYr 44
QY 343 AAAGTCCCTGATGACATCTCTTCTTCAACCAAGAACATAGATCTGAGCTTCAACCCCTTG 402
DB 45 LysIleProAsnPhaLeuProPhaSerThrIlyAsnLeuAspLeuSerPhaAsnProLeu 64
QY 403 AAGATCTTAAAAAGCTATAGCTTCTCCAAATTTTTCAGAACTTCAAGTGCATTTATTC 462
DB 65 ArgIAsnLeuGlySerIySerPhaSerPhaProGluLeuGlnValLeuAspLeuSer 84
QY 463 AGGTGTGAATTTGAACAAATTGAGACAGACAGACAGCTGCTTACACCACTCTTCAAC 522
DB 85 ArgCySgIuIleGlnThrIleGluAspIyAlaTyrgInSerLeuSerHisLeuSerThr 104
QY 523 TTGATATGACAGAGAAACCTATCCAGAGTTTTCCCGAGAGATTTCTGAGTAACA 582
DB 105 LeuIleLeuThrIyAsnProIleGlnSerLeuAlaLeuGlyAlaPhaSerGlyLeuSer 124
QY 583 AGTTTGAACAATCTGGTGGCTGTGGAGACAAATTTGGCTCTAGAAAGCTTCCATT 642
DB 125 SerLeuGlnIyLeuValAlaValGluThraAsnLeuAlaSerLeuGluAsnPhaProIle 144
QY 643 GACAGAGCTTAAACCTTAAAGAACTCAATGGTGCATTTTATATCTCTGTAAG 702
DB 145 GlyIlyAsnLeuIySthrLeuIySgIuLeuAsnValAlaHisAsnLeuIleGlnSerPhaYs 164
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DB 165 LeuProGluTyryPhaSerHisLeuThraAsnLeuGluHisLeuAspLeuSerSerHisIys 184
QY 763 ATTCAAACTATTTATGTCAACGACTTACAGTTTCTACGTGAAAAATCCAAAGTCAATGC 822
DB 185 IleGlnSerIleTyryCyThraSpleuIyrgValLeuHisGlnMetProLeuLeuAsnLeu 204
QY 823 TCTTTAGCATGTCTTTTGAACCAATTGACTTCAATTTCAAGACCAAGCTTTCAAGGAAT 882
DB 205 SerLeuAspLeuSerLeuAsnProMetAsnPhaIleGlnProGlyAlaPhaIySgIuIle 224
QY 883 AAGCTCCATGAACTGACTTAAGAGTAAATTTTATAGCTCAAAATATATGAAAACTTGC 942
DB 225 ArgLeuHisIySpleuThraIyrgAsnAsnPhaAspSerLeuAsnValMetIlySthrCyS 244
QY 943 CTTCAAAAAGCTGGCTGTTTACACGCTCATCGGTGATCTTGGGAGAAATTTAAAGATGA 1002
DB 943 CTTCAAAAAGCTGGCTGTTTACACGCTCATCGGTGATCTTGGGAGAAATTTAAAGATGA 1002

DB 245 IleGlnIyLeuAlaGlyLeuGlnValHisArgLeuValLeuGlyIyPhaArgAsnGlu 264
QY 1003 AGGAATCTGGAATTTTGAACCTCTATCATGAGAGACTATGATGATGACATTTGAT 1062
DB 265 GlyAsnLeuIySpleuAspIySserAlaLeuGlnGlyLeuCySAsnLeuThrIleGlu 284
QY 1063 GAGTTCAAGTTTAAATATACAAATGATTTTTCAGATGATTTGTAG--TTCCATTTGC 1119
DB 285 GluPhaIyrgLeuAlaTyryLeuAspTyryTyryLeuAspAspIleIleLeuAspLeuPhaAsnCyS 304
QY 1120 TTGGCGAATGTTTCTGCAATGTCTCTGGCAGGGTGATCTTAAATAATTTCAAGAGATTT 1179
DB 305 LeuThraAsnValSerSerPhaSerLeuValSerValThrIleGlnIyrgValIyAspPhe 324
QY 1180 CTTAAACATTTCAAAATGCGCAATCTTATCATATGATAGATGCAACTAAG--CAGTTTCCA 1238
DB 325 SerTyryAsnPhaGlyTyryGlnHisSleuGlnLeuValAsnCySAspPheGlyGlnPhaPro 344
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QY 1299 TTTAAAAAGTGGCCCTTACCAAGTCTCAGCTATCTAGATTTTGAATAATGCACTGAGC 1358
DB 365 PhaSerGluValAspLeuProSerLeuGluPhaLeuAspLeuSerArgAsnGlyLeuSer 384
QY 1359 TTTTAAAGTGGCTGTTCTTATCTGATTTTGGGAAACAAACGCTGAGACCTTGAACCTC 1418
DB 385 PhaIySgIyCySserGlnSerAspPheGlyThraThrSerLeuIySpleuAspLeu 404
QY 1419 AGCTTCAATGGTGCATATATAGTGCACAAATTTCAAGGCTGTAGAAAGCTGCAGAC 1478
DB 405 SerPhaAsnGlyValIleThrMetSerSerAsnPhaLeuIyLeuGlnGluLeuHis 424
QY 1479 CTGATTTTTCAGACCTCTTCTTAAAGAGGTCACAGAAATTTCTCAGCTTCTTATCTCT 1538
DB 425 LeuAsp-PhaGlnHisSerSerAsnLeuIySgIuMetSergIuPhaSerValPhaLeuSerIle 444
QY 1539 TGAAGACTACTTACTTACCTGACATCTCTTATACACCAAAATGACTTCGATGTAT 1598
DB 444 HisArgAsnLeuIleTyryLeuAspIleSerHisIySthrIySthrArgValAlaPhaAsnGlyIle 464
QY 1599 ATTCTGGCTTGCACAGTCTCAACACATTTAAATAATGGCTGCGCAATCTTTCAGACAA 1658
DB 464 ePhaAsnGlyLeuSerSerLeuGlnValLeuIySMeclAglIyAsnSerPhaGlnGluIyAs 484
QY 1659 CACCCTTCAAAATGCTTTTGCAAAACACACAAACTTGCATTCCTGGATCTTCTAAATG 1718
DB 484 nPhaLeuProAspIlePhaThrGluLeuArgAsnLeuThrPhaLeuAspLeuSerGlnCy 504
QY 1719 TCAATTGGAACAAATATCTGGGGGGTATTGACACCCCTCCATAGACTTCAATTATTA 1778
DB 504 SgIuLeuGlnGluLeuSerProThraAlaPhaAsnSerLeuSerSerLeuGlnValLeuAs 524
QY 1779 TATAGTCAACAACATATATGTTTGTGATTCATCCCATTAATAACAGCTGATTTCCCT 1838
DB 524 nMetSerHisAsnAsnPhaSerHisSerLeuAspThrPhaProTyryIySgIySpleuAsnSerIle 544
QY 1839 CAGCACTTGTGATGACGTTTCAATGCGATAGACATCT--AAAGAAATACTGCACAA 1895
DB 544 uGlnValLeuAspTyrySerLeuAsnHisIleMetThrSerIySpleuGlnIyLeuGlnIle 564
QY 1896 TTTTCCAAAGAGTCTTACTTCTTCAATCTTACATCAAAATTCGTGCTGTGATATGTA 1955
DB 564 sPhaPheSerSerLeuAlaPhaLeuAsnLeuThrGlnAsnAspPhaIleCySthrCySgI 584
QY 1956 ACATCAGAAATTCCTGCAAGTGGTCAAGAGAACAGAACAGATTTCTGTGATGTGGAAC 2015
DB 584 uHisGlnSerPhaLeuGlnIyryIySAspGlnArgGlnLeuLeuValGluValGluArg 604
QY 2016 AATGACATGTGCAACACTGTAGAGATGAATACCTCTTATGTTGGATTTTAATATTC 2075
DB 604 gMetGluCySAlaIyThraProSerAspIySgIuGlnIyMetProValLeuSerLeu--AsnIle 623

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QY 2076 TACCTGTATATGTACAAGACATCATGTCAGTGTGTCAGTGTGATTTGATGTAATC 2135
D 623 eThCyeGlmetLeuTherThrlleleGlyValSerValLeuSerValLeuValSe 643
QY 2136 CACTGTAGACATTTTGTATATACCATTTTACCTGATTAATTTATTTGCTGCTGTA 2195
D 643 rValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysI 663
QY 2196 AAATACAGCAGAGAGAAACATCTATGATGCAATTTGTGATCTTACTGATCAGAAATGA 2255
D 663 eLysTyrCylYarGlyGluAenIleTyrAspAlaPheValIleTyrSerSerGlnAspG 683
QY 2256 GGACCTGGGTGAATGATGCTGTAAAGATTGTAAGAAAGAGAGGCCCGCTTCACT 2315
D 683 uAspTyrValArGAsnGluLeuValLysAsnLeuGluGluValIleProPheGlnLe 703
QY 2316 CTGCTTCACTACAGACATTTATTTCTGTGTATGATGATGCTGCAATCATCTACAGGA 2375
D 703 uCysLeuHisTyrArGAspPheIleProGlyValAlaIleAlaIleAlaIleIleHisG 723
QY 2376 AGGCTTCCACAGAGCCGGAAGTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2435
D 723 uGlyPheHisTyrSerArGlyValIleValValSerGlnHisPheIleGlnSerAr 743
QY 2436 TTGGTATCTTTGATATGATGATTTGCTCAACATGGCAGTTTGTGACAGCCGCTGTG 2495
D 743 GTTCyaleIlePheGluTyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArGlnA 763
QY 2496 CATCATCTTCAATTTCTTGAAGAGTTGAGAGTCCCTGTGAGGAGCAGGTGGAATT 2555
D 763 yIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArGlnGlnValGluLe 783
QY 2556 GTATCGCTTTTGAAGAAACACCTTACCTGGAATGGAGAGCAATCTCTGGGAGAGCA 2615
D 783 uTyrArGLeuLeuSerArGAsnTrIleTyrLeuGluTrpGlnAspSerValLeuGlyArG 803
QY 2616 CATCTTCTGAGAGACTTAAATAATGCCCTATTTGATGGAAGAAAGCTGGAATCTCGAGA 2675
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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Pred. No.: 1,136-259 Length: 799
Score: 2675.50 Matches: 532
Percent Similarity: 79.82% Conservative: 97
Best Local Similarity: 67.51% Mismatches: 155
Query Match: 51.68% Indels: 5
DB: 10 Gaps: 3

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QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGATATAGCTTCTTCAATTTTTCAGAACTT 444
D 21 LeuSerPheAsnProLeuArGHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY 445 CAGTGGCTGATTTATTCAGGTGTGAATTTGAACATTTGAAGCAAGCAGCATGGC 504
D 41 GlnValLeuAspLeuSerArGysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
QY 505 TTACACCACCTTCAACCTTGATATCTGACAGAAACCTTATCCAGATTTTTCACAGGA 564
D 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY 565 AGTTTCTGTGATCAACATTTTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 624
D 81 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 100
QY 625 CTGAAATCTTCCCTATTTGAGACAGCTTATACCTTAAAGAAACCATGTCGTCACAAAT 684
D 101 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
QY 685 TTATACATTCCTGTAAATGATTAAGTCAATTTTTCATCTGACGAACCTAGATATGTG 744
D 121 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 140
QY 745 GATCTTCTTATATATATATTAATCAACTATTACTGTACAGCACTTACAGTTTCTTACG 804
D 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArGValLeuHisGln 160
QY 805 AATCCCAAGATCAATCTCTTATAGACATGCTTTGAACCCATTTGACCTTCATTCAGAC 864
D 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProPheCAsnPheIleGlnPro 180
QY 865 CAAGCTTTCAGGAAATTAAGTCCATGACATGACCTTAAGAGGTATTTTAATAGCTCA 924
D 181 GlyAlaPheLysGluIleArGLeuHisLysLeuThrLeuArGAsnAsnPheAspSerLeu 200
QY 925 AATATATGAATTAACCTGCTTCAAAACCTGCTGCTTTTACAGTCCATCGGTGATTTG 984
D 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValAlaHisArGLeuValLeu 220
QY 985 GGAGATTTTAAAGTAAGAAAGAAATCTGGAATTTTGAACCCCTTCAATGAGAAAGACTA 1044
D 221 GlyGluPheArGAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 240
QY 1045 TGTGATGTGACATTTGATGATTCAGGTTAATCAATATCAATGATTTTTCAGATGATAT 1104
D 241 CysAsnLeuThrIleGluGluPheArGLeuAlaTyrLeuAspLysTyrTyrLeuAspAspIle 260
QY 1105 GTTAAG---TTCAATGCTTGGGAGATGTTTTCGCAATGTCTGTGAGAGGTATATCTATA 1161
D 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280

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QY 1222 CAACCTAG-CAGTTTCAACTCTGAGATCTTACCTTTCTTAAAGATTGACCTTAACTATG 1280
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QY 301 LYSBHEGLYGLNPHPROTHLEULYSEULYSERLEULYSARGLEUTHPHETHSER 320
QY 1281 AACAAGGCTATACAGTTTAAAAAGTGGCCCTTACCAATCTCAGTACTATGATCTT 1340
Db      ::::::::::::::::::::|
QY 321 ASNLVSEGLYGLASMDALAPHESERGLUVALASPLEUPROSERLEUGLULPHLEUASPLEU 340
QY 1341 AGTAGAATGACCTAGCTTAGTGTGCTGTCTTATCTTGAATTGGGAACAACAGC 1400
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QY 341 SERTAGENGLYSEURPHELYSEGLYCYSEYSESERGINSEARPHNEGLYTHTHSER 360
QY 1401 CTGAGACCTTAGCCTGAGCTTCAATGTCSCATCATTAATGAGTCCCAATTTGAGGT 1460
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QY 361 LEULYSTRYLEUASPLEUSERPHEANGLYVALILETHMETSESERASNPHLEUGLY 380
QY 1461 CTAGAGAGCTGACGACCTGATTTTACGACTCTTAATAAAGAGGACACAGATT 1520
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QY 381 LEUGLUGLNULEUGLULHISLEUASP-PHEGLNHISERASNLEULYSEGLINMETSERGLUPH 400
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QY 400 ESERVALPHEUSERLEUARGANLEULIETYLEUASPLEULESERHISHTHISHTHAR 420
QY 1581 AATGACTCTGATGATATTTCTTGCTTGACAGCTCAACATTAATAAATGGCTGG 1640
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QY 420 GVALALAPHENGLYLEPHEANGLYLEUSERSERLEUGLULVALLEULYSEMEALAGL 440
QY 1641 CAATCTCTTCAAGACACACCTTTCAATGCTTTGCAACAACACACAACTTGACTT 1700
Db      ::::::::::::::::::::|
QY 440 YASNSERHEGLINGLUAENPHEUPROASPLIEPHEHTRGLUEARGANLEUTHPH 460
QY 1701 CCTGATCTCTTAATGCTCAATTTGGAACAATAATCTGGGGGATTTGACACCTTCA 1760
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QY 460 ELEUASPLEUSERGLNCYSGINLEUGLULHLEUSERPROTHRALAPHEANSEULUSE 480
QY 1761 TAGACTTCAATTAATTAATGAGTACACAAATCTATTTGTTTGAATCCCATTA 1820
Db      ::::::::::::::::::::|
QY 480 RSEULEUGLULVALLEUANMETSERHISASNAPHEPHESEULEUAPRTHPRHEPROLY 500
QY 1821 TAACAGCTGTATTCCTCAGACACTCTGATTTGACGTTTCAATGCCAAGACATCT-- 1878
Db      ::::::::::::::::::::|
QY 500 RLYSEYSELEUANSERLEUGLULVALLEUASPLYRSEULEUASNHISILEWETINSELY 520
QY 1879 -AAAGGAATCTGCAACATTTTCCAAAGAGCTAGCCTTTCTTCAATCTTAAACAATTC 1937
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QY 520 SLYSGINLULLEUGLULHISPEHROSERSEULEUAPHELEUASPLEUTHRGINASNA 540
QY 1938 TGTGCTTGTATATGTAAGATCAGAAATCTCTGAGTGGGTCAAGAAAGACAGATT 1997
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QY 540 PHHEALACYSTRHCYSGIUNHISGLINSERPHELEUGLINTPRILEYSAEPGLINARGLILE 560
QY 1998 CTGGTGAATGTTGAACAATGACATGTGCAACACTGTAAGATGAATACCTCTTATGT 2057
Db      ::::::::::::::::::::|
QY 560 ULLEUVALGLULVALGUARGMETGLUCYSALATHRPROSEARSPLYSGINLYMETPRIVA 580
QY 2058 GTTGATATTTAATATCTTACCTGTTATATGTAACAAGCAATCATCAGTGTGCTAGTGT 2117
Db      ::::::::::::::::::::|
QY 580 LLEUSERLEU--ASNLLETHCYSGIMETASNLVSHTRILEILEGLYVALSERVALLE 599
QY 2118 CAGTGTGATTTGATTCACCTAGTACATTTCTGATATACCACTTCTAATTTTCACTTAT 2177
Db      ::::::::::::::::::::|
QY 599 USERVALLEUVALSERVALVALALVALLEUVALYRILYSPHELYRPHENHISLEUME 619
QY 2178 ACTTATGCTGCTGTAAAAAGTACAGAGAGGAGAAACATCTATGATGCTATTTGTAT 2237
Db      ::::::::::::::::::::|
QY 619 TLEUENULIAGLYCYSLIETLYRGLYARGGLYGLUENULIETRYARPALAPHEVALI 639
QY 2238 CTACTCGATGTCAGATGAGAGCTGGGTGAGAAATGAGCTGGTAAGAATTATGAAGAAG 2297

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QY 639 EYRSESERGLINAPGLUBSPTRVALARGANGLULEVALLYEASNLEUGLULGL 659
QY 2298 AGTGCCCGCTTTACCTCTGCTCTTCACTACAGAGACTTATTCCTGCTGTATGCCATTGC 2357
Db      ::::::::::::::::::::|
QY 659 YVALPROPHOPEGLINLEUCLYSEULHSTRYARGAPRPHLEIETROGLYVALALALEAL 679
QY 2358 TGGCAATCATCATCAGGAAGCTTCCACAGAGCCGGAAGGATTATGTGTAGTGTAG 2417
Db      ::::::::::::::::::::|
QY 679 AALASNLILEILEHISGLINULYPHEHISLYSEARAGLYSVALILEVALVALSERGL 699
QY 2418 ACACTTATTCAGAGCCGTGTGTATCTTTGAATATGAGATTGCTCAACATGCGAGTT 2477
Db      ::::::::::::::::::::|
QY 699 NHISPEHLEGLINSEARLYTRPCYSILEPHEGLIUTYRGLULILEGLINTHTRPGINPH 719
QY 2478 TCTGAGAGCCGCTCTGCGACATCTTCAATTTGCTTGAAGAGCTTGAAGAGTCCCTGCT 2537
Db      ::::::::::::::::::::|
QY 719 ELEUSERSEARXALAGLYLEILEPHEILEVALLEUGLULYSEVALGLULYSTRILEUE 739
QY 2538 GAGGACAGAGTGAATGTATGAGCTTCTTACAGAAACACCTACCTGGAATGGAGGA 2597
Db      ::::::::::::::::::::|
QY 739 UARGINGLULVALGLULUEUTYRARGLEUUSERARGANTRHYRLEUGLUTRPGIUB 759
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QY 759 PSERVALLEUGLYARGHISILEPHEHTRPARGLUEARGLYEALALEUENUPGLYLY 779
QY 2658 AGCCTCGAATCTGAGCAACA 2679
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Db      ::::::::::::::::::::|

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Alignment Scores:
Pred. No.: 1,13e-259 Length: 799
Score: 2675.50 Matches: 532
Percent Similarity: 79.82% Conservative: 97
Best Local Similarity: 67.51% Mismatches: 155
Query Match: 51.68% Indels: 3
DB: 14 Gaps: 3

US-09-396-985b-46 (1-2951) x US-10-128-166-7 (1-799)
QY 325 ATGATACAGAACTCAGCAAAAGTCCCTGATGACATTTCTTCAACCAAGACATAGAT 384
Db      ::::::::::::::::::::|
QY 1 METGLUENUNPHELYRVLISLEPROASPSANLEUPROHSEARTHLYSASNLASASP 20
QY 385 CTGAGCTTCAACCCCTGGAAGATCTTAAAGACTATGCTTCTTCCCAATTTTTCAGAACTT 444
Db      ::::::::::::::::::::|
QY 21 LEUSERPHEANSPROBLUNARGHISLEUGLISERTYSERPHEPESRPHPROGLIDU 40
QY 445 CAGTGTGATTTATTCAGGTGTGAATGAATGAACAAATGAAGCAAGGATGCGATGCC 504
Db      ::::::::::::::::::::|
QY 41 GLINLLEUENUPLEUSERARGCYSGULILEGLINTHTRILEGLUBSPGLYALATYRGLINSE 60

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QY 505 TTACACACCTCTGAACTGTAGTACGAGGAAACCTATCCAGATTTCCTCCAGAGA 564
 Db 61 LeuserhlsleuserThleuileuinhglsanpfoileginsleuialaleuily 80
 QY 565 AGTTCTCTGAGCTAACAGATTAGACAATCTGTGTGCTGTGAGACAAATTTGGCTCT 624
 Db 81 AlapheserlglyleuserSerleuglnlyleuvalalavalgluthrAsnleuAlaser 100
 QY 625 CTAGAAAGCTTCCTATTGAGCAGCTTAACTTAAAGAACTCAATGTGGCTCACAT 684
 Db 101 LeuglnsnphleuProileglnhlsleuylsThleuylsGlnleuAsnValAlhlsan 120
 QY 685 TTTATACATCTCTGAACTGCTGACATATTTTCCATTTGAGGAACTGATCATCTG 744
 Db 121 LeuileginsleuThleuylsleuProglulThrleuserleuinhAsnleuGlnhlsleu 140
 QY 745 GATCTTTCTTAACTATATTAATCAATCTATCTGACAGACTTACAGTTTCTACGTGA 804
 Db 141 AspleuserSerleuAsnlylelglnserllyrCysThrAspleuArgValleuilegln 160
 QY 805 AATCCACAAGTCATCTCTTTAGACATGTCTTTGAACCCAAATTGACTTATTCAGAC 864
 Db 161 MetProleuAsnleuAsnleuSerleuAsnleuSerleuAsnPrometAsnPhlelglnPro 180
 QY 865 CAAGCTTTGAGGAGTTAAGCTCCATGCTGACCTGAAGGTTAATTTAATTAAGTCA 924
 Db 181 GlyAlaphelysGlnleuArgleuinhlsleuThleuArgAsnAsnPhaspleu 200
 QY 925 AATATTAATGAAGAACTTGCTTCAAAACCTGGCTGTTTACAGTTCACGTGCTGATCTTG 984
 Db 201 AsnValMetCysThrCyslllelglnlyleuAlaglyleuGlnValhlsArgleuValleu 220
 QY 985 GGAAGATTTAAAGTGAAGAAATCTGGAATTTTGAACCTCTATCATGGAAGACTA 1044
 Db 221 GlyleuPheArgAsnGlnGlyAsnleuGlnlyrPheAsnlyrSerAlaleuGlnGlyleu 240
 QY 1045 TGTGATGAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
 Db 241 CysAsnleuThrlelglnGlnPheArgleuAlaThrleuAsnlyrThrleuAsnAsnlyr 260
 QY 1105 GTTAAG--TTCCATTTGCTGGCAGATGTTTCTGCAATGTCTGCGACAGTGTATCTA 1161
 Db 261 IleAsnleuPheAsnlyrleuThrAsnValSerSerPheSerleuValSerValThrle 280
 QY 1162 AATATCTCAAGAGTGTCTTAAACATTTCAATGGCAATCTTATCATTAAGATGT 1221
 Db 281 GlnArgVallyAsnAsnleuSerlyrAsnPhleGlyThrGlnhlsleuGlnleuValAsn 300
 QY 1222 CAACCTAAG-CAGTTTCCAACTCGATGATGATGATGATGATGATGATGATGATGATG 1280
 Db 301 LysPheGlnGlnPheProThleuLysleuLysSerleuLysValGlnleuThrPheThrSer 320
 QY 1281 AACAAAGGCTCTATCAGTTTAAAGAGTGCCCTTACCAAGTCTCAGCTATCTAGATCT 1340
 Db 321 AsnlyleGlnyAsnAlapheserGlnValAsnleuProSerleuGlnPheleuAsnleu 340
 QY 1341 AGTGAAGATGCACTGAGCTTTAGTGTGGCTGTCTTATTTGTATTTGGGAAACAACAC 1400
 Db 341 SerTrgAsnGlnlyleuSerPheLysGlyCysCysSerGlnserAsnPhleGlyThrThrSer 360
 QY 1401 CTGAGACACTTGAAGCTCAGCTTCAATGGCCATTCATTAATGATGCAATTTAGGCT 1460
 Db 361 LeuylsThrleuAsnleuSerPheAsnGlyVallleThrMetSerSerAsnPhleGlnly 380
 QY 1461 CTAGAGAGCTGAGCACTGAGATTTTTCAGACCTTCACTTAAAGAGGCTCAGAGATT 1520
 Db 381 LeuGlnGlnleuGlnhlsleuAsp-PheGlnhlsleuSerAsnleuLysGlnMetSerGln 400
 QY 1521 CTGAGCGTTTATTCCTTGAAGAACTTATTAACCTTGAACATCTTATTAACCTAACA 1580
 Db 400 eSerValPheleuSerleuArgAsnleuLyleuThrleuAsnlyrleuSerhlsThrThrAr 420

QY 1581 AATGACTGAGATGATATTTCTTGCTTGACCAAGCTCTCAACATTTAAATAGGCTG 1640
 Db 420 gvalAlaphesnlyllePheAsnGlnlyleuSerSerleuGlnValleuylsMetAlag 440
 QY 1641 CAATCTTTCAAGAACAAACCTTTCAAAATGTCTTTGCAAAACAACAACCTTGACATT 1700
 Db 440 YAsnSerPheGlnGlnubsnPheleuProAsnPhleThrGlnleuArgAsnleuThrPh 460
 QY 1701 CTTGATCTCTTCAAAATGCTCAATTTGGAACAAATCTTTGGGGGATATTGACACCTTCA 1760
 Db 460 eleuAsnleuSerGlnCysGlnleuGlnleuSerProThrAlapheserleuSe 480
 QY 1761 TAGACTTCAATTTAATATGAGTCAACAATCTATGTTGTTTGGATTCATCCCATTA 1820
 Db 480 rSerleuGlnValleuAsnMetSerhlsAsnAsnPheserleuAsnPhrPheProTy 500
 QY 1821 TAACCAAGCTGTATTCCTTCAAGACCTTGTATTTGAGTTCAATGCAATGACATGCT 1878
 Db 500 rlyCysleuAsnSerleuGlnValleuAsnlyrSerleuAsnhsileMetThrSerly 520
 QY 1879 -AAAGAACTGCAATTTTCCAAAGACTTACCTTCTTCAATCTTATTAACAATTC 1937
 Db 520 slyeGlnGlnleuGlnhlsPheProSerSerleuAlaphleuAsnleuThrGlnAsnAs 540
 QY 1938 TGTGCTTGTATATGTGACATCAGAAATTCCTGACAGTGTGCTGAGGAAACAAGACATT 1997
 Db 540 pHeAlCysThrCysGlnhlsGlnserPheleuGlnThrlyAsnGlnhlsGlnle 560
 QY 1998 CTGTGTAATGTTGAACAAATGACATGTGCAACCTGTAGAGATGAATACCTTCTAGT 2057
 Db 560 uleuValGlnValGlnArgMetGlnCysAlaThrProSerAsnlyrGlnGlnMetProva 580
 QY 2058 GTTGGAATTTAATATCTACCTGTATATGTATGACAAACAATCATCAGTGTGACAGTGT 2117
 Db 580 lleuSerleu--AsnleThrCysGlnMetAsnlyrThrleleGlyValSerValle 599
 QY 2118 CAGTGTATGTTGGTATCCACTGAGCATTTCTGATGATGATGATGATGATGATGATGAT 2177
 Db 599 uSerValleuValValSerValValAlaValleuVallyrLysPheThrPhehlsleuMe 619
 QY 2178 ACTTATGCTGCTGTAAAGTACAGACAGAGAGAGAAACATCTATGATGATTTGTAT 2237
 Db 619 tleuLeuAlaglyCyslleuThrGlyArgGlyGlnAsnleuThrAsnPhleValle 639
 QY 2238 CTATCGAGTCAAGATGAGACTGGGTGAGAAATGAGCTGTAAAGATTTGAAGAGAG 2297
 Db 639 eTySerSerGlnAsnlyrAsnlyrValArgAsnGlnleuVallyAsnleuGlnGln 659
 QY 2298 AGTGCCCGCTTCACTGCTGCTTCACTGACAGACTTATTCCTGCTGAGCATTTGC 2357
 Db 659 yValProProPheGlnleuCysleuThslyrArgAsnPhelleProGlyValAlaileAl 679
 QY 2358 TGCCAAATCATCCAGAGAGGCTTCCAAAGAGCCGGAAGGTTATTTGTGATGTCTAG 2417
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 QY 2418 ACACTTATTCAGACCCGTTGGTGTATCTTTGAATATGATGATGCTTAAACATGGCAGT 2477
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 QY 2478 TCTGAGACGCGCTGAGCATCATCTTCAATGCTTGAAGAGGTTGAGAAGTCCGCT 2537
 Db 719 eleuSerSerArgAlaGlyllePhelelleValleuGlnlyValGlnlysrThrleu 739
 QY 2538 GAGGACAGAGTGAATTTGATGACCTTTTACAGAAACAACCTGAGATGGAGAGA 2597
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 QY 2598 CAATCTCTGGGAGGACATCTTTGAGAGAACTTAAATGAGCCCTATTTGATGAGAAA 2657
 Db 759 pSerValleuGlnlyArghlslePheThrArgArgleuArglyAlaAlaLeuLeuAsnlyr 779
 QY 2658 AGCTGCAATCTGAGCAACA 2679

QY	Db	Sequence	Score	Percent Similarity	Best Local Similarity	Query Match
QY	Db	560 uleValGlulValGluaGrMetGlucYalalathrProserxapbrysgInglYmeProVa	580	100%	100%	100%
QY	Db	2058 GTTGAGATTTTAATAATTTCTACTGTTATATAGTACAAGACAATCATCACTAGCTGTCAGTGT	2117	100%	100%	100%
QY	Db	580 lIeusereUe---AsnIlethnCysglMeetAsnlyshrllellelleglYalserValle	599	100%	100%	100%
QY	Db	2118 CAGGTGATNTGGNGATNCCACTGTAGACATTTCTGATATACCACTCTCATTTTTCACCTGAT	2177	100%	100%	100%
QY	Db	599 uSerValIeuValIserValIalAlaValIeuValIyrlYrsPheIyrPheHslEume	619	100%	100%	100%
QY	Db	2178 ACTATATGCTGAGCTGTAAAGATACAGACAGAGAGAGAAAGCATCTATAGATTTGTGAT	2237	100%	100%	100%
QY	Db	619 tIeuUeuaIaeIyCyrlleIySryrGlYArGlYglUeuaenlleIyrbapAlaPheValIl	639	100%	100%	100%
QY	Db	2238 CTACTGAGTCAGATAGAGACCTGGGTGAGAAATGAGCTGTAAAGATTTAGAGAGAG	2297	100%	100%	100%
QY	Db	639 eIySerserGlnaPrgIuMaPrtPValIArgaSncluleValIyIsaenleuGlulGl	659	100%	100%	100%
QY	Db	2298 AGTGGCCCCGCTTCACTCTGCTCTCATACAGAGACTTTATCTCGGTGATGCCATTGC	2357	100%	100%	100%
QY	Db	659 yValIProPheGlnleuCySleuHslEyrArGsbPheIleProglYValAlaIleAl	679	100%	100%	100%
QY	Db	2358 TGCCAACTCATCCAGAGAGGCTTCAACAAGCCGGAAGGTTATTTGNGATGTCTAG	2417	100%	100%	100%
QY	Db	679 aIaIasnllelleHslglUglYpHeHslYserArGlYsValIleValIalserGl	699	100%	100%	100%
QY	Db	2418 ACACCTTATTCAGAGCCGCTGTGATCTTTGAAATAGATGATGCTCAACATGAGCAGTT	2477	100%	100%	100%
QY	Db	699 nHlsPheIleGlnserArGtrPcYsllePheGlulYrGlulIeAlaGlInthrlrPglInP	719	100%	100%	100%
QY	Db	2478 TCTGAGCAGCCGCTCTGCGCATCATTTTATTTGCTCTGAGAGAGTTGAGAGTCCCTGCT	2537	100%	100%	100%
QY	Db	719 eIeuserserArGlAglYlellePheIleValIleuInIySValGlulYsrHleUe	739	100%	100%	100%
QY	Db	2538 GAGGACAGAGGTGAGATGTATGCGCTCTTAGACAGAAACCTACCTGGAATGGAGGA	2597	100%	100%	100%
QY	Db	739 uArGlInGlInValGlulPheUryrArGlueUeSerArGsbHrlyrIeugIulrPgluAs	759	100%	100%	100%
QY	Db	2598 CAATCTCTGAGGAGACACATCTTCTGAGAGAACTTAAATGCGCTTATGATGAGAA	2657	100%	100%	100%
QY	Db	759 pSerValIeuGlYrHsllePheIlePrtPArGrGlueUryrYsAlaIeUeUaPglYly	779	100%	100%	100%
QY	Db	2658 AGCCTCGAATCTTGACAAACA	2679	100%	100%	100%
QY	Db	779 sSerTrpAsnProgluGlYThr	786	100%	100%	100%
RESULT 5						
US-10-732-796A-8						
Sequence 8, Application US/10732796A						
Publication No. US20040197865A1						
GENERAL INFORMATION:						
APPLICANT: Gupta, Shalley K.						
APPLICANT: Ghosh, Taron K.						
TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines						
FILE REFERENCE: 58182US004						
CURRENT APPLICATION NUMBER: US/10/732,796A						
CURRENT FILING DATE: 2003-12-10						
NUMBER OF SEQ ID NOS: 23						
SOFTWARE: PatentIn version 3.2						
SEQ ID NO 8						
LENGTH: 799						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-10-732-796A-8						
Alignment Scores:						
Pred. No.: 1,13e-259						
Score: 2675.50						
Percent Similarity: 79.82%						
Best Local Similarity: 67.51%						
Query Match: 51.68%						
Length: 799						

DB:	16	Gaps:	3
US-09-396-985B-46 (1-2951) x US-10-732-796A-8 (1-799)			
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QY	385	CTGAGCTTCAACCCCTTGAGAGATCTTAAAAAGCTATAGCTTCTCCATTTTTCAGACTT	444
	21	LeuSerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGluLeu	40
QY	445	CAGTGGCTGGATTTATCCAGGTGGAAATTTGAACAATTTGAAGCAAGACATGCGATGCG	504
	41	GlnValLeuAspLeuSerArgCysGlnTLeGlnThrLLeGluAspGlyAlaTyLInSer	60
QY	505	TTACACCAACCTCTAAACTTATAGTACGACAGAAACCTTATCCAGAGTGTTTTCCCAAGA	564
	61	LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly	80
QY	565	AGTTTCTCTGGACTTACACAGTTTGAACAATCTGGTGGCTGTGAGACAAAATGGCTCT	624
	81	AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer	100
QY	625	CTAAGAAAGCTTCCCTATTTGACACAGCTTATACCTTTAAAGAAACCTAATGTGGCTCACAT	684
	101	LeuGlnAsnProPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn	120
QY	685	TTTATACATTCCTGTAAAGTTACCTGCAGATTTTTCACATCTGACAGAACCTTGTACATGTG	744
	121	LeuIleGlnSerPheLysLeuProGluTyPheSerAsnLeuThrAsnLeuGlnHisLeu	140
QY	745	GATCTTTCTTATTAACCTATTTCAACTATTACTGTCAACGACTTACAGTTTCTACGTGAA	804
	141	AspLeuSerSerAsnLysIleGlnSerIleTyCysThrAspLeuArgValLeuHisGln	160
QY	805	AATCCACAGTCATCTCTCTTGAACATGCTTTGAACCCCAATTGACTTCACTCAACAGC	864
	161	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro	180
QY	865	CAACCTTTTCAGGAAATTAAGCTCCATGACCTGACCTTAAAGAGGTAAATTTAATAGTCA	924
	181	GlyAlaPheLysGluTLeaArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu	200
QY	925	AATATTAATGAAAACCTGCTTCAAAACCTGGCTGGTTTACACGTCAATCGGTGATCTTG	984
	201	AsnValMetCysThrCysIleGlnGlyLeuAlaIleLysGluValHisArgLeuValLeu	220
QY	985	GGAGAAATTTAAAGATGAAGAGATCTGGAATTTTGAACCCCTTATCATGGAAGACTA	1044
	221	GlyLysIlePheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu	240
QY	1045	TGTCATGTGACCAATGATGAGTTGACGTTTAAACATATCAAAATGATTTTTCAGATGATTT	1104
	241	CysAsnLeuThrIleGlnGluPheArgLeuAlaTyxLeuAspTyxTyxLeuAspAspLe	260
QY	1105	GTTAAG--TTCCATGCTCTGGCAAGATTTTCTGCAATGTCCTCGGAGAGGTATCTATA	1161
	261	IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	280
QY	1162	AAATATCTAGAGAGTGTCTTAACATTTCAATGCGAATCTTATCATCATTAAGATGT	1221
	281	GluArgValLysAspPheSerTyxAsnPheGlyTyxGlnHisLeuGluLeuValAsnCys	300
QY	1222	CAACTAAG-CAGTTTCAACCTCGGATCTACCCCTTCTTAAAGTTTGAAGTTTAACATGATG	1280
	301	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer	320
QY	1281	AAACAAAGGCTCTATCAGTTTAAAAAAGTGCGCCCTTACCAAGTCTCACATCTTATGATCTT	1340
	321	AsnLysGlyGlyAsnAlaPheSerGlnValAlaAspLeuProSerLeuGlnPheLeuAspLeu	340
QY	1341	AGTAGAAATGACCTGAGCTTTAGTGGTGGCTGTTCTTATTTCTGATTTGGGAACAACAGC	1400

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Db      341 SerArgAnGIYLeuSerPheLYeGIYCySeSerGIInSerAerPheGIYThrThrSer 360
QY      1401 CTGAGACACTTAAGACCTTCAGCTTCAATGAGGCCATCATATGATGACCAATTTATGAGT 1460
Db      361 LeuYerTYrLeuAerPheSerPheAnGIYAlIeThrMetSerSerAerPheLeuGI 380
QY      1461 CTAGAAAGCTGACACCTGATTTTTCAGACCTTCACTTAAAGAGGACAGAAATT 1520
Db      381 LeuGIInLeuGIInuGIInleuAerP- PheGIInISeSerAnleuYSeGIInMetSerGIInPh 400
QY      1521 CTCAGCGTTCTTAATCCCTTGAAGAACTTACCTTGAACATCTTATATCAACCA 1580
Db      400 eSerValPheLeuSerLeuAerGAnleuIleTYrLeuAerPheSerHisThrHisThrAr 420
QY      1581 AATTGACTGATGATGATATTTCTTGAGTTCACAGCTTCACAACTTAATAAAGCTCG 1640
Db      420 gValAlaPheAnGIYIlePheAnGIYLeuSerSerLeuGIInValIleuYSeMetAlaGI 440
QY      1641 CAATTCTTTCAAGACAAACACCTTTCAAATGCTTTTGCAAAACAAACAACTTGACATT 1700
Db      440 YArSerPheGIInGIInuGIInPheLeuProAerPheIlePheThrGIInleuAerGAnleuThrPh 460
QY      1701 CTGGAATCTCTTAATGTCAATGTGAACAAATATCTTGAGGAGGTATTTGACACCTTCCA 1760
Db      460 eLeuAerPheSerGIInCySeGIInleuGIInleuSerProThrAlaPheAnSerLeuSe 480
QY      1761 TAGACTTCAATTAATAATAGATCAACAATCTATGTGTTTGGATTCATCCCATTA 1820
Db      480 rSerLeuGIInValIleuAnMetSerHisASAnAerPheSerLeuAerPheProTY 500
QY      1821 TAAACAGCTGATATTCCTTCAGACACTTGTATGAGCTTTCAGATGACATCATCT- 1878
Db      500 rlyCySeleuAerSerLeuGIInValIleuAerPheTYrSerleuAerHisIleMetThrSerly 520
QY      1879 -AAAGAAATCTGCAACATTTTCAAGAGCTTGAAGCTTCTTCAATCTTACAAATTC 1937
Db      520 slyGIInGIInleuGIInHisPheProSerSerLeuAlaPheLeuAnleuThrGIInAerAs 540
QY      1938 TGTGTCTGTATATGTGAACATCAAGAAATTCCTGACAGGCTGACAGAAACAGACGTT 1997
Db      540 pPheAlaCyThrCySeGIInHisGIInSerPheLeuGIInTrIleYSePheGIInAerGIInLe 560
QY      1998 CTGAGTGAATGTTGAACAATGATGATGCAACACTGTAGACATGAATGAAATCCTCTT 2057
Db      560 uLeuValGIInValIleuAerMetGIInCySeAlaIleThrProSerAerPheGIInMetProVa 580
QY      2058 GTTGGATTTTAATAATCTTACCTGTATATGTATGATCAAGCAATCATCACTGTGTCAGTGT 2117
Db      580 lLeuSerLeu---AsnIleThrCySeGIInMetAsnIleThrIleIleGIYValSerValle 599
QY      2118 CAGGTGATGTTGTGATTCACATGATGATCTTGTATATACACATCTTATTTTCACTGAT 2177
Db      599 uSerValleuValIleSerValIleAlaValleuValTYrIleYSePheTYrPheHisIleMet 619
QY      2178 ACTTATGCTGCTGTAAAGAAAGTACAGACAGAGAAAGCATCTATGATGATGATTTGTGAT 2237
Db      619 tLeuLeuAlaGIYCySeIleYSeTYrGIYArGIYGIInuAnIleTYrAerPheAlaPheValI 639
QY      2238 CTATCTGAGTCAGATGAGACTGAGTGTGAGAAATGAGCTGTGTAAGATTTTGAAGAAG 2297
Db      639 eTYrSerSerGIInAerPheIleAerPheValIleAerGAnGIInleuValIleAerGIInuGI 659
QY      2298 AGTGGCCCGCTTCACTCTGCTTCACCTACATACAGAGACTTTATCTGTGTAGACCATTC 2357
Db      659 YValProProPheGIInleuCySeleuHisTYrAerAerPheIleProGIYValAlaIleAl 679
QY      2358 TGGCAACATCATCCAGAAAGCTTCCACAGAGCGGAGGATTTGTGAGTGTAG 2417
Db      679 aAlaAnIleIleHisGIInGIInleuHisIleYSeAerTYrGIYValIleValIleValSeGI 699
QY      2418 ACACTTATTCAGAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCAACATGGCAGTT 2477

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Db      699 nHisPheIleGIInSerAerTYrPheCysIlePheGIInTYrGIInIleAlaGIInThrTrpGIInPh 719
QY      2478 TCTGAGACCGCGCTGCGACATCATCTTCAATGCTTGTGCTGAGAGGTTGAGAAATCCCTGCT 2537
Db      719 eLeuSerSerAerAlaGIYIleIlePheIleValleuGIInuValGIInuYSeThrIleuLe 739
QY      2538 GAGGACAGCAGGTGAAATTTGATGCGCTTCTTACAGAAACACCTTACCTGGAATGGAGGA 2597
Db      739 uArGIInGIInValGIInleuTYrAerTYrAerleuSerAerGAnThrTYrleuGIInuTYrGIInuAs 759
QY      2598 CAATCTCTGGGAGGACATCTTCTGAGAAACATTTAAAGCCCTATTTGATGAGAAA 2657
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Db      779 sSerTrpAerProGIInuGIYThr 786

RESULT 6
US-10-114-893-10
; Sequence 10: Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racle, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Metberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-114-893-10

Alignment Scores:
Score: 1,38e+48 Length: 661
Percent Similarity: 579.50 Matches: 185
Best Local Similarity: 47.54% Conservative: 124
Query Match: 28.46% Mismatches: 305
DB: 11.19% Indels: 37
Gaps: 16

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QY      289 TGCATAGAGGTAGTCTCTAATATTACCTTACCAATGCATGATCAAGAAACTCAGCAAGTC 348
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QY      349 CTGATGACATCTCTTCTTCAACCAAGACATAGATGTGAGCTTCAACCCCTTGAAGATC 408
Db      48 ProAerPheProAerProAerThrGIInuPheLeuGIInuPheAerPheAerPheLeuProThr 67
QY      409 TTAAGAAAGCTATAGCTTCTTCAATTTTTCAGAACTTCAAGGCTGATTTATCAAGGTGT 468
Db      68 lIleHisAerAerTYrPheSerAerGIYleuMetAsnleuThrPheleuAerPheThrArGIY 87
QY      469 GAAATTTGAACAAATTGAAGCAAGGACATGCTTACACCACTCTCAAACTTGATA 528

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Db 88 GlnleAsnTrpIleHisGluAspThrPheGlnSerHisIleGlnLeuSerThrLeuVal 107
 QY 529 CTGACAGGAACCCCTATCCAGAGTTTCCCGAGAGATTTCTGTGACTTAACAAGTTTA 588
 Db 108 LeuThrGlyAsnProLeuIlePheMetCysIleThrSerLeuAsnGlyProLysSerLeu 127
 QY 589 GACATGTGTGGCTGTGAGACAAATGGCTCTTGAAGAGCTTCCCTATTGACAG 648
 Db 128 LysHisLeuPheLeuIleGlnThrGlyLeSerAsnLeuGlnPheIleProValHisAsn 147
 QY 649 CTTATACCTTAAGAACTCAATGTGGCTCAATTTTATACATCTCTGTAAGTACT 708
 Db 148 LeuGlnSerLeuGlnSerLeuTyrlleuGlySerAsnHisIleSerSerIleLysPhePro 167
 QY 709 GCATATTTTTCATCTGACAGCTTGTACATGATGATCTTTCTTATATATATTCAA 768
 Db 168 LysAspPhePro--AlaArgAsnLeuLysValLeuAspPheGlnAsnAlaIleHis 186
 QY 769 ACTATTAATCTCAACGACTTCAAGTTTCTTACGTGAAATCCACAAATCATCTCTTTA 828
 Db 187 TyrIleSerArgGluAspMetCysSerLeuGln-----AlaIleAsnLeuSerLeu 204
 QY 829 GACATGTCTTGAACCAATGACTTCACTTAAGACCAAGCTTTGACGGAATTAAGCTC 888
 Db 205 AsnPheAsnGlyAsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPhe 224
 QY 889 CATGACGACTCTAAGAGTAAATTTTATAGCTCAATATATAGAAACTGTGCTTCAA 948
 Db 225 GlnSerLeuAsnPheGlyLysThrProAsnLeuSerValIlePheAsnGly--LeuGln 243
 QY 949 AACCTGGCTGTGTTACACGCTCATCGTGTGATCTTTGGAGAAATTAAGATGAAGAGAT 1008
 Db 244 AsnSerThr-----ThrGlnSerLeuThrPheGlnLysThrPheGlnAspIleAspAsp 260
 QY 1009 CTGGAATTTTGAACCTCTATCATGAGAGACTATGTGATGTGACCATGATGAGTTC 1068
 Db 261 GluAspIle--SerSerIleMetLeuLysGlyLeuGlyMetSerValGlnSerLeu 279
 QY 1069 AGCTTAACATATACAATGATTTTTCAGAT--GATATGTGTAAGTTCATGCTGCGC 1125
 Db 280 AsnLeu--GlnGlnHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThr 298
 QY 1126 AATGTTTCTGCAATGTCTGTGACAGTGTATCTATTAATAATCTGAAGATGTCCTTAA 1185
 Db 299 GlnLeuGlnGlnLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSerGlyMetLys 318
 QY 1186 CATT-----CAAAATGCAATCCTTATCATCAT-----TAG 1217
 Db 319 GlyLeuAsnLeuLeuLysLeuValLeuSerValAsnHisPheAspGlnLeuGlyGln 338
 QY 1218 ATGTCACTAAGAGCTTTCACACTCTGATCTACCCCTTTCTTAAAGTTTGAATCTTAACT 1277
 Db 339 IleSerIleAlaAsnPheProSerLeuThrHisLeuTyrlleArgGlyAsnValLysLys 358
 QY 1278 ATGAACAAGAGGTATATCATGTTTAAAAAGTGGCCCTACCAAGCTCAGCTATCTTAAAT 1337
 Db 359 LeuHisLeuGlyValGlyCysLeuGlnLys-----LeuGlyAsnLeuGlnThrLeuAsp 376
 QY 1338 CTTAGTAGAAATGACAGCTTGTAGTGTGGCTGTCTTATTTGATTGGAAACAAC 1397
 Db 377 LeuSerHisAsnAspIleGluAlaSerThrCysSerSerLeuGlnLeuLysAsnLeuSer 396
 QY 1398 AGCTTGAGACACTTGAAGCTCAGCTCATGTGGCAT--ATTAGAGTGGCAATTTT 1454
 Db 397 HisLeuGlnThrLeuAsnLeuSerHisAsnIleProLeuGlyLeuGlnSerGlnAlaPhe 416
 QY 1455 ATGGGTCTAGAAGAGCTGACACCTGGATTTTTCAGACACTCTTAAAAAGGTGCAC 1514
 Db 417 LysGlnCysProGlnLeuGlnLeuLeuAspLeuAla-PheThrArgLeuHisIleAsnAl 436
 QY 1515 AGAATTCGACGGTCTTATCCCTGAAAGCTTACTTGAATCTTGTATACTTAA 1574
 Db 436 AProGlnSerProPheGlnAsnLeuHisPheLeuGlnValLeuAsnLeuThrTyrlleCysPhe 456

QY 1575 CACCAAAATGACTTCGATGATATATTCTTGCTTACCGACTCAACATTAATAAAT 1634
 Db 456 eLeuAspThrSerAsnGlnHisLeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLe 476
 QY 1635 GGCTGGCAATTTCTTCAAGAACAACCTT-----TCAAATGCTTTTGCAAAACACAC 1688
 Db 476 LysGlyAsnHisPheGlnAspGlyThrIleThrLysThrAsnLeuGlnThrValGln 496
 QY 1689 AAATTTGACATCTCTGATCTCTTAAATGTCATTTGGAACAATATCTTGGGGGTATT 1748
 Db 496 YSerLeuGlnValLeuLeuLeuSerSerCysGlyLeuLeuSerIleAspGlnAlaPhe 516
 QY 1749 TGACACCCCTCATGACTTCAATTAATTAATAGTCACACAATCTTATTTG-----TT 1802
 Db 516 eHisSerLeuGlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSe 536
 QY 1803 TTGTGATTTCA--TCCCATTAATAACAGCTGTATTTCCCTGACACCTTGTATGACGTTT 1859
 Db 536 rIleAspSerLeuSerHisLeuLysGlyIleTyrlle-----LeuAsnLeuAlaI 552
 QY 1860 CAATGCAATGAGACATCTTAAAGAAATCTGCAACATTTTCCAAAGAGTCAAGCTTCTT 1919
 Db 552 aAsnSerIleAsnIleIleSerProArgLeuLeuProIleLeuSerGlnGlnSerThrI 572
 QY 1920 CAATCTTATTAACAATCTGTGCTTGTATATATGAAATCAAGAAATCTGACGTGGGT 1979
 Db 572 eAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPheLeuThrTyrl 592
 QY 1980 CAAGAAACAGAAAGAGTCTTGTGTAATGTGAACAATGACATGTGCCAACACCTGTAGA 2039
 Db 592 rLysGlnAsnLeuHisLysLeuGlnGlnLysSerGlnGlnThrThrCysAlaAsnProSe 612
 QY 2040 GATGAAT-----ACCTCCTTAGTGTGATTTTAATTAATCTTACCTGTATAT 2087
 Db 612 rLeuArgGlyValLysLeuSerAspValLysLeuSerCysGlyIleThrAlaIleGlyI 632
 QY 2088 GTACAAACAATCATGCTGTGTCAGTGTGACAGTGTGATGCTGATCCACTGAGCATT 2147
 Db 632 ePhePheLeuIleValPheLeuLeuLeuLeuAlaIleLeuLeuPheAlaValLysTy 652
 QY 2148 TCTGATATACACTTCTATTTTTCACCTG 2175
 Db 652 rLeuLeuArgTrpLysTyrlleGlnHisIle 661

RESULT 7
 US-10-038-854-134
 : Sequence 134, Application US/10038854
 : Publication No. US20040022781A1
 GENERAL INFORMATION:
 APPLICANT: Spytek, Kimberly A
 : APPLICANT: Li, Li
 : APPLICANT: Wolenc, Adam R
 : APPLICANT: Vernele, Corine
 : APPLICANT: Bisen, Andrew J
 : APPLICANT: Liu, Xiaohong
 : APPLICANT: Malysankar, Uziel M
 : APPLICANT: Shinkets, Richard A
 : APPLICANT: Tchernev, Velizar
 : APPLICANT: Spaderna, Steven K
 : APPLICANT: Gorman, Linda
 : APPLICANT: Keltuda, Ramesh
 : APPLICANT: Paturajan, Meera
 : APPLICANT: Gusev, Vladimyr Y
 : APPLICANT: Gangolli, Baha A
 : APPLICANT: Guo, Xiaojia S
 : APPLICANT: Shenoy, Suresh G
 : APPLICANT: Rastelli, Luca
 : APPLICANT: Casman, Stacie J
 : APPLICANT: Boldog, Ferenc
 : APPLICANT: Burgess, Catherine E
 : APPLICANT: Edinger, Shlomit R
 : APPLICANT: Ellerman, Karen

```

; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT FILING DATE: 2003-01-22
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 134
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-134

Alignment Scores:
Pred. No.: 1,38e-48 Length: 661
Score: 579.50 Matches: 185
Percent Similarity: 47.54% Conservative: 124
Best Local Similarity: 28.46% Mismatches: 305
Query Match: 11.19% Indels: 37
DB: Gaps: 16

US-09-396-985b-46 (1-2951) x US-10-038-854-134 (1-661)
QY 289 TGCATAGAGTAGTTCCTAATATTACCTCAATGCATGCATGACAGAACTGACGAAAGTC 348
DB 28 CysilegilyysguilaasnllythrtyrancygsluauenllyleuSerGluile 47
QY 349 CCTGATGACATTCCTTCTTCAACCAAGAAACATAGATCGAGCTTCAACCCCTTGAAAGTC 408
DB 48 ProasprhrlleuProasnthrthrGluPheleuglupheSerPheAsnPhelauProthr 67
QY 409 TTAAGAGCTAGCTTCCTCAATTTTTCAGAACTTCAAGTGGCTGAGATTTCAGAGGT 468
DB 68 lIehlsanarglthrhPheSerArgleuMetasnlthrPheleuAspLeuThrArgCys 87
QY 469 GAAATGAAACATTTGAAGACAGGATGAGATGAGCTTACACCACTTCAAACTGTGATA 528
DB 88 GlnleAentprllehlsGluAsrphrheGlnSerhshlsGlnleuSerThrleuVal 107
QY 529 CTGACAGAAACCTATCCAGAGTTTTCGCCAGGAAGTTTCTCGACTAACAAGTTTA 588
DB 108 leuhrgrglYaaenProleuilePheMetlAgluthrSerleuAsnGlyProlySerleu 127
QY 589 GACATCGTGGGTGGAGAGCAAAATTTGGCTCTAGAAAGCTTCCATTGGAGACAG 648
DB 128 LyshtleuPheleuileGlnThrGlyleSerleuAsnGluPheleProvalhlsAsn 147
QY 649 CTATTAACCTTAAAGAACTCAATGTGCTGACAAATTATATACATTCCTGTAGTTACT 708
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DB 148 leuGluAsnleuGluSerleuTyrlleuGlySerAsnshlsleSerSerleuYrphPro 167
QY 709 GCATATTTTCCAAATGACGAGACCTAGTACATGGAGTCTTTCTATACATATTCAA 768
DB 168 LysAsrPhePro--AlaArgAsnleuYvalleuAsrPheGlnAsnAsnAllehis 186
QY 769 ACTATTATCTGACACGATTCAGTTTCTACSTGAAATCCACAGATCAATCTCTTTTA 838
DB 187 TyrlleSerArgGluAsrMetArgSerleuGlnGln-----AlalleuAsnleuSerleu 204
QY 829 GACATGCTTTGAAACCAATTCATTCATTCAGACCAACCCCTTCAAGGAATTAAGTC 888
DB 205 AsnPhenAsnGlyAsnAsnVallyGlyleGlnleuGlyAlaPheAsrPheSerThrValPhe 224
QY 889 CATGACCTGACSTGACAGGATATTTTAATAGSTCAATATTAAGAAATCTGCTGCA 948
DB 225 GlnSerleuAsnPhelGlyGlyThrProAsnleuSerVallePheAsnGly--LeuGln 243
QY 949 AACCTGGCTGTTTACACSTGCATCGGTATCTGTGGAGAAATTTAAAGTGAAGAGAT 1008
DB 244 AsnSerThr-----ThrGlnSerleuThrleuGlyThrPheGlnAsrPheleAsr 260
QY 1009 CTGAAATTTTGAACCTCTATCATGAAAGACATATGTGATGACATTAATGACTTC 1068
DB 261 GlnAsrPhe--SerSerAlaMetleuYrGlyleuGlySerleuGlyMetSerValGlySerleu 279
QY 1069 AGGTAAACATATCAATATGATTTTTCAGAT---GATATGTGAAGTCCATGCTGGCG 1125
DB 280 Asnleu---GlnGluhlsArgPheSerAsrPheleSerSerThrThrPheGlnCysPheThr 298
QY 1126 AATGTTTCTGCAATGTCTGTGACAGGTGTATCTAAATATATGATGAAAGTCTTAA 1185
DB 299 GlnleuGlnleuAsnleuAsrleuThrAlaThrnlleuYrGlyleuPProserGlyMetLys 318
QY 1186 CATTT-----CAATGSCAATCTTATCATATAT-----TAG 1217
DB 319 GilyleuAsnleuYrGlyleuValleuSerValAsnshlsPheAsrGlnleuGlyGln 338
QY 1218 ATGTCAACTAAGACGTTTCCACSTGCATGATCCCTTCTTAAAGTTGAGTTTAAT 1277
DB 339 lIleSerAlaAsnPhrProSerleuThrnlleuYrTleArgGluAsnVallyGlyLys 358
QY 1278 ATGAAACAAAGGCTCTATCACTTTTAAAAAAGTGCCCTTCAACATGCTCACTATGAT 1337
DB 359 leuhtleuYrValGlyGlyleuGlnLys-----leuYrAsnleuGlnThrleuAsr 376
QY 1338 CTTAGTGAATAAGCATGACCTTATAGTGTGCTGCTCTTATGCTGATTTGGGAACAAC 1397
DB 377 leuSerhlsAsnAsrPheleGluAlaSerAsrCysSerSerleuGlnleuYrAsnleuSer 396
QY 1398 AGCTGACACATTAAGCCTCAGCTTCAATGAGTGGCATC--ATTATGAGTGGCAATTC 1454
DB 397 hlsleuGlnThrleuAsnleuSerhlsAsnGlnProleuYrleuGlnSerGlnAlaPhe 416
QY 1455 ATGGGCTGAAGAAGGCTGACGACACCTGATTTTTCAGACACTTACTTTAAAGGCTCAC 1514
DB 417 LysleuGlyAsrProGlnleuGlnleuAsrleuAla-PheThrArgleuhtlsleAsnAl 436
QY 1515 AGAATTCAGCGCTTTTATCCCTTGAAAAGCTATCTTACCTTGACATCTCTATACATA 1574
DB 436 AsrProGlnSerProPheGlnAsnleuhtlsPheleGlnValleuAsnleuThrTyGlyAsr 456
QY 1575 CACCAAAATTGACCTGATGATATTTCTTGGCTTGACCAAGTCAACATTAATAAT 1634
DB 456 eleuAsrPheSerAsnGlnhlsleuAsnAlaGlyleuPProvalleuYrhtlsleuAsnle 476
QY 1635 GAGCTGACATTTCTTCAAGAACAAACCTT-----TCAATGTCTTTCGAAACACAC 1688
DB 476 ulysGlyAsnshlsPheGlnAsrGlyThrTleThrlyThrAsnleuGlnThrValGly 496
QY 1689 AACTTGACATTCCTGAGCTCTTGAATATGCAATTTGAAACAAATATCTTGGGGGGTAT 1748
DB 496 YserleuGlnValleuileuSerSerCysGlyleuSerleuSerleuAsrGlnGlnAlaPhe 516
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Db      189 SerIyegIuaepMetSerSerLeuGInGln-----AlaThrAenLeuSerLeuAenLeu 206
Qy      835 TCCTTGAACCAATGACTTCATTCACAGACCAACGCTTCAGGAAATTAAGCTCCAGAA 894
Db      207 AenGlyAenAerIleAglYIleGlnProGlyAlaPheAerSerAlaValPheGlnSer 226
Qy      895 CTGACCTGAAGAGGTAATTTAATAGCTCAATATTAATGAAAACCTGCTCAAAACCTG 954
Db      227 Leu-----AenPheGlyGlyThrGlnAenLeuValIlePheGlyGlyLeu 242
Qy      955 GCTGGTTACACGTCATCGGTTGATCTTGAGAAATTAAGATGAAAGAAATCTGGAA 1014
Db      243 LysAenSerThrIleGlnSerLeuTrpLeuGlyThrPheGlnAerMetAspArgLysAer 262
Qy      1015 ATTTTGAACCTGATCATGGAAGAACTATGATGATGACCATGATGATGATGATGATGAT 1074
Db      263 Ile---SerProAlaValPheGlnGlyLeuGlySerValGlySerIleAenLeu 281
Qy      1075 ACATATACAAATGATTTTTCAGATGATATGTTAAGTTCCATGCTGGCGAATGTTTCT 1134
Db      282 GlnIyehIstYrPhePheAenIleSerSerAenThrPheHISCySPheserGlyLeuGln 301
Qy      1135 GCAATGCTCTGGCAGGTGATCTATAAATATCTAGAAGATGTTCTTAACATTTTC--- 1191
Db      302 GluLeuAerLeuThrAlaThr-----HisLeuSerGluLeuProSerGlyLeuVal 318
Qy      1192 -----NAATGGCAATCCTTTATCATC 1212
Db      319 GlyLeuSerThrLeuValLeuValLeuSerAlaAenLysPheGlnAenLeu----- 336
Qy      1213 ATTAGATGTCAACTAGACAG-----TTTCAACTGTGATCTACACCTTCTTAAAAAGT 1265
Db      337 -----CysGlnIleSerAlaSerAenPheProSerLeuThrHisLeuSerIleLysGly 354
Qy      1266 TTGACTTTAACTAGAACAAAGGCTATCATGATTTAAAAAGTGGCCCTCAACAAGTCTC 1335
Db      355 AenThrLysAerGlyLeuGlnLeuGlyThrGlyCysLeuGlnAen-----LeuGlnAenLeu 372
Qy      1326 AGCATCTAGATCTTAGTAGAAATGCACTGAGCTTATGAGTGGCTGTCTTATTCGAT 1385
Db      373 ArgGluLeuAerLeuSerHisAerAerPheIleGluThrSerAerCySAsnLeuGlnLeu 392
Qy      1386 TTGGGAACAACAGCCTGAGACACTTAGACCTCAAGCTCAATGGTGCATATTAGAGT 1445
Db      393 ArgAenLeuSerHisLeuGlnSerLeuAenLeuSerGlyArgGlnProLeuSerLeuLys 412
Qy      1446 GCCAAT--TTCATGGCTTAGAAGAGCTGACAGCCTGGAATTTTTCAGACCTACTTT 1502
Db      413 ThrGluAlaPheLysGlyCysProGlnLeuGlnLeuAerLeuAla-PheThrArgLe 432
Qy      1503 AAAAAGGTCACAGAAATCTCAGCGCTTTATCCTTGAAAAGTACTTACCTTGACAT 1562
Db      432 uLysValLysAerAlaGlnSerProPheGlnAenLeuHisLeuLeuLysValLeuAenLe 452
Qy      1563 CTCCTATACTAAACCAAAATTAAGCTTGATATTTCTTGCGTTCGACCAAGCTTCAA 1622
Db      452 uSerHisSerLeuAerPheIleSerSerGlnLeuPheAerGlyLeuProAlaLeuGly 472
Qy      1623 CACATTAATAATGCGTGGCAATTTTTCAAAAGACAAACCTT-----TCAATGTCTT 1676
Db      472 nHisLeuAenLeuGlnGlyAenHisAerProLysGlyAenIleGlnLysThrAenSerLe 492
Qy      1677 TGCAAAACACAAACCTTGACATTCCTTGATCCTTTAAATGCAATTTGGAACAAATTC 1736
Db      492 uGlnThrLeuGlyAerGlyLeuGlnIleLeuValLeuSerPheCySAsnLeuSerSerLeAs 512
Qy      1737 TTGGGGGGTATTTGACACCTTCATAGACTCAATATTAATTAATGATCAACAATCT 1796
Db      512 pGlnHisAlaPheThrSerLeuLysMetMetAsnHisValAerLeuSerHisAerAlaGlyLe 532
Qy      1797 ATTTGTTTTGAT-----TCAATCCATTTATAACAGCTGATTCCTCAGACACTCT 1847
Db      532 uThrSerSerSerIleGlnAlaLeuSerHisLeuLysGlyIleTy-----Le 548

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Qy      1848 TGATTCAGTTTCATTCAGTCATAGACATCTAAAGAAATCTGCAACATTTCCAAAAG 1907
Db      548 uAenLeuAlaSerAenHisIleSerIleIleLeuProSerLeuAerProIleLeuSerGly 568
Qy      1908 TCAGCCTTCTTCAATCTTATCAATCAATCTGTGTGTATATATGAAACATCAGAAAT 1967
Db      568 nGlnArgThrIleAenLeuAerGlnAenProLeuAerCySThrCysSerAenIleTyRph 588
Qy      1968 CTCGCACTGGGTCAAGAACAGAACTTCTTGGAATGTTGAAACAAATGACATGTGC 2027
Db      588 eleuGluTrpTyLysGlyLysAenMetGlnLysLeuGlnAerThrGlnAerThrLeuCySgI 608
Qy      2028 AACACCTGATGAGATGAT-----ACCTCCTTAGTGTGATTTTAATTAATTC 2075
Db      608 uAenProProLeuLeuAerGlyValAlaArgLeuSerAerAerValThrLeuSerCySserMetAl 628
Qy      2076 TACCTGTATATATGACAAACAAATCATCACTGTGTGATGATGATGATGATGATGAT 2135
Db      628 aAlaValAlaGlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePh 648
Qy      2136 CACTGTAGCATTTCTGATATACCATTCATTTTTCACCTG 2175
Db      648 eAlaValLysTyRPhLeuAerGlyTrpLysTyRglnHisIle 661

RESULT 9
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Rameesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: PatluraJan, Meera
APPLICANT: Groose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verneet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malysankar, Uriel M
APPLICANT: Kothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigattu, Muraidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060

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QY 2028 AACACCTGTAGATGAAT-----ACCTCTTAGTGTGATTTTAATATTC 2075
Db 608 uasnpProleuLeuArglyValAlaArgLeuSerAspValThrLeuSerCysSerMetAl 628
QY 2076 TACCTGTTAATATGACAAAGACATCATCAGTGTCTCATGTGTGATGATGTTGATC 2135
Db 628 aAlaValGlyrIlePhePheLeuIleValrPheLeuValrPheAlaIleLeuLeuIlePh 648
QY 2136 CACTGTAGCATTTCTGATATACCACTTCTATTTTCACCTG 2175
Db 648 eAlaValIleYrPheLeuArgrTrpYrGlnHisIle 661

RESULT 10
US-09-954-987B-192
; Sequence 192, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-987B-192

Alignment Scores:
Pred. No.: 1,99e-46 Length: 1032
Score: 559.00 Matches: 253
Percent Similarity: 38.61% Conservative: 157
Best Local Similarity: 23.82% Mismatches: 353
Query Match: 10.80% Indels: 300
DB: 10 Gaps: 42

US-09-396-985B-46 (1-2951) x US-09-954-987B-192 (1-1032)
QY 211 ATGCGTCC-----TGGCTCTGGCTAGACCTGTGATCATG-----GCA 249
Db 4 MetProGlnInsrTrpIleLeuThrCysPheCysLeuLeuSerSerglyThrSerAla 23
QY 250 CTGTTCTCTCTGCTGACACACAGAAAGCTTGATCTCTTCATAGAGTGATTCCTAAT 309
Db 24 ILePheHisIlyAlaAsnYrSerArgrSerYr---ProCysAspGlnIleArgrHisAsn 42
QY 310 -----ATTACCTTACCATGATGATGATGATGAAAGCTCAGCAAGTCCCTGATGACATTCCT 363
Db 43 SerLeuValIleAlaGlyCysAsnHisArgrGlnLeuHisIleGluValrProGlnThrIleGly 62
QY 364 TCTTCAACCAAGACATGATCTGACCTTCAACCCCTTCAAGATCTTAAAAAGCTATAGC 423
Db 63 LysrTrValrThrAsnIleAspLeuSerAspAsnAlaIleThrHisIleThrIleGluSer 82
QY 424 TTCTCCAAATTTTTCAGAACTTCAGTGCCTGATTTATCCAGGTGTGAATGAA-----477
Db 83 PheGlnYrLeuGlnAsnLeuThrIlyrIleAspLeuAsnHisAsnAlaYrGlnGlnHis 102
QY 478 -----ACATTTGAAGCAAGCATGGCATGGCTTACACAC 513
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Db 103 ProAsnGluAsnYrAsnGlyMetAsnIleThrGlnGlyAlaLeuLeuSerLeuArgrAsn 122
QY 514 CTCTCAACTGTGATCTACACAGAAACCTATTCAGAGTTTTC-----CCAGGA 564
Db 123 LeuThrValLeuLeuLeuGlnYrAspAsnGlnIleYrThrIleProAlaGlyLeuProGln 142
QY 565 AGTTTCTGAGCATACAAAGTTTACCAATCTGCGTGCCTGGAGCAAAA-----615
Db 143 SerLeuYrGlnLeuSerLeuIleGlnAsnAsnIlePheGlnValrThrYrAsnAsnThr 162
QY 616 -----TTGGCTCTCTAGAAAGCTTCCCTATTTGA-----645
Db 163 PheGlyLeuArgrAsnLeuGlnArgrLeuYrLeuGlyrTrpAsnCystrYrPheYrCysAsn 182
QY 646 -----CAGCTTATTAACCTTAAAGAACTTCAT 672
Db 183 GlnThrPheYrValrGlnArgrAlaPheYrAsnLeuIleHisIleYrValrLeuSer 202
QY 673 GTGGCTCACAAAT-----TTTATACATTCCTGTAGCTTACCTGCA-----711
Db 203 LeuSerPheAsnAsnLeuPheYrValrProProYrLeuProSerSerLeuArgrYrLeu 222
QY 711 -----711
Db 223 PheLeuSerAsnAlaYrIleMetAsnIleThrGlnGluAspPheYrGlyLeuGluAsn 242
QY 711 -----711
Db 243 LeuThrLeuLeuAspLeuSerGlyAsnCySProArgrCystrYrAsnAlaProPheProCys 262
QY 711 -----711
Db 263 ThrProCysYrGluAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY 712 -----TATTT 717
Db 283 GlnLeuLeuYrIleAsnLeuSerSerThrSerLeuArgrThrIleProSerThrTrpPhe 302
QY 718 TCCAACTGACGACCTGATGATGATGATCTTTCTTATACAT--ATTCAACATATT 774
Db 303 GluAsnLeuSerAsnLeuYrGlnLeuHisIleGlnIlePheAsnYrLeuValrGlnIle 322
QY 775 ACTGTACAGACCTTACGTTCTACGGAAGAAATCCACAGTCAATCTCTTACGATG 834
Db 323 AlaSergly-----AlaPheLeuThrYrLeuProSerLeuGlnIle---LeuAspLeu 339
QY 835 TCTTTGAACCAATGATGATTCATTCAGAACCAAGCTTTCAAGGAAATTAGTCCATGAA 894
Db 340 SerPheAsn-----PheGlnYrYrGlnYrLeuGlnIlePheIleAsnIle-----354
QY 895 CTGACTTAAGAGTAATTTTATAGCTCAAAATATATATGAAGAACTTCCTCAAAACCTG 954
Db 355 -----SerSerAsnPheSerYr-----LeuArgrSerLeu 364
QY 955 GCTGTTTACAGCCATCGCTGATCTTGAGGAATTTAAGATGAAGAAAGAAATCTGAA 1014
Db 365 LysrYrLeuHisIleuArgrGlyrTrValrPheArgrGlnLeuYrYrYrHis-----381
QY 1015 ATTTTGAACCTCTATCATCATGAGGAAGCATATGTATGTGACCATGTGAGTTCAAGTTA 1074
Db 382 ---PheGlnHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
QY 1075 ACATATACAAATGATTTTTCAGATGATATTGTTAAGTTCATGTTGCTTGCGAAATGTTTCT 1134
Db 399 AsnPheIleGlnYrIle-----AspPheYrAlaPheGlnAsnPheSerYrYrLeuAsp 416
QY 1135 GCATGTCTGTGGCAGGTGTATCTATTAATATCTGAAGAAGTGTCTTAACATTTGAAA 1194
Db 417 ValIleYrLeuSerGlyAsnArgrIleAlaSerValLeuAspGlyrThrAspYrSerSer 436
QY 1195 TGGCAATCTT-----ATC 1208
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US-10-272-502A-31

Alignment Scores:

Pred. No.:	1,996-46	Length:	1032
Score:	559.00	Matches:	253
Percent Similarity:	38.61%	Conservative:	157
Best Local Similarity:	23.82%	Mismatches:	353
Query Match:	10.80%	Indels:	300
	14	Gaps:	42

US-09-396-985B-46 (1-2951) x US-10-272-502A-31 (1-1032)

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QY 211 ATGCGTCC-----TGGCTCTGCTAGACCTGATCATG-----GCA 249
Db 4 MePrProGlnSerTrpIleuThrCySerPheCySerLeuSerSerGlyThrSerAla 23
QY 250 CTGTTCTTTCTCTGCTGACACCCAGAACTTGATCCCTGCATAGAGTATTCCTAAT 309
Db 24 IlePheHisIyValAdeNlyrSerArgSerTy---ProCySerGluIleArgHisAsn 42
QY 310 -----ATTACCTCAATGATGATGATCAGAACTCAGAAAGTCCCTGATGATTCCT 363
Db 43 SerLeuValIleAlaGluCyAsnHisArgGlnLeuHisGluValProGlnThrIleGly 62
QY 364 TCTTCAACCAAGACATAGATCTGAGCTTCAACCCCTTGAGATCTTAAAGCTATAGC 423
Db 63 LysTyValThrAsnIleAspLeuSerAspAsnAlaIleThrHisIleThrIyGluSer 82
QY 424 TTTCCCAATTTTCAAGACTTCAAGTGGCTGATTTATTCACAGTGTGAATTGAA----- 477
Db 83 PheGlnIySerGlnAsnLeuThrIyValIleAspLeuHisHisAsnAlaIySerGlnHis 102
QY 478 -----ACAATTGACCAAGCATGCGATGCGTTCACACAC 513
Db 103 ProAsnGlnAsnIyAsnGlyMeCAsnIleThrGlnGlyAlaLeuLeuSerIleuArgAsn 122
QY 514 CTCTCAACTTGTATGATGACAGAAACCTATCCAGAGTTTTC-----CCAGA 564
Db 123 LeuThrValIleLeuLeuGlnAspAsnGlnLeuTyThrIleProAlaGlyLeuProGlu 142
QY 565 AGTTTCTCTGAGCTTACAGATTAGACAACTGTGCTGCTGAGACAAA----- 615
Db 143 SerLeuIySerGlnLeuSerIleGlnAsnIlePheGlnValThrIyAsnAsnThr 162
QY 616 -----TTGGCTCTGATGAAAGCTCCCTATGGA----- 645
Db 163 PheGlyLeuArgAsnLeuGlnArgLeuTyIleuGlyTrpAsnCyTyrPheIySerAsn 182
QY 646 -----CAGCTTATACCTTAAAGAACTCAAT 672
Db 183 GlnThrPheIyValGlnAspGlyAlaPheIyAsnLeuIleHisIleLeuValLeuSer 202
QY 673 GTGGCTCACAAAT-----TTATACATTCCTGTAAGTTACCTGCA----- 711
Db 203 LeuSerPheAsnAsnLeuPheTyValProProIySerLeuProSerSerIleuArgIyLeu 222
QY 711 ----- 711
Db 223 PheLeuSerAsnAlaIyValIleMeCAsnIleThrGlnGlnAspPheIySerGlyLeuGlnAsn 242
QY 711 ----- 711
Db 243 LeuThrIleuAspLeuSerGlyAsnCySerProArgCyTyrAsnAlaProPheProCyS 262
QY 711 ----- 711
Db 263 ThrProCyIySerGlnAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY 712 -----TATTTT 717
Db 283 GlnLeuLeuTyIleuAsnLeuSerSerThrSerLeuArgThrIleProSerThrTrpPhe 302
QY 718 TCCAACTGACGAACCTAGTACATGTGAGTCTTTCTTAACTAT--ATTCAAACTATT 774

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Db 303 GlnAsnLeuSerAsnLeuIySerGlnLeuHisIleLeuGlnPheAsnIyIleuValGlnGluIle 322
QY 775 ACTGTACAACATTAACGTTTCTACAGTAAATCCCAAGTCAATGCTCTGTTAAAGATG 834
Db 323 AlaSerGly-----AlaPheLeuThrIyLeuLeuProSerLeuIleu----LeuAspLeu 339
QY 835 TCTTGAACCCCAATGATGCTTATTCAAAGCAAGCCTTTCAGAGGAATTAAGTCCATGAA 894
Db 340 SerPheAsn-----PheGlnTyIyGluGlyIleuGlnPheIleAsnIle----- 354
QY 895 CTGACTTGAAGGTAATTTTAATAGCTCAAAATGATAAGAACTTGCCCTTCAAAACCTG 954
Db 355 -----SerSerAsnPheSerIyS-----LeuArgSerLeu 364
QY 955 GCTGTTTACACGTCCATCGGTTGATCTTGAGGAATTTAAAGATGAAGAAATCTGAA 1014
Db 365 IyIyIySerHisIleuIyArgIyTyValPheArgIyIleuIySerIyIyHis----- 381
QY 1015 ATTTTGAACCCCTATCATGAGGAAGCTATGTGATGTGACCATGATGAGTTACAGGTTA 1074
Db 382 ----PheGlnHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
QY 1075 ACATATACAAATGATTTTTCAGATGATATGTTAAGTTCCATTGCGGAAATGTTTCT 1134
Db 399 AsnPheIleGluIySile-----AspPheIyAlaPheGlnAsnPheSerIySleuAsp 416
QY 1135 GCATGCTCTGGCAGGCTGATATCTATTAATATCTGAAGAGATGTCTCTAAACATTTGAA 1194
Db 417 ValIleTyIleuSerGlyAsnArgIleAlaSerValLeuAspGlyThrAspTyIySerSer 436
QY 1195 TGGCAATCCTT-----ATC 1208
Db 437 TrpArgAsnArgIleuArgIySProLeuSerThrAspAspAspGluPheAspProHisVal 456
QY 1209 AATCATTAATGTCACTAAACAGATT-----CCAAC 1241
Db 457 AsnPheTyHisSerThrIySProLeuIleIyProGlnCyThrAlaTyIyGlyVala 476
QY 1242 CTGATTTACCTTT----- 1256
Db 477 LeuAspLeuSerLeuAsnAsnIlePheIleIleGlyIySerGlnPheGlnIyPheGln 496
QY 1257 ----CTTAAAGTTTGACTTAACTATGACAAAGGCTATCATGTTTAAAAAAGTG--- 1310
Db 497 AspIleAlaCySleuAsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGlu 516
QY 1311 -----GCCCTACCAAGTCTCAGCTATCTAGATCTTATGTAAGAAATGCACTGACCTT 1364
Db 517 PheSerSerMetProHisIleIyTyIeIyLeuAspLeuThrAsnAsnArgLeuAspPheAsp 536
QY 1365 GGTGGCTGTTCTTATTTCTGATTTTGGGAACAAACAGCCTGAGACCTTACAGCTTTC 1424
Db 537 AspAsnAsnAlaPheSerIlePheLeu-----HisAspLeuGlnValIleuAspLeuSerHis 554
QY 1425 AATGTGCATCATTAATGAGTGCCAAT-----TTCATGGCTCTA 1463
Db 555 AsnAlaHisTyIyPheSerIleAlaGlyValThrHisArgIleuGlyPheIleGlnAsnLeu 574
QY 1464 GAAGAGCTGACGACCTGATTTTTCAGACCTTATTAAGGATGACAGAA----- 1518
Db 575 IleAsnLeuArgValIleuAsnLeuSer-HisAsnGlyIleTyIyThrIleuThrGlnGluSe 594
QY 1518 ----- 1518
Db 594 GlnLeuLeuSerIleSerLeuIySerGlnLeuValPheSerGlyAsnArgIleuAspHisSle 614
QY 1519 -----TTTCAGCGTTTATTCCTTGAAGAAAGCTATTTA 1553
Db 614 UTTPAsnAlaAsnAspGlyIySerTyIyTrpSerIlePheIySerLeuGlnAsnLeuIleArg 634
QY 1554 CTTGACATCTTTATATCAACACAAATGCACTTGATGTATATTTCTTGCGCTTG-- 1611

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Db      634 glenAspLeuSerTyrAsnAsnLeuGlnGlnIleProAsnGlnValAAspLeuAsnLeuPr 654
Qy      1412 -ACGAGTCTCAACATTAATAATGGCTGCAATCTCT-----TTCAAGACACACACCTT 1664
Db      654 ogLSerLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 674
Qy      1665 TTCAATATGCTTTGCAACACACACACACACACACACACACACACACACACACACACACACAC 1724
Db      674 uLeuGlnTyrPhe-----ProHISLeuHISLeuLeuAspLeuSerAAsnGlnIle 691
Qy      1725 GGAACAATATCTTTGGGGGGATTTGACACACCTCCATAGACTTCATATTAATATGAG 1784
Db      691 uTyPheLeuProAsnGlnSerLeuSerTyrPheAAsnISerLeuGlnIleLeuLeuLeu 711
Qy      1785 TCACACAACTATATGTTTGGATGATCCCATTAATACACAGCTGATTCCTCCACAGAC 1844
Db      711 rHisAsnHISpHeSerHISLeuProSerGlnPheLeuSerGlnValAAsnLeuValHIS 731
Qy      1845 TCTTGAATGACATTTCAATCCGATAGAG--ACATCTAAGAAATACTGACAAATTTTCC 1901
Db      731 sLeuAspLeuSerPheAsnHISLeuMetIleAsnLeuSerSerLeuGlnHISLeuSme 751
Qy      1902 AAAG--AGTCTACCTCTTCAATCTTAACATCTTCTGCTGTATATGACAA 1958
Db      751 tTyPheThAsnLeuSerIleLeuGlnLeuHISGlnTyPheAspCysThrCysAspIle 771
Qy      1959 TCAGAAATTCCTGACAGGCTGCAAGAACAGACAGCTC-----TTGGTCA 2006
Db      771 eSerAspPheArgSerTyrLeuAspGlnAsnLeuAsnIleThrIleProGlnLeuValAs 791
Qy      2007 TGTGGAACAATGACATCTGCAACACCTGTAGACATGATACCTCTTATGTTGATTT 2066
Db      791 nVal-----IleCysSerAsnProGlnAspGlnLeuSerSerIleMetSerIle 808
Qy      2067 TAATTAATTAACCTGTTATATGATACAGACATCATCATGCTGACAGCTGATGAT 2126
Db      808 uAspLeuThrThrCysValSerAspThrThrAlaValLeuPheLeuThrPheLe 828
Qy      2127 TGTGATATCCATGTA-----GCATTTCTGATATACAC----- 2160
Db      828 uThrThrSerMetValMetLeuAlaValLeuValHISLeuPheTyrTyrAspValTr 848
Qy      2161 -TTCTATTTTCACTG-----ATACTTATGCTGCTGTAATAAAGTACACAGAGAGA 2213
Db      848 pHeIleTyrHISMetCysSerAlaValLeuLeuGlnTyTrArgThrSerSerThrSerGln 868
Qy      2214 AAGCATCTATGATCATTTGATCTACTGACATGACAAAT-----GAGACCTGGGT 2264
Db      868 nThrPheTyrAspAlaTyrIleSerTyrAspThrTyrAspAlaSerValThrAspTrpVa 888
Qy      2265 GAGAAATGAGCTGTAAGAATTTAGAAGAGAGAGTCCCGC-----TTTCACTCTGCT 2321
Db      888 lIleAsnGlnLeuArgTyrHISLeuGlnIleGlnSerGlnAspTyrSerValLeuLeuCysLe 908
Qy      2322 TCATCAAGAGACCTTATCTGCTGATGACCAACATGCTGCAACATCCAGAGAGCTT 2381
Db      908 uGlnGlnArgAspTrpAspProGlnLeuProIleIleAspAsnLeuMetGln---SerIle 927
Qy      2382 CCACAGAGCCGAGAGGTTATTTGATGATGCTGACAACTTTATTCAGAGCCGTTGGTG 2441
Db      927 eAsnGlnSerTyrSerThrIlePheValLeuThrIleTyrSer----- 941
Qy      2442 TATCTTGAATATAGATGTCTCAACATGCGACTTTCTGAGC----- 2484
Db      942 -----AlaTySerTyrPAsnPheTyrThrAlaPheTyrIleuAlaLe 955
Qy      2485 -----AGCCGCTCTGACATCATCTTCAATCTTCTGGAAGAGTTGA 2525
Db      955 uGlnArgLeuMetAspGlnAsnMetAspValIleIlePheIleLeuLeuGlnUpProValLe 975
Qy      2526 GAAGTCCCTGCTGAGGACGAGGATGGAATTGTATCGCTTTCAGCAAAACACTTACT 2585
Db      975 uGln-----TyrSerGlnTyrLeuArgLeuArgGlnArgIleCysTyrSerSerIleLe 993

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Qy      2586 GGAATGGAGAGCAATCTCTGGGGAGCACATCTTCTGGAAGACTTAATAATGCCCT 2645
Db      993 uGlnTrpProAsnAsnProGlnAlaGlnAsnLeuPheTrpIleuSerLeuAsnValVa 1013
Qy      2646 ATTG 2649
Db      1013 lLeu 1014

RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041,70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Alignment Scores:
Pred. No.: 1,99e-46 Length: 1032
Score: 559.00 Matches: 253
Percent Similarity: 38.61% Conservative: 157
Best Local Similarity: 23.82% Mismatches: 353
Query Match: 10.80% Indels: 300
DB: Gaps: 42

US-09-396-985b-46 (1-2951) x US-10-407-952-32 (1-1032)
Qy      211 ATGCGTCCC-----TGCGTCTGCTAGAGACTTGATCATG-----GCA 249
Db      4 MetProGlnGlnSerTrpIleLeuThrCysPheCysLeuLeuSerSerGlnThrSerAla 23
Qy      250 CTGTTCTTCTCTGCTGACACACAGAGCTTGAATCCCTGCATAGAGTATTCAT 309
Db      24 lIlePheHISLysAlaAsnTyrSerArgSerTyr---ProCysAspGlnIleArgHISAsn 42
Qy      310 -----ATTACCTTACCAATGATGATGATGACAAACTGACAAAGTCCCTGATGACATTCT 363
Db      43 SerLeuValIleAlaGlnCysAsnHISArgGlnLeuHISGlnValProGlnThrIleGln 62
Qy      364 TCTTCAACCAAGACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAATAAGCTATAGC 423
Db      63 LysTyrValThrAsnIleAspLeuSerAspAsnAlaIleThrHISIleTrnLysGlnSer 82
Qy      424 TTCTCAATTTTTCAGAACTTCAAGTGCCTGATTTATCCAGGTGTGAATGAA----- 477
Db      83 PheGlnLysLeuGlnAsnLeuThrLysIleAspLeuAsnHISAsnAlaLysGlnGlnHIS 102
Qy      478 -----ACAAATTGAAGACAAAGGCAATGATGATGCTTACACAC 513
Db      103 ProAsnGlnAsnLysAsnGlnMetAsnIleThrGlnIleValAlaLeuLeuSerLeuArgAsn 122
Qy      514 CTCTCAACTTCTTACTGACAGAGAAACCTTACAGAGTTTTC-----CCAGCA 564
Db      123 LeuThrValLeuLeuLeuGlnAspAsnGlnLeuTyrThrIleProAlaGlnLeuProGln 142
Qy      565 AGTTTCTGACATCAACAACTTGAACATCTGAGTGGCTGTGAGACAA----- 615
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QY 646 -----CAGCTTATTAACCTTAAAGAACTCAAT 672
Db 183 GluThrPheLeuValGluArgGlyAlaPheLeuAsnLeuIleHisLeuValLeuSer 202
QY 673 GTGGCTCAACAT-----TTTATACATTCCGTGAAGTTACTGCA----- 711
Db 203 LeuSerPheAsnAnleuPheTyrValProPheLeuProSerSerLeuArgGlyLeu 222
QY 711 ----- 711
Db 223 PheLeuSerAnlaValIleMetAsnIleThrGlnGluAspPheLeuGlyLeuGluAsn 242
QY 711 ----- 711
Db 243 LeuThrLeuLeuAspLeuSerGlyAsnCySerProArgCySerTyrAnlaProPheProCys 262
QY 711 ----- 711
Db 263 ThrProCysArgGluAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY 712 -----TATTTT 717
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Db 303 GluAsnLeuSerAnleuLeuValGluLeuHisIleGluIlePheAsnTyrLeuValGlnGluIle 322
QY 775 ACTGTCAACGACTTAACGTTTCTACGTGAATCCAAAGTCAATCTCTCTTGAACATG 834
Db 323 AlaSerGly-----AlaPheLeuThrLeuProSerLeuGlnIle--LeuAspLeu 339
QY 835 TCTTTGAACCCATTTGACTTCATTCAGAACCAAGCCCTTTCAGGAACTTAAGCTCATGAA 894
Db 340 SerPheAsn-----PheGlnTyrLeuGluTyrLeuGlnPheIleAsnIle----- 354
QY 895 CTGACTCTAAGAGGTAAATTTAATAGCTCAAAATTAATGAAGAACTGCTTCAAAACCTG 954
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QY 955 GCTGCTTACACGTCATCGTGTATCTGTGGAGAAATTTAAAGATGAAGAAATCTGGAA 1014
Db 365 LysLeuLeuHisIleLeuArgGlyTyrValPheArgGluLeuGlyLysHis----- 381
QY 1015 ATTTTGAACCTCTATCATGAGAGACTATGTATGATGACCATTTGATGAGTTCAGGTTA 1074
Db 382 ----PheGluHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
QY 1075 ACATATACAAATGATTTTTCAGATGATATTTGTAAGTTCCATTCGCGCAATGTTTCT 1134
Db 399 AsnPheIleGluLysIle-----AspPheLysAlaPheGlnAsnPheSerLeuAsp 416
QY 1135 GCAATGTCTCTGGCAGGTGTATCTTAATAAATATCTAGAAGTGTCTTAAACATTTCAA 1194
Db 417 ValIleTyrLeuSerGlyAsnArgIleAlaSerValLeuAspGlyThrAspTyrSerSer 436
QY 1195 TGGCAATCTT----- 1208
Db 437 TyrPheAsnArgLeuArgGlyLeuProLeuSerThrAspAspAspGluPheAspProHisVal 456
QY 1209 AATCATTTAGATGTCAACTAAGCAGTTT-----CCAACCT 1241
Db 457 AsnPheTyrHisSerThrLysProLeuIleLysProGlnCysThrAlaTyrGlyLysAla 476
QY 1242 CTGAGTCAACCTTT----- 1256
Db 477 LeuAspLeuSerLeuAsnAsnIlePheIleIleGlyLysSerGlnPheGlnGlyPheGln 496

QY 1257 ----CTTAAAGTTTGACTTTAATCATGAACAAAGGCTATCATGTTTAAAGAGTG--- 1310
Db 497 AspIleAlaCysLeuAsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGlu 516
QY 1311 -----GCCCTACCAAGTCTCAGCTATCTAGATCTTTATGAAATGACATGACCTTTAGT 1364
Db 517 PheSerSerMetProHisIleLysTyrLeuAspLeuThrAsnAsnArgLeuAspPheAsp 536
QY 1365 GGTGGCGTTCTATTCATTTGATTTGGGAACAAAGCTGACACATTTAGCTCAGCTTC 1424
Db 537 AspAsnAsnAlaPheSerAspLeu-----HisAspLeuGluValLeuAspLeuSerHis 554
QY 1425 AATGTGGCATCATTAATGAGTCCAAAT-----TTCATGGGCTTA 1463
Db 555 AsnAlaHisTyrPheSerIleAlaGlyValThrHisArgLeuGlyPheIleGlnAsnLeu 574
QY 1464 GAAGAGCTGACAGACCTGATTTTTCAGCACTCTATTTAAAGGCTCACAGA----- 1518
Db 575 IleAsnLeuArgValLeuAsnLeuSer-HisAsnGlyIleTyrThrLeuThrGluGluSe 594
QY 1518 ----- 1518
Db 594 GlnLeuLysSerIleSerLeuLysGluLeuValPheSerGlyAsnArgLeuAspHisIle 614
QY 1519 -----TTCTCAGCGTTCTTATCCCTTGAAAGCTACTTTA 1553
Db 614 uTPheAnlaAsnAspGlyLysTyrTyrPheSerIlePheLysSerLeuGlnAsnLeuIleArg 634
QY 1554 CTTTGACATCTCTTAATCAACCAAAATTTGACTTCGATGTATATTCTTGCGCTTG-- 1611
Db 634 GluAspLeuSerTyrLysAsnLeuGlnGlnIleProAsnGlyAlaPheLeuAsnLeuPyr 654
QY 1612 -ACCAGTCAACACATTTAAATGCTGGCAATCTCT-----TTCAAGAACCAACCT 1664
Db 654 ogInSerLeuGlnGluLeuLeuIleSerGlyAsnLysLeuArgPheAsnThrPheIle 674
QY 1665 TTCAAATGTCTTTGCAACACAAACAACTTGACATTCCTGGATCTCTTAATGTCAATT 1724
Db 674 uLeuGlnTyrPhe-----ProHisLeuHisIleuLeuAspLeuSerArgAsnGluLe 691
QY 1725 GAAACAAATATCTTGGGGGTATTTTGACACCCCTCATGACTTCATTAATTAATGAG 1784
Db 691 uTyrPheLeuProAsnCyLeuLeuSerLysPheAlaHisIleSerLeuGlnThrLeuLeuSe 711
QY 1785 TCAACAACTATTTGTTTGTGATCATCCCATTAATTAACAGGTGATCCCTCAGCAC 1844
Db 711 ThrAsnHisPheSerHisIleuProSerGlyPheLeuSerGluAlaArgAsnLeuValHis 731
QY 1845 TCTTGATTTGAGTTTCAATGCAATAGAG--ACATCTAAAGAAATCTGCAACATTTTCC 1901
Db 731 GluAspLeuSerPheAsnThrIleLysMetIleAsnLysSerSerLeuGlnThrLysMe 751
QY 1902 AAAG--AGTCTACCTTTCTCAATCTTAAACAATCTGTGGTCTGTATATGTGAACA 1958
Db 751 ClysThrAsnLeuSerIleLeuGlnLeuHisGlyAsnTyrPheAspTyrThrCysAspIle 771
QY 1959 TCAGAATTCCTGACGTGGGTCAAGAACAGAGCAAGTTC-----TTGCTGAA 2006
Db 771 eSerAspPheArgSerTyrLeuAspArgGluAsnLeuAsnIleThrIleProLysLeuValAs 791
QY 2007 TGTTTGAACAAATGACATGTCCAAACACCTGTAGAGATGAATACCTCTTAGTGTGGATT 2066
Db 791 nVal-----IleCysSerAsnProGlyAspGlnLysSerIleMetSerIle 808
QY 2067 TAATTAATTTAATCTGTTATATGTAACAAGACATCATCATGCTGTACAGTGTCACTGTGAT 2126
Db 808 uAspLeuThrThrCysValSerAspThrThrAlaAlaValLeuPhePheLeuThrPheLe 828
QY 2127 TGTGATTCACAGTGA-----GCATTTCTGATATACAC----- 2160
Db 828 uThrThrSerMetValMetLeuValAlaLeuValHisIleuPheTyrTyrAspValItr 848
QY 2161 -TTCTATTTTCACCTG-----ATACTTATTTGCTGCTGTAAAGAAATGACAGAGAGAGA 2213

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Db      848 pHeilleTyHismetCySerAlalyLeuylsglyTyArGThrSerSerThrsGcl 868
Qy      2214 AAGCATCATGATGATTTGGATCTACTGAGTACAGAT-----GAGACTGGCT 2264
Db      868 nThpHeTyArspAlaTyrlleSerTyArspThryAspAlaSerValThraPTrpVa 888
Qy      2265 GAGAAATGAGCTGGTAAAGAAATTTAGAAGAAGAGTGGCCGAC--TTTCACTTGGCT 2321
Db      888 lIlaSngluLeuArGyThrlsleugluGluSerGluAspLysSerValleuLeuCySle 908
Qy      2222 TCACACTAGAGACTTATTTCTGTGTAGACATTCCTGCAATCATCATTCAGACCGTTG 2381
Db      908 uglUgluArGAspTrpAepProGlyLeuProIlelleAspEnleuMetGln--Ser11 927
Qy      2382 CCAGAGAGCCGGAAGGTTATTTGTGTAGTGTCTAGACACTTATTCAGACCGTTG 2441
Db      927 eAsngluSerLysThrllePheValleuThrlsLysSer11 941
Qy      2442 TATCTTGAATATGATGATTTGCTCAACATGACAGTTTCTGAGC----- 2484
Db      942 -----AlaLysSerTrpAsnPhelyThrlaPheTyrlleuAlaLe 955
Qy      2485 -----AGCCGCTGTGCAATCATCTTCAATGTCTTGAAGAGTTGA 2525
Db      955 ugluArGleuMetAspGluAsnMetAspValIlellePheIleleuGluProValle 975
Qy      2526 GAACTCCTGCTGAGCGACGCGAGTGAATTTATGCTTCTTACAGAAACACTTACT 2585
Db      975 uGln-----TySerGlnTyrlleuArGleuArGlnArGlieCyLysSerSerIlele 993
Qy      2586 GGAATGGAGAGACATCTCTGGGGAGGACATCTTGGAGAGACTTAATAATGCGCT 2645
Db      993 uGlnTrpAsnProLysProLysAlaGluAsnleuPheTrpGlnSerleuLysAsnValva 1013
Qy      2646 ATTG 2649
Db      1013 lIeu 1014

RESULT 13
US-09-954-987B-187
; Sequence 187, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-987B-187

Alignment Scores:
Pred. No.: 4,11e-45 Length: 1059
Score: 546.00 Matches: 264
Percent Similarity: 39.32% Conservative: 165
Best Local Similarity: 24.20% Mismatches: 359

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Query Match: 10.55% Indels: 304
DB: 10 Gaps: 45
US-09-396-985B-46 (1-2951) x US-09-954-987B-187 (1-1059)
Qy      162 TCGTCAATGTTCTTCATGAGCGCTCCACATGTTGAGAAATGCGAGATGATGCTCCCTG 221
Db      9 SerSerCySerleuGlyLysGluThr-LysLysGluAsn-----Me 22
Qy      222 GCTCTGCTGAGACTGCTGATCATGACATGCTTTCTC-----TCTGCTGAC 269
Db      22 tPheleuGlnSerSerMetLeuThrCyrllePheleuLeuIleSerGlySerCySgIule 42
Qy      270 ACCAGAGACTTGAAT-----CCCTGATAGAGGTAGTTCTTAAT----- 309
Db      42 uCyAlaGluGluAsnPheserArGserTyTrpCysAspGluLysLysGlnAsnAspSe 62
Qy      310 -ATTACCTACCAATGATGATGATGAGAAATCGAGAAATGCTGATGACATTCCTTCTC 368
Db      62 rValIleAlaGluCySerSerAsnArGArGleuGlnGluValProGlnThrValGlyLysTy 82
Qy      369 AACCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
Db      82 rValThrGluLeuAspLeuSerAspAsnPheIleThrHisIleThrAsnGluSerPheG1 102
Qy      429 CAATTTTCAAGACTTCAAGTGGCTGATTTATCC----- 462
Db      102 nGlyLeuGlnAsnleuThrLysIleAsnLeuAsnHisAsnProAsnValGlnHisGlnAs 122
Qy      463 -----AGGTGTGAATTTGAACATTTGAAGACAGGATGATGATGATGATGATGAT 506
Db      122 nGlyAsnProGlyLysleuSerAsnGlyLeuAsnIleThrAspGlyAlaPheleuAsnle 142
Qy      507 ACACCACTCTCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
Db      142 uLysAsnleuArGluLeuLeuLeuGluAspAsnGlnleu-----ProGln11 158
Qy      567 TTTCTGAGACTA--ACAAGTTTGAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
Db      158 eProSerGlyLeuProGluSerleuThrGluLeuSerleuIleGlnAsnIleTyAs 178
Qy      624 TCTAGAAAGCTTCCCTTATGAGACAGCTTATTAACCTTAAGAACTCAATGCTGCTCAAA 683
Db      178 nIleThrLysGluGlyLysleuArGleuIleAsnleuLysAsnleuTyrlleAlaTrpAs 198
Qy      684 T-----TTTATACATTCCTGTAATTA-----CTGCAATTTTTCATTC 725
Db      198 nCyTyTrpAsnLysValCySgIuLysThraSnIleGluAspGlyValPheGluThrle 218
Qy      726 GAGGAACCTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 785
Db      218 uThraSnleuGluLeuLeuSerleuSerPheAsnSerleuSerHisValSerProLysle 238
Qy      786 CTTACAGTTTCTACGTTGAATCCACAAGTCAATCTCTTTTGAACATGCTTTGAACCC 845
Db      238 uProSerSerleuArGlys-----leuPheLeuSerAsnThrG1 251
Qy      846 AATTGACTTATTCAGACCAAGCCTTTCAGGGA--ATTAAAGCTCATGAATGACTCT 902
Db      251 nIleTyTrpLysleuSerGluGluAspPheLysGlyLeuIleAsnleuThrleuLeuAspLe 271
Qy      903 AAGAGTAAAT-----TTTAAT----- 918
Db      271 uSerGlyAsnCySerProArGCySphesAsnAlaProPheProCySValProCySAspGlyG1 291
Qy      919 -----AGCTCAATATATGAAAACTTGCCTTCAAAACCTGCTGTTTACAC----- 966
Db      291 yAlaSerIleAsnleuAspArGpheaIaPheGlnAsnleuThrGlnleuArGyTrleuAs 311
Qy      967 -----GTCCATGCTTGAATCTTGGGAGAAATTTAAAGATTAAGAAAGAAATCT 1010
Db      311 nLeuSerSerThrSerleuArGlySleAsnAlaAlaTrpPheLysAsnMetProHisle 331

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QY 1011 GGAATTTTGA-----CCCTATCATGGAAGA----- 1041
 Db |||
 331 ulysvalleuasrleuclupheantylrleuvalglyllelaserglylaaphene 351
 QY 1042 -----CTATGTGATGACCATTTGATGATTCAGTTAACATA 1079
 Db |||
 351 uThMetleuProArgleugluilleAsrleuSerPheantyllelysglySery 371
 QY 1080 T-----ACAAATGATTTTCA----- 1095
 Db |||
 371 rProGlnHileanlleSerArganPheSerleuSerleuArgalaleuH 391
 QY 1096 -----GATGATATTGTATGATTCATTCCTT 1121
 Db |||
 391 sIeuArgglylYrValrPheGlnGluIeuArgGluAsrAsrPheGlnrProIeuMetGlnle 411
 QY 1122 GGGCAATGTTTTCGCAATGTCCTGCGAGGTATCTATTAATAATATCTAGAAATGTTCC 1181
 Db |||
 411 uProAsnleuSerThrIleAsnleuGlylleAsnPheilleysGlnlleAsp----- 428
 QY 1182 TAAACATTTGAA-----TGGCAATCCTTATCATCATCTT----- 1215
 Db |||
 429 -----PheylleuPheGlnAsnPheSerAsnleuGlnlleIeYrleuSerGluAs 446
 QY 1216 -----AGATGTCAACTAAGACAGTTTCCA 1238
 Db |||
 446 nArgIleSerProleuVallyAsrPheThrArgGlnSeryrAlaAsnSerSerPheG 466
 QY 1239 ACTCTGATC-----TA 1250
 Db |||
 466 nArgHilellyAsrArgSerThrAsrPheGlnPheAsrProHileSerAsnPheTy 486
 QY 1251 CCCTTTCTT-----AAAGTTTGACCTT 1273
 Db |||
 486 rHAsrPheThrArgProleuIlelyProGlnCyAlaAlaIeYrGlysalaleuAsrPle 506
 QY 1274 AACTATGACAA-----GGGTCTATCAGTTTAAAGATG----- 1310
 Db |||
 506 uSerleuAsnSerIlePhePheIleGlyProAsnGlnPheGlnuAsnleuProAsrIleAl 526
 QY 1311 -----GC 1312
 Db |||
 526 aCyIeuAsnleuSerAlaAsnSerAsnAlaGlnValleuSerglyThrgIupheSerAl 546
 QY 1313 CCTACCAAGTCCTAGCTATCTAGATCTTAGTAAAGACACTGAGCTTATGCTGCTG 1372
 Db |||
 546 alIePheHileVallystyIleuAsrPleuthrAsnAsnArgleuAsrPheAsnAlaSe 566
 QY 1373 TTTCTATTTCTGATTTGGAAACAACAGCTGAGACACTTAGACCTTCAATGCTGC 1432
 Db |||
 566 rAlaIeuThrGluIeu-----SerAsrPleuGluValleuAsrleuSerTyraAsnSerH 584
 QY 1433 CATCATTTATGAGTCC-----AATTTCATGGCTT 1462
 Db |||
 584 sTyrPheArgIleAlaGlyValThrHAsnleuGluPheIleGlnAsnPheThrAsnle 604
 QY 1463 AGAA-----GAGTGGACAGCCTGGATTTTTCAGCACTTAAAGGGTTCACAG 1516
 Db |||
 604 ulysValleuAsnleuSerHileAsnAsnIleTyThrIeu-ThrAsrPlystyraAsnleug 624
 QY 1517 AATTCTGAGCGTCTTATCCCTTGAAGAACTACTTTAC-----CTTGACATCT 1564
 Db |||
 624 IuSerIys-----SerleuValGluIeuValrPheSerglyAsnArgleuAsrIlel 641
 QY 1565 CTATTAACACCAAAATTTGACTTCATGGTATATTTCTTGCTTGACAGTCTCAACA 1624
 Db |||
 641 eutPAsnAsrAsrAsrAsnArgTyrlleSerIlePheIyGlyleuIyAsnleuThra 661
 QY 1625 CATTAATAAATGGCGGCAATCTTTCAAGACAACACCTTCAAAATCTTTGCAAC- 1663
 Db |||
 661 rgluIeuAsrleuSerleuAsnArgleuIys-----HsIleProAsnGlnAlaPheleuAsn 680
 QY 1684 --ACAACAACCTTGACATTCCTGATCCTTCTAATATGCATGTGGAACAATATCTTGGG 1741

Db |||
 680 eutProAlaSerleuThrGlnIleuHilelAsnAsrAsnMetleuIysrPheAsnTrp 700
 QY 1742 GGGTATTTGACACCCCTCCATACCTTCAATTTAATAATAGATCACAACAATCTATGT 1801
 Db |||
 700 hTrleuIeuGlnGlnPheProArgleuGlnIleuIeuAsrGlyAsnIlyleuIeuP 720
 QY 1802 TTTTGATTCATCCCATTTATACACGCTGATTCCTCGACACCTTGTATGAGTTTCA 1861
 Db |||
 720 heIeuThrAsrSerleuSerAsrPheThrSerSerleuAlaGlnrIleuIeuSerHile 740
 QY 1862 ATCGATA-----G 1870
 Db |||
 740 snArgIleSerHileuProSerglyPheIeuSerGluValSerSerleuIyAsnIleuA 760
 QY 1871 AGACATCTAAGAAATPCTCAACATTTCCAAAGCT----- 1908
 Db |||
 760 sPheSerSerleuIleuIyThrIleAsnIySerAlaIeuGluThrIyThrThT 780
 QY 1909 -----CTAGCCTTCAATCTTACTAACAATCTGTGTGCTTGTATGTGAACATGAGA 1963
 Db |||
 780 hTrlyIeuSerMetleuGluIleuHileGlyAsnProPheGluCyThrCyAsrIleGlyA 800
 QY 1964 AATTCTGCACTGAGTCAAGAAACAGAGCACTTCTGTGAATGTTGAA----- 2013
 Db |||
 800 sPheAsrArgTrpMetAsrGluHile-----LeuAsnVallyIleProArgl 816
 QY 2014 -----CAATGACATGTGCAACACCTGTAGAGATGAATACCTCTTATAGTGTGATTTA 2068
 Db |||
 816 euValAsrValIleCyAlaIeSerProGlyAsrIuArgIyIySerIleValSerleug 836
 QY 2069 ATAACTCTACTGTGTATGTATGATACAGACATCTACAGTGTGTCAGTGTGATTTG 2128
 Db |||
 836 IuIeuThrThrCyValSerAsrValThrAlaValIleIeuPhePheThrPhePheI 856
 QY 2129 TGGTATCCACTGA-----GCATTTCTGATATACCACTTATTTTAC----- 2172
 Db |||
 856 leThrIleMetValMetleuAlaIleuAlAsnIleuPheTyTrpAsrValTrp 876
 QY 2173 -----CTATACTTTATGCTGCTGTAAAGATACAGACAGACAGAAA 2215
 Db |||
 876 heIleTyraAsnValCyIleuAlaIyIlelysglyTyraSerleuSerThrSerIeTrp 896
 QY 2216 GCATCTATGATGATTTGTGATGATCACTGAGTCAAGAT-----GAGACACTGGTGA 2266
 Db |||
 896 hTrPheTyraPAlaIyrlleSerTyraPThrIyAsrPAlaIeSerValThrAsrTrpVal 916
 QY 2267 GAAATGAGCTGTAAAGAAATTTAGAAAGAGAGTGGCCGC-----TTTACCTGTGCTTC 2323
 Db |||
 916 IeAsnGluIeuArgTyHileuGlnIuSerIyAsrIyAsnValleuIeuCyIeuG 936
 QY 2324 ACTACAGACCTTATTTCTGCTGTAGCCATTCCTGTCACATCATCCAGAAAGCTTCC 2383
 Db |||
 936 IuGluIyAsrTrpAsrProGlyIleuAlaIleIleAsrAsnIleuMetGln---SerIleA 955
 QY 2384 ACAAGACCGGAAGTATTTGTGTAGTGTCTAGACACTTATTTACAGACCGTGTGTA 2443
 Db |||
 955 enGlnSerIyIyIyThrValrPheValleuThrIyIyIyTy 968
 QY 2444 TCTTTGAATATGAGATTGCTCAACATGAGCTTCTGAC----- 2484
 Db |||
 969 -----AlaIySerTrpAsnPheIyThrAlaPheTyIleuAlaIeuG 983
 QY 2485 -----AGCCGCTGTGGCATCATCTTCAATTTGTCCTTGAAGAGTTTGA 2527
 Db |||
 983 IuArgleuMetAsrGluAsnMetAsrValIleIlePheIleIeuGlnProValIeuG 1003
 QY 2528 AGTCCCTGCTGAGACAGCAGGTGAATGTATAGCCTTTAGACAGAAACACCTGCG 2587
 Db |||
 1003 IuHile-----SergIuTyIleuArgleuArgGlnArgIleCyIyIySerSerIleuG 1021
 QY 2588 AATGGAGAGCAATCTCTGTGGAGGAGGACATCTTCTGAGAGAACTTAAATGCTCTAT 2647
 Db |||


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Qy 1311 -----GC 1312
Db 526 aCysLeuAsnLeuSerLysAsnSerAsnAlaGlnValLeuSerGlyThrGluPheSerAl 546
Qy 1313 CCAACCAAGCTCAGCTATCTAGATCTTGAAGAAATGCACTGAGCTTTAGTGGTGCCTG 1372
Db 546 aAlleProHisValLysThrLeuAspLeuThrAsnAsnArgLeuAspPheAsnAlaase 566
Qy 1373 TTTCTATTCTGGGAAACAAACGCTGAGACACTTGAAGCTTCGCTTCAATGGTGC 1432
Db 566 rAlaLeuThrGluLeu-----SerAspLeuGluValLeuAspLeuSerGlyAsnSerHis 584
Qy 1433 CACCATATGAGTGC-----AATTCAATGGCT 1462
Db 584 sTyrPheArgLleAlaGlyValThrHisLeuGluPheLleGlnAsnPheThrAsnLe 604
Qy 1463 AGAA-----GAGCTGAGACACTGATTTTTCAGACCTTACTTAAAAAGGCTCAG 1516
Db 604 ulysValLeuAsnLeuSerHisAsnAsnLleTyrThrLeu-ThrAspLysTyrAsnLeuG 624
Qy 1517 AATTCTGAGCTTTATTCCTTGAAGAGCTACTTAC-----CTTGACATCT 1564
Db 624 lAsnLys-----SerLeuValGluLeuValPheSerGlyAsnArgLeuAspLleL 641
Qy 1565 CTATATACACCAAAATGACCTGATGCTATATTTCTTGGCTGACAGCTTCAACA 1624
Db 641 eutTrAsnAspAspAspAsnArgTyrLleSerLlePheLysGlyLeuLysAsnLeuThra 661
Qy 1625 CATTAATAATGGCTGGCAATCTTTCAAGACACACCTTTCAATGCTTTTGAAC- 1683
Db 661 rGluLeuAspLeuSerLeuAsnArgLeuLys--HisLleProAsnGluAlaPheLeuAsnL 680
Qy 1684 --ACAAACAATCTGACATCTCTGATCTCTTAATATGCAATGGAACAATATCTGGG 1741
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Qy 1742 GGGTATTGACACCTCAGCTCAATGATTAATTAATGAGCACACAATATATTTGT 1801
Db 700 hTrLeuLeuGlnGlnPheProArgLeuGluLysLeuLeuAspLeuArgGlyAsnLysLeuEur 720
Qy 1802 TTTTGAATTCATCCCATTAATACAGCTATATCTCTGACAGCTTGTGATGCAATTCA 1861
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Qy 1862 ATGGCAAA-----G 1870
Db 740 snArgLleSerHisLeuProSerGlyPheLeuSerGluValSerSerLeuLysHisLeuA 760
Qy 1871 AGACATCTAAAGAAATCTGCAACATTTTCCAAAGAGT----- 1908
Db 760 sPLeuSerSerAsnLeuLysThrLleAsnLysSerAlaLeuGluThrLysThrTrt 780
Qy 1909 -----CTAGCCTTCTTCACTTACTTAACAATCTGTGTGTTATATGTAACATCAGA 1963
Db 780 hTrLysLeuSerMetLeuGluLeuHisGlyAsnProPheGluCytThrCysAspLleGlyA 800
Qy 1964 AATTCTGCACTGGCTCAAGACAAAGACAGTTCTTGTAAGTTGAA----- 2013
Db 800 sPLeuAspArgTrpMetAspGluHis-----LeuAsnValLysLleProArgL 816
Qy 2014 -----CAATGACATGTGCACTGTGAGATGAAATACCTCTTATGTTGATTTTA 2068
Db 816 euValAspValLleLysValaSerProGlyAspGlnArgLysSerLleValSerLeuG 836
Qy 2069 ATAATCTACCTGTATATGTACAAGCAATCATCAGTGTGTCAGTGTGATGATTTG 2128
Db 836 luleuThrThrCysValSerAspValThrAlaValLleLeuPhePheThrPhePheI 856
Qy 2129 TGGTATCCACTGTA-----GCATTTCTGATATACACTTTATTTTTCAC----- 2172
Db 856 lethrThrMetValMetLeuAlaAlaLeuAlaHisLysLeuPheTyrTrpAspValTrp 876

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Qy 2173 -----CTGATCTATTATTCCTGCTGTAAAGTAACAGCAGAGAGAA 2215
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Qy 2216 GCATCTATGATGCAATTGTGATCTACTCGAGTCAGAAAT-----GAGGATGGGTGA 2266
Db 896 hPheTyrAspAlaTyrLleSerTyrAspThrLysAspAlaSerValThrAspTrpVal 916
Qy 2267 GAAATGAGCTGGTAAAGAAATTTAGAAAGAGAGACTGCCCGC-----TTTCACTCTGCTTC 2323
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Qy 2324 ACTACAGAGACTTAAATCTGTGTGAGCCATTCCTGCAACATCATCCAGAAAGCTTCC 2383
Db 936 lueGluArgAspTrpAspProGlyLeuAlaLleLleAsnLeuMetGln--SerLleA 955
Qy 2384 ACAAGAGCCGGAAGTTATTTGTGTAGTGTCTAGACACTTATTCAGAGCCGTTGGTGA 2443
Db 955 snGlnSerLysLysThrValPheValLeuThrLysLysTyr----- 968
Qy 2444 TCTTGAATATGAGATTGCTCAAAACATGCGAGTTTCGAGC----- 2484
Db 969 -----AlaLysSerTrpAsnPheLysThrAlaPheTyrLeuAlaLeuG 983
Qy 2485 -----AGCCGCTGCGCATCATCTTCAATGTCTTGAAGAGTTGAGA 2527
Db 983 lAspGluMetAspArgLysAsnMetAspValLleLlePheLleLeuGluProValLeuG 1003
Qy 2528 AGTCCCTGCTGAGCGACAGCTGGAATTTATGCTCTTTCAGACAAACACTTACTGG 2587
Db 1003 lHis-----SerGlnTyrLeuArgLeuArgLysGlnArgLysSerSerLleLeuG 1021
Qy 2588 AATGGAGAGCAATCTCTGCGGAGAGGACACTTTTCGAGACAACTTAAATAGCCCTAT 2647
Db 1021 lAspProAspAspProLysAlaGluGlyLeuPheTrpGlnThrLeuArgAsnValVal 1041
Qy 2648 TG-----GATGAAAAGCCTCGAAT 2667
Db 1041 eutThrGluAsnAspSerArgTyrAsnAsn 1050

RESULT 15
US-10-753-267-30
Sequence 30, Application US/10753267
Publication No. US20050037946A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Scagliano, Nancy E.
APPLICANT: Healy, Aileen
APPLICANT: Acton, Susan L.
APPLICANT: Galvin, Katherine M.
APPLICANT: Donoghue, Mary A.
APPLICANT: Rodriguez-Way, Amelie
APPLICANT: Tomlinson, James E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
TITLE OF INVENTION: 10653, 9255, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
TITLE OF INVENTION: 1468, 12822, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 9955,
TITLE OF INVENTION: 23345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
TITLE OF INVENTION: 42028, 110291, 13886, 13942, 1673, 54946 OR 2419
FILE REFERENCE: MP103-003P1NOMINIM
CURRENT APPLICATION NUMBER: US/10/753, 267
CURRENT FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US 60/439, 683
PRIOR FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/445, 216
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/448, 036
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/454, 189
PRIOR FILING DATE: 2003-03-12

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PRIOR APPLICATION NUMBER: US 60/457,541
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/466,411
PRIOR FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/469,041
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/477,414
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: US 60/478,560
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/489,772
PRIOR FILING DATE: 2003-07-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1059
TYPE: PR1
ORGANISM: Homo Sapiens
US-10-753-267-30

Alignment Scores:
Pred. No.: 4,11e-45 Length: 1059
Score: 546.00 Matches: 264
Percent Similarity: 39.32% Conservative: 165
Best Local Similarity: 24.20% Mismatches: 359
Query Match: 10.55% Indels: 304
DB: 17 Gaps: 45

US-09-396-985b-46 (1-2951) x US-10-753-267-30 (1-1059)
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DB 9 SererCyserLeuGlyLysGluThr-LysLysGluAsn-----Me 22
QY 222 GCTCTGCTGAGTCACTGATCATGAGCATGCTTCTTC-----TCCTGCTGAC 269
DB 22 tPhleuclnserSerMetLeuThrCyrllePhleuclnleuSerGlyserCyrglule 42
QY 270 ACCGAGAACTTGAT-----CCCTGCTAGAGTGAAGTTCCTAAT----- 309
DB 42 uCyalaGluGluAsnPheserArGserTyProCysAspGluLysGlnAsnAspSe 62
QY 310 -ATTACCTACCAATGATGATGATGAAATCGAGAAATGCGTATGATGATTCCTTCTC 368
DB 62 rValilleaGluCyserAsnArgArgLysGlnGlnValProGlnThrValGlyLysTy 82
QY 369 AACCAAGAACATAGATGATGATGATCAACCCCTGGAAGATCTTAAAGACTATAGCTTCTC 428
DB 82 rValilleaGluLeuAspLeuSerAspAsnPhelileThrileThrAsnGluSerPheG 102
QY 429 CAATTTTTCAGACTTCAGTGGCTGATTAATCC----- 462
DB 102 nGlyleuGlnAsnLeuThrLysLleAsnLeuAsnHleAsnProAsnValGlnHleGlnAs 122
QY 463 -----AGCTGTGAATTTGAACAATTTGAACAATGCAAGCATGCGATGCTT 506
DB 122 nGlyAsnProGlyLleGlnSerAsnGlyLeuAsnHleThrAspGlyAlaPhleuAsnLe 142
QY 507 AACACCCCTCTCAATGATGATGATGAGAAACCTTACAGAGTTTTCCTCCAGAGAG 566
DB 142 uLysAsnLeuArgGluLeuLeuLeuGlnAspAsnGlnLeu-----ProGlnH 158
QY 567 TTTCTCTGAGTA--ACAAGTTTAGACAATCTGCTGCTGCTGAGACAAATTTGGCTC 623
DB 158 eProSerGlyLeuProGlnSerLeuThrGluLeuSerLeuHleGlnAsnAsnHleTyAs 178
QY 624 TCTGAAGAAGCTCCCTATTGAGACAGCTTATACTTAAAGAACTCAATGCTGCTCACA 683
DB 178 nileThrLysGlnGlyLleSerArgLeuLleAsnLeuLysAsnLeuTyLeuAlaTyPAs 198
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GenCore version 5.1.6
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

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2	3903.5	11.8	799	14	US-10-128-166-7	Sequence 7, Appli
3	3903.5	11.8	799	16	US-10-732-563-8	Sequence 8, Appli
4	3903.5	11.8	799	16	US-10-732-796A-8	Sequence 8, Appli
5	3903.5	11.8	799	16	US-10-732-796A-8	Sequence 26, Appli
6	563.5	1.7	661	15	US-10-038-854-135	Sequence 135, App
7	563.5	1.7	661	15	US-10-037-417-107	Sequence 107, App
8	561.5	1.7	784	10	US-09-950-041-4	Sequence 4, Appli
9	561.5	1.7	784	15	US-10-456-947-46	Sequence 46, Appli
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ALIGNMENTS

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; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950, 041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

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; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

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RESULT 2

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 ; Publication No. US20030077279A1
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 ; APPLICANT: ARDITI, MOSHE
 ; APPLICANT: RAJAVASHISTH, TRIPATHI
 ; APPLICANT: SHAH, PREMIDAN K.
 ; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
 ; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
 ; FILE REFERENCE: 81476-0255398
 ; CURRENT APPLICATION NUMBER: US/10/128,166
 ; CURRENT FILING DATE: 2002-04-23
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 799
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-128-166-7

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 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
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 DB 131 PheSerAsnleuThrAsnleuGlnHieIleuAspLeuSerSerAsnlysaIleGlnSerIle 150
 QY 12549 TATTGCACAGCTGGGGGTCTTACATCAAAATGCCCTTACTCAATCTCTCTTGAACCTG 12608
 DB 151 TyCysThrAspLeuAspValleuHieGlnMeCProleuAsnleuSerleuAspLeu 170
 QY 12609 TCCCTGAACCTTATGAATTTATGCAACAGGTGCATTTAAGAAATTAAGGCTTCATPAG 12668
 DB 171 SerleuAsnProleuAsnPheIleGlnProGlyAlaPheIlysaGlnIleArgleuHieIly 190
 QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAAATGTAAGAACTTGTATTCAAGTCTG 12728
 DB 191 LeuThrleuArgAsnAsnPheAspSerleuAsnValMeCysThrCysIleGlnlyleu 210
 QY 12729 GCTGCTTTAAGATTCCTCGTTGGTCTGGAGAAATTTAGAAATGAAGAACTTGGAA 12788
 DB 211 AlaGlyleuGlnValHieArgleuValleuGlyGlnPheArgAsnGlnlysaIleGln 230
 QY 12789 AAGTTTGAACAATGCTCTAGAGAGGCTGGCAATTTGACCATTAAGAAATTCGATTA 12848
 DB 231 LysPheAspLysSerAlaIleGlnlyleuCyAsnleuThrIleGlnlysaArgleu 250
 QY 12849 GCATCTTAGACTACTACCTCGATGATATTAATGACTTAATTTAATGTTTGAACAATGTT 12908
 DB 251 AlaTyLeuAspTyTyTyLeuAspAspIleIleAspLeuPheAsnCysleuThrAsnVal 270
 QY 12909 TCTTCATTTTCCCTGGAGTGTGACTATTTGAAGAGGTAAGACTTTTCTTAATATTC 12968
 DB 271 SerSerPheSerleuValSerValThrIleGlnlysaPheSerTyAsnPhe 290
 QY 12969 GGAATGCAATTTAAGATTAATTAATTAATTAATTTGAAGAGGTAAGACTTTTCTTAATATTC 13028
 DB 291 GlyTyPheGlnHieIleuGlnleuValAsnCysIlyPheGlyGlnPheProIleuIlyleu 310
 QY 13029 AAATCTCTCAAAAGGCTTACTTCACTTCACTCAAAAGGTGGGAATGCTTTTCAAGATT 13088
 DB 311 LysSerleuLysArgleuThrPheThrSerAsnlysaGlyGlnAlaPheSerGluVal 330
 QY 13089 GATCTCAACAGCTTGATTTCTAGATCTCAGTGAAGAAATGGCTTGAGTTCAAGATTGC 13148
 DB 331 AspLeuProSerleuGlnPheLeuAspLeuSerArgAsnIlyleuSerPheIlyGlyCys 350
 QY 13149 TGTTTCAAGATTAATTTGGGAGACACAGCCTAAGATTTAGTCTGAGGTTCAATGGT 13208
 DB 351 CysSerGlnSerAspPheGlyHieThrSerleuLysTyTyLeuAspLeuSerPheAsnGly 370
 QY 13209 GTTATTACATGATTCAACTTCTGGGCTTGAACAACTAGAACATCTGATTTCCAG 13268
 DB 371 ValIleThrMetSerSerAsnPheleuGlyleuGlnGlnleuGlnHieIleuAspPheGln 390
 QY 13269 CATTCCAATTTGAACAATAGAGTGTTCAGTATTCCTATCACTCAGAAACCTCAAT 13328
 DB 391 HieSerAsnleuLysGlnMetSerGlnPheSerValPheleuSerleuArgAsnleuIle 410
 QY 13329 TACCTGACATTTCTACTACTCAGACAGAGTGTTCATGAGCACTTCAATGGCTTG 13388
 DB 411 TyTyLeuAspLysSerHieThrHieThrArgValAlaPheAsnGlyIlePheAsnGlyleu 430
 QY 13389 TCCAGTCTCGAAGCTTTGAATAGGCTGAGCAATTTCTTCCAGAAAACTTCCCTTCAGAT 13448

Db 431 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheProAsp 450
QY 13449 ATCTTCACAGAGCTGAGAAACCTTGAACCTTCTGACCTCTGATGTCACCTGAGACAG 13508
Db 451 IlePheThrGluLeuAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
QY 13509 TTGTCTCCACAGCATTTAATCTCACTCTCCAGTCTTCAAGTACTTAATATGAGCACAC 13568
Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTCATTTGATGATGATGCTTCTTAATGATGTCGAACTCTCCAGGTTCTTGAT 13628
Db 491 AsnPheSerSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCATGACATTAATGACTTCCAAAACAGAGACATGACGACTTTTCCAGAGT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTAACTGACAAATGACTTTGCTGACTTGTGAACACAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
QY 13749 CTGCAATGATCAAGACACAGAGGACCTCTTGAGTGAAGTTGAACGAATGGAATGTGCA 13808
Db 551 LeuGlnThrLysAspGlnAspGlnLeuValGlnValGlnAspMetGlnCysAla 570
QY 13809 ACACCTTCAGATTAAGCAGGCGATGCTGTGTGCTGAGTTGAATATCAGCTGTGACATGAAT 13868
Db 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnHisIleThrCysGlnMetAsn 590
QY 13869 AAGACATCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13928
Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 610
QY 13929 GTCTAATAGTTCTATTTTCACTGATGCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13988
Db 611 ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlnLysGly 630
QY 13989 GAAACATCTATGATGCTTTTGTATCTATCTCAAGCCAGATGAGAGTGGGTAAAGAAAT 14048
Db 631 GluAsnHisLysAspAlaPheValIleTyrSerSerGlnAspGlnAspThrValAlaAsn 650
QY 14049 GAGCTAATAAAGATTAAGAAAGAGGAGCTCTCATTTGACCTGCTGCTGCTGCTGCTGCTG 14108
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QY 14109 GACTTATTCCTCGGTGTGGCCATGTGCTCCAAATCATTCATGAAGTTTCCATAAAGC 14168
Db 671 AspPheIleProGlyValAlaIleAlaAlaAsnHisIleHisGlnGlyPheHisLysSer 690
QY 14169 CGAAGGTGATGT 14228
Db 691 ArgLysValIleValValValSerGlnHisPheHisGlnSerAspGlyProCysIlePheGln 710
QY 14229 TATGAGATTTGCTGACCTGACATTTCTGAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14288
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QY 14289 CTGCAAGGTGAGAAAGACCTGCTCAAGCAGCAGGCTGAGAGTGAACCGCTTCTGACG 14348
Db 731 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGlnLeuValArgLeuLeuSer 750
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Db 751 ArgAsnHisTyrLeuGlnTyrGlnAspSerValLeuGlyArgHisIlePheThrArgArg 770
QY 14409 CTGCAAAAAGCCCTGAGAGTGAATCATGAATCAGAAAGAAACAGGTGGTACAGGA 14468
Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerThrAsnProGlnGlnValGlnValGlnGly 790
QY 14469 TGCATTTGGCAGAGCAACATCTATC 14495
Db 791 CysAsnThrProGlnGlnAlaThrSerIle 799

RESULT 3
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Pink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 16 Gaps: 1
US-09-396-985b-47 (1-18989) x US-10-732-563-8 (1-799)
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QY 12249 CAGACATTTGAAGATGGGGCATATCAGAGCCTTAAGCCACTCTTCACTTAATATGACA 12308
Db 51 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisIleuSerThrLeuIleLeuThr 70
QY 12309 GAAACCCCATCCAGAGTTTGAAGCCCTGGAGCCCTTTTCTGACTATATGAATTAACAGAG 12368
Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 90
QY 12369 CTGTGGCTGTGGAGCAAACTTACGATCTTACAGAACTTCCCAATTTGACATTTGACA 12428
Db 91 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlnHisLeuLys 110
QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTAAGTAT 12488
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QY 12489 TTTTCTAATGTACCAATCTAGAGCACTTGAACCTTTCCAGCAAAAGATTCAAAGTAT 12548
Db 131 PheSerAsnLeuThrAsnLeuGlnHisIleuAspLeuSerSerAsnLysIleGlnSerIle 150
QY 12549 TATTTGACAGACTTGGGGTTCATCAATGCAATGCCCTACTCAATCTCTTTAGACCTG 12608
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QY 12609 TCCCTGAACCTTGAACCTTATATCAACACAGTGCATTTAAAGAAATTAAGCTTCATAG 12668
Db 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGlnIleArgLeuHisLys 190
QY 12669 CTGACTTAAGAAATAATTTGATGATTAATGTAATGAATACTTGATTTCAAAGTCTG 12728
Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetCysThrCysIleGlnGlyLeu 210
QY 12729 GCTGCTTTAAGTCCATCGTTTGTCTTGGGAAATTTGAATGAAGAACTTGGA 12788
Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnGlyAsnLeuGln 230
QY 12789 AAGTTTGAACAAATCTGCTAGAGGCGCTGCAATTTGAACATTTGAAGATTTCCGATTA 12848

Db 231 LysBheAspLysSerAlaLeuGluGlyLeuCyAsnLeuThrIleGluGluPheArgLeu 250
 QY 12849 GCATCTAGACTACTACCTCGATGATATATATGATTTATTTGTTGACAAAGTT 12308
 Db 251 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnCyLeuThrAsnAla 270
 QY 12909 TCTTCATTTTCCCTGAGTGTGATCTATTTGAAAGGTAAGAAAGCTTTCTTATATTTTC 12968
 Db 271 SerSerPheSerLeuValSerValThrIleGluArgVallySerPheSerTyrAsnPhe 290
 QY 12969 GGATGGCAACATTTAGATTAGTTAACTGTAATTTGGACAGTTTCCCACTTGAACATC 13028
 Db 291 GlyTyrGlnIleuGluLeuValAsnCyLysPheGlyGlnPheProThrLeuLysLeu 310
 QY 13029 AAATCTCAAAAGGCTTACTCTTCACTTCCAAAGGTGGAGTTCCTTTTTCAGAGTT 13088
 Db 311 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyLysAlaAlaPheSerGluVal 330
 QY 13089 GATCTACCAAGCTTGAATTTCTAGATCTCAGTAAATGGCTTGAATTTCAAGTTGC 13148
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 QY 13149 TGTTCCTCAAGTGAATTTTGGACACCAAGCTTAAAGTATTTAGATCTGAGCTTCAATGCT 13208
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 QY 13209 GTTATTCACATGATGTAATTTCTTGGGCTTAGAACCAAGTTCAGTTCGATTTCCAG 13268
 Db 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHISLeuAspPheGln 390
 QY 13269 CATTCATTTTGAACAAATGAGTGAATTTTCAATTTCTATGACTCAGAAACCTCAT 13328
 Db 391 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAspAsnLeuIle 410
 QY 13329 TACCTGACATTTTCTCATPACTCACAACAAGTCTCTTCAATGAGCATTTCAATGCTTG 13388
 Db 411 TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
 QY 13389 TCCAGTCTCGAAGCTTGAATAATGGCTGGCAATTTTCCAGGAAATCTTCTCCAGAT 13448
 Db 431 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 450
 QY 13449 ATCTTCACAGAGCTGAGAAATCTGACCTTCTGAGACCTCTCTCAGTGTCACTGAGACG 13508
 Db 451 IleHeThrIleGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
 QY 13509 TTGTCTCCAAACAGATTAACTCACTCTCCAGTCTTCAAGTACTAAATATGAGCCACAC 13568
 Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
 QY 13569 AACTTCTTTTCAATGATGATCTTCTTATTAAGTGTGAACTCCCTCCAGGTTCTTGAT 13628
 Db 491 AsnPheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 510
 QY 13629 TACAGTCTCAATCATATATGACTTCCAAAAAACAAGAACTACAGCAATTTCCAAAGTGT 13688
 Db 511 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 530
 QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTTCCTTGTACTTGTGAACACAGAGTTTC 13748
 Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
 QY 13749 CTGCAATGATTCAGAGACCAAGGACACTCTTGGTGAAGTGAACGAATGGAATGTGCA 13808
 Db 551 LeuGlnIleTyrLeuAspGlnArgGlnLeuLeuValGlnValGluArgMetGlnCysAla 570
 QY 13809 ACACTTCAGATTAAGCAGGAGCATCTGTGCTGATTTGAATATCACCTGTCAATGAAT 13868
 Db 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
 QY 13869 AAGACATCATGCTGTGTGCTGCTCTCAAGTGTGCTTGTAGTATGTTGTGACAGTTCTG 13928
 Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeu 610

QY 13929 GTCTATAGTTCTCATTTTCACTGATGCTTCTGCTGGCTGCATAAAGTATGTAGAGGT 13988
 Db 611 ValTyrLysPheTyrPheHisLysMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
 QY 13989 GAAACATCATAGATGCTTGTATTTACTCAAGCCAGATGAGACTGGGTAAAGAAAT 14048
 Db 631 GluLeuIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTrpValArgAsn 650
 QY 14049 GAGCTAGTAAAGATTTTGAAGAAAGGGGTGCTTCATTTTCAAGCTTGTGCTTCACTACGA 14108
 Db 651 GluLeuValLysAsnLeuGluGlnGlyValProProPheGlnLeuCyLeuHisLysTyrArg 670
 QY 14109 GACTTATTCCTCCGGTGTGGCAATTTGCTGCCAATCATCCATGAAGGTTTCCATAAAGC 14168
 Db 671 AspPheIleProGlyValAlaIleAlaIleAsnIleHisGlnGlyPheHisLysSer 690
 QY 14169 CGAAGGTGATTTGTGTGTGTCCACAGCACTTCATCCAGACCGCTGGTGTATCTTGA 14228
 Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 710
 QY 14229 TATGAGATTTGCTCAGACCTGGCAGTTTCTGACAGTGTGTGTGTATCATTTTCAATGTC 14288
 Db 711 TyrGlnIleAlaGlnIleThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
 QY 14289 CTGCAGAAAGGTGAGAAAGACCTTGTCTCAGGACAGGAGGTGAGTGTACCCGCTCTCAGC 14348
 Db 731 LeuGlnLysValGluLysTrpIleLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 750
 QY 14349 AGGAACACTTACCTGAGTGGAGAGACAGTGTCTCTGGGGCGGCACATTTCTGAGACGA 14408
 Db 751 ArgAsnThrTyrLeuGluTrpGluAspSerValLeuGlyArgHisIlePheTrpArgArg 770
 QY 14409 CTCAGAAAGCCTGCTGTGATGCTTAATCATGCAATCAGAAAGAAACAGTGGGTACAGGA 14468
 Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGly 790
 QY 14469 TGCATTTGGCAGAGACACATCATCTATC 14495
 Db 791 CysAsnTrpGlnGluAlaTrpSerIle 799

RESULT 4
 US-10-732-796A-8
 : Sequence 8, Application US/10732796A
 : Publication No. US20040197865A1
 : GENERAL INFORMATION:
 : APPLICANT: Gupta, Shalley K.
 : APPLICANT: Ghosh, Tarun K.
 : APPLICANT: Fink, Jason R.
 : TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
 : FILE REFERENCE: 58182US004
 : CURRENT APPLICATION NUMBER: US/10/732,796A
 : NUMBER OF SEQ ID NOS: 23
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 8
 : LENGTH: 799
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-10-732-796A-8

Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 16 Gaps: 1

US-09-396-985b-47 (1-18989) x US-10-732-796A-8 (1-799)
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QY 12309 GGAAGCCCACTCCAGAGTTTAGCCCTGGAGACCTTTTCTGGACATATCAAGATTACAGA 12368
Db 71 GlyAsnProIleGlnSerIleuAlaIleuGlyAlaPheSerGlyLeuSerSerIleuGlnIlys 90
QY 12369 CTGGGCTGTGGAGACAATCTAGACATCTCTAGAGAATCCCGCATTTGACATCTCAAA 12428
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QY 12429 ACTTTGAAAGAACTTAATGTGGCTCACAATCTTATCCAAATTTTCAAAATTAACCGACTAT 12488
Db 111 ThrIleuysGluLeuAsnValAlaH1AsnLeuIleGlnSerPheIysLeuProGluTyx 130
QY 12489 TTTTCTATCTGACCAATCTAGAGCACTTGGACCTTCCAGACAACAAGATTCAAAATATT 12548
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Db 151 TyxSerThrAspLeuArgValIleuH1sGlnMetProLeuLeuAsnLeuSerIleuAspLeu 170
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Db 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuH1Ilys 190
QY 12669 CTGACTTTAAGAATAATTTTGTAGATTAAATGAAATACTTGATTCAGAGCTCTG 12728
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QY 12849 GCATCTAGTACACTACTCCGATGATATTAATGACTTATTAATGTTTGAACAATGTT 12908
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Db 271 SerSerPheSerLeuValSerValThrIleGluArgValIysAspPheSerTyxAsnPhe 290
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QY 13389 TCCAGTCTCGAAGCTTGAATAATGGCTGGCAATCTTCCAGGAAAATTCCTTCAGAT 13448
Db 431 SerSerIleuGluValLeuTyxMetAlaGlyAsnSerPheGlnGluAsnPheProAsp 450
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QY 13509 TTGCTCCAAACAGCATTTAACTGACTCCAGCTTCCAGGTACTAAATATAGACCAAC 13568
Db 471 LeuSerProThrAlaPheAsnSerIleuSerIleuGlnValIleuAsnMetSerH1Asn 490
QY 13569 AACTTCTTTTCAATGGATACGTTTCTTAATAGTGTGAACTCCCTCCAGGTTCTTGAT 13628
Db 491 AsnPheSerIleuAspThrPheProTyxTyxLeuAsnSerIleuGlnValIleuAsp 510
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QY 13809 ACACCTTCATATAGACGGGACGCTGTGCTGAGTTGAATATTCACCTTCAGATGAAT 13868
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Db 591 LysThrIleIleGlyValSerValIleuSerValLeuValIaSerValIaValIaLeu 610
QY 13929 GTCTATAGTCTTATTTTCACTGATGCTTCTTGCTGGCTGCAATTAAGTATGTAAGGT 13988
Db 611 ValTyxTyxPheTyxPheH1sIleuMetLeuLeuAlaGlyTyxIleTyxGlyArgGly 630
QY 13989 GAAAACATCTATGATGCTTTTGTATTAATCAAGCCAGATGAGAGCTGGGTAAAGAAAT 14048
Db 631 GluAsnIleTyxAspAlaPheValIleTyxSerSerGlnAspGluAspTrpValArgAsn 650
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QY 14109 GACTTATTTCCGGTGTGGCAATTTGCTGCCAACATCATCAATGAAGTTTCCATAAAGC 14168
Db 671 AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleH1sGluGlyPheH1sIysSer 690
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Db 691 ArgIysValIleValIaValIaSerGlnH1sPheIleGlnSerArgTyxValIlePheGlu 710
QY 14229 TATGAGATGGCTCAGACCTGAGATTTCTAGACAGTGTGCTGGTATCATTTCAATGTC 14288
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QY 14289 CTGCAGAAAGTGAAGAAACCTGCTCAGGACGAGGATGAAGCTGACCGCTTCTCAGC 14348
Db 731 LeuGlnIysValGluTyxThrLeuLeuArgGlnIaValGluLeuTyxArgLeuLeuSer 750
QY 14349 AGGAACACTTACCTGAGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGAGCA 14408
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QY 14409 CTCGAAAAGCCCTGCTGATGTAAATCATGAGATCAGAGAACAGTGGGTACAGGA 14468
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Db 771 LeuhtgysalaleuLeuabpGlyysSerTrpserProgluGlyThValGlyThrcly 790
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RESULT 5
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-26
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
Gaps: 1
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QY 12309 GGAACCCCATCCAGAGTTTACGCTGGAGACCTTTTCTGACATTCAGATTACAGAG 12368
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QY 12369 CTGGGTGCTGAGAGACAAATCTAGCATCTCTAGAGACTTCCCATTTGAGCATCTCAA 12428
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QY 12429 ACTTTGAAAGAACTTAATGTGGCTCAACATCTTATTCATCTTTCAAATTAAGTAT 12488
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Db 149 ThrLeuIlysgluLeuAsnValAlaHisAsnLeuIleGlnSerPheIlyLeuProgluIlyr 168
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QY 12489 TTTTCTAATCTGACCAATCTAGACACTTGGACCTTTTCAGAACAAAGATTCAAGTAT 12548
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Db 169 PheSerAsnLeuThrAsnLeuGluHisLeuAspLeuSerSerAsnIlyIleGlnSerile 188
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QY 12609 TCCCTGAACCTTAAAGCTTTATCCAAACGAGTCAATTTAAAGAAATTAGGCTTCATAG 12668
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| | | | |
QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAAATGAAACCTTGATTAAGAGCTG 12728
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QY 12969 GGATGGCAACTTTAGAAATTTAGTTAACTGTAAATTTGGACAGCTTTCCACATTTGAAATC 13028
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QY 13029 AATCTCTCAAAAGGCTTACTCTTCACTTCCAAAGAGTGGGAATGCTTTTTCAGAGTT 13088
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QY 13089 GATCTACCAAGCTTGAATTTCTAGATCTCAGTGAAGAAATGCTTGAATTAAGATTC 13148
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| | | | |
Db 389 CysSerGlnSerAspPheGlyThrThrSerLeuIlyTyrLeuAspLeuSerPheAsnGly 408
| | | | |
QY 13209 GTTATTTACATGAGTTGAACTTCTGGGCTTAGAACAACTAGAACTCTGATTTCCAG 13268
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Db 409 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHisLeuAspPheGln 428
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QY 13389 TCCAGTCTCGAAGCTTGAAGAAATGAGTGGCAATCTTTCCAGAAACTTCTCCAGAT 13448
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QY 13569 AACTTCTTTTCATGAGATGATCTTCTTAATAGTGTGAACTCCCTCCAGGTTCTTGAT 13628
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Qy	13689	CTAGCTTCTTAAATCTTACTCTACGAATGACTTTGGCTTGTAACCTTGGAACACCAAGGTTTC	13748
Db	569	LeuAlaPheLeuAsnLeuTrpGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe	588
Qy	13749	CTGCATATGATCAAGACGACAGAGGACAGCTTTGGTGGAACTTGAAAGAAATGGAATGTCGA	13808
Db	589	LeuGlnTrpLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGluCysAla	608
Qy	13809	ACACCTTCAGATTAAGCAGGCGCATGCTGTGCTGATGATTGAATATCACTGTCAGATGAAT	13868
Db	609	ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn	628
Qy	13869	AAGACATCATATGGTGTGTGGGTCCTCCAGTGGCTTGTAAGTCTGGTTTACAGATTCG	13928
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Qy	13929	GTCATATAGTTCATATTTTCACTGATGCTTTCTTGCGGTGCATAAAGTATGATGAGGT	13988
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Db	709	AspPheIleProGlyValAlaIleAlaIleAlaIleAlaIleIleHisGlnGlyPheHisLysSer	728
Qy	14169	CGAAAGGTGATGTGTGTGTGTGCCAGACTTTCATCAGACCGCGGTGTATCTTTGAA	14228
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Qy	14409	CTCAGAAAAGCCCTGCTGATGTGTAAATCATGTGAATCCAGAAAGAACAGTGGGTACAGGA	14468
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RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1

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; APPLICANT: Spytek, Kimberly A
;
; APPLICANT: Li, Li
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; APPLICANT: Wolenc, Adam R
;
; APPLICANT: Vernet, Corine
;
; APPLICANT: Eisen, Andrew J

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APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shinkete, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kektad, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoli, Esha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Macdougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-038-854-135

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Alignment Scores:	
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QY 12447 GTGGCTCAACAATCTTATCCAACTTTTCAATACCTGAGTATTTTCTTAATCTGACCAAT 12506
Db 156 LeuGlySerAsnHisIleSerSerIleLysLeuProLysGlyPheProThr---GlnLys 174
QY 12507 CTAAAGCACTTGACCTTTCCAGCAACAAGTTCAAAAGTATTATTGACAGACTTGGCG 12566
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QY 12627 TTATCCAAACGAGTGCATTTTAAAGAAATTAGGCTTCAAGCTGACTTTAAGAAATAT 12686
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QY 12807 CTAGAGGCGCTGTGCATTTGACCAATTGAGAAATTCGATTAGCACTTAGACTACTAC 12866
Db 268 PheGlnGlyLeuGlyGlnMetSerValGlnSerIleAsnLeu---GlnLysHisTyrPhe 286
QY 12867 CTGCATGATATTATTACTATTATTAATTGTTTGAACAAATGTTTCTTCAATTTCCCTGGTG 12926
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QY 12927 AGTGTGACTATTGAAGGGTAAAGACTTTCTTATATATTGAGAGGCAATTTAGAA 12986
Db 299 -----GlyLeuGlnGlnLeuAsp 304
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QY 13041 AGGCTTACTTTCACCTTCCACAACAAGTGGGAAAT-----GCTTTTTCAGAAATTGATCTA 13094
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Db 345 ProSerLeuThrHisIleSerIleLysGlyAsnThrLysArgLeuGlnLeuGlyLys 364
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QY 13140 AAAGGTTGCTGTTCTCAAAGTATTTGGGACAAACGAGCTTAAAGTATTAGATCTGAGC 13199
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QY 13200 TTCAATGGTGTATTATACATGATGTTCAAC---TTCTTGGGCTTAGAACAACCTGAACAT 13256
Db 405 TyrAsnGlnProLeuSerLeuLysThrGlnAlaPheLysGlnLysProGlnLeuGlnLeu 424
QY 13257 CTGGATTTCAGACATTCCAATTTGAAACAATGAGTGGTTCAGTATTCCTATCACTC 13316

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Db 425 LeuSerLeuAlaPheThrArgLeuLysValLysAspAlaGlnSerProPheGlnAsnLeu 444
QY 13317 AGAAACCTCATTTTACCTTGACATTTCTCATCTACACACAGAGTGGCTTTCAATGGCATC 13376
Db 445 HisLeuLysValLeuAsnLeuSerHisIleSerLeuAspIleSerGlnGlnLeu 464
QY 13377 TTCAATGGCTGTGCAGTCTGAGAGTTCGAAAGCTTGAAGAAATGCGGCAATTTCTTCAGGAAAC 13436
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QY 13491 CAGTGTCACTGAGACAGCTTGTCTCCAAACAGATTTTATCTACCTCTCCAGCTTCAGGTA 13550
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Db 595 AsnMetGlnLysLeuGlnAspThrGlnAspThrLeuLysGlnAsnProProLeuLeuArg 614
QY 13827 GGCATGCTGTGCTGAGTTTGAATATCATCTGTGACATGATGAATGACCATATGGTG 13886
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QY 13887 TCGGCTCCTCAGTGTGCTTGAATATCATCTGTGACATGCTGCTTAAGTTAT 13943
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RESULT 7
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameeh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spletke, Kimberly A
; APPLICANT: Patrudajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Vernert, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Eilerman, Karen
; APPLICANT: Malvanekar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G

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Db      542 HisLeuLysGlyIleYrLeuAsnLeuAlaSerHisIleSerIleIle----- 558
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Qy      13707 ACTCAGATGACTTGGCTTGTACTTGTGACACAGAGTTTCTTCGCAATGATGATCAAGAC 13766
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Qy      13767 CAGAGGAGCTCTGTGGAGAGTTGAACGAATGAAGAAATGGAACACCTTCGATTAACAG 13826
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Db      615 GlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaValGlyIlePhePhe 634
Qy      13887 TCGGTCTCAGTGTGCTTGTGATATCTGTGTGACAGCTTGTGCTTAATGTTCTAT 13943
Db      635 LeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaValIysTyPhe 653

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RESULT 8

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US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XX1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-4

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Alignment Scores:

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Pred. No.:      1,24e-44      Length:      784
Score:          561.50      Matches:      220
Percent Similarity: 41.59%      Conservative: 121
Best Local Similarity: 26.83%      Mismatches: 260
Query Match:    1,70%      Indels:      219
DB:            10      Gaps:      38

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US-09-396-985b-47 (1-18989) x US-09-950-041-4 (1-784)

Qy 12246 ATCCAGCAATTGAGATGGGCGCATATCAGAGCCTTAAGCACTCTCTACCTTAATATTG 12305

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Db      88 IleAsnThrIleGluGluAspSerPheSerSerLeuIleSerLeuGluHisLeuAspLeu 107
Qy      12306 ACGAAGAACCCCATCCAGATTTAGCCCTTGAGACCTTTCTGACATATCAAGTTTCAG 12365
Db      108 SerTyraAsnYrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
Qy      12366 AAGCTG-----GTGCTGTGAGACAAT 12389
Db      128 PheLeuAsnLeuLeuGluAsnProTyIysThrLeuGluIleThrSerLeuPheSerHis 147
Qy      12390 CTAGACATCTGTAGAGAACTTCCCATTTGACATCTCAAACT----- 12431
Db      148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
Qy      12432 -----TTGAAGAAGCTTAATGTGGTCAACATCTTAATCAA 12467
Db      168 LysAspPheAlaGlyLeuThrPheLeuGluGluLeuIleLeuAlaSerAspLeuGln 187
Qy      12468 TCTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTGACCTTCC 12527
Db      188 SerTyroIu---ProLysSerLeuLysSerIleGlnAsnValSerHisIleLeuHis 206
Qy      12528 AGCAACAAG-----ATTCAAAGTATTATTC 12554
Db      207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
Qy      12555 ACAGACTTGGGGGTTTCAATCAAAAGCCCTACTCAATCTCTTGTAGACCTGCTCC 12614
Db      227 LeuGluLeuArg-----AspThrAspLeu 234
Qy      12615 AACCCATTAAGCTTT-----ATCCAAACAGAGTCAATTAAGAAATTAAGGCTTCATAG 12668
Db      235 AspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---IleLysLys 253
Qy      12669 CTGACTTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAAACTTGT 12716
Db      254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
Qy      12717 -----ATTCAAGTCTGGCTGTTTGAAGTCCATGCTTTGGTTCG-----GGA 12761
Db      274 AsnGlnIleSerGlyLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly 293
Qy      12762 GAATTTGAAATGAAAGAACTTGGAAGAAAGTTTGACAAATCTGCTAGAGGCGCTGTC 12821
Db      294 AsnPheArgAlaSerAspPheAspArgValIleAspProGlyLysValGlu----- 310
Qy      12822 AATTTGACATTTGAGAAATTCGATTAGCA-----TACTTAGACTTACCTCGATGAT 12875
Db      311 ThrLeuThrIleArgArgLeuHisIleProArgPheTyIleuPheTy-----Asp 327
Qy      12876 ATTAATGACTTATTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGACT 12935
Db      328 LeuSerThrLeuYrSerLeuThrGluArgValLys-----ArgIleThr 342
Qy      12936 ATTGAAGAGGTAAAGACTTTCTTAATTTGGATGGACATTTAGATTAAGTTTAAC 12995
Db      343 ValGluAsnSerValPhe-----LeuValPro 352
Qy      12996 TGTAAATTGGACAGTTTCCACATTTGAATCAAAATCTCTCAAAAAGCTTACTTTCAC 13055
Db      353 CysLeuLeuSerLys----- 357
Qy      13056 TCCAAACAAGGTGGAGAAAGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTTCAAT 13115
Db      358 -----HisLeuLysSerLeuGluTyIysLeuAsp 366
Qy      13116 CTCAGTAGAAAT-----GGCTGAGTTTCAAAAGCTTGCTGTCTCAAACT 13160
Db      367 LeuSerGluAsnLeuMetValGluGluTyIysLeuLysAsnSerAlaCys----- 382
Qy      13161 GATTTTGGGACAAACAGCCTTAAGTATTTAGATCTGAGCTTCAAGTGTTATTATTAACATG 13220

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Db      383  GLuAspAla1trpProSerLeuGlnThrLeu11LeuArgGlnAsn----- 397
QY      13221 AGTTCAAACTTTGGGCTTAAGAAACAATAAGCATGTGATTTCCAGATTCGAATTTG 13280
Db      398  -----HisLeu-----AlaSerLeu 402
QY      13281 AAACAAATGAGTAGTTTTCAGATTCCTATCACTCAGAAACCTCATTTTACCTTGACATT 13340
Db      403  GlnUlyeThrGlyGlu-----ThrLeuThrLeuUlyeAsnLeuThrAsn11LeuArg1Le 420
QY      13341 TTCATATCTACACACAGAGTTGCTTTCATATGGCATTTTCATATGGCTTTGTCAGATCTCGAA 13400
Db      421  SerUlye----- 422
QY      13401 GTCTTGAAATATGGCTGAGCATTTCTTCCAGAAAACTTCTCCAGATATCTTCACAGAG 13460
Db      423  -----AenSerPheHisSer-----MetProGlnUthrCysGlnTrp 434
QY      13461 CTGAGAAACTTGACCTTCTGACACTCTCTCACTGATGTCATGACAGAGAGTTGCTCT----- 13514
Db      435  ProGlnUlyeMetUlyeTyrlLeuAsnLeuSerSerThrArg1LeHisSerVal1ThrGlyCys 454
QY      13515 ---CCAAAGACATTTAACTCACTCTCCAGTCTTCAGGTAAGTAAATATGAGCCACACAC-- 13568
Db      455  IlePro-----LysThrLeuGlnUlyeLeuAspVal1SerAsnAsnAsn 468
QY      13569 ---AACTTCTTTTCATTGGAT----- 13586
Db      469  LeuAsnLeuPheSerLeuAsnLeuProGlnLeuUlyeGlnUlyeUlyeTr11SerArgAsnUlye 488
QY      13587 ---ACGTTTCTCT--TATTAAGTGTCTGAACCTCTCCAGAGTTTCTTGATTAACAGTCTC 13637
Db      489  LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuVal1LeuUlyeSerArg 508
QY      13638 AATCACATATGACTTCCAAAAACAGAACTACAGCATTTTCCAACTAGTCTTACGTTTC 13697
Db      509  AsnAla11eThrThrPheSerUlyeGlnGlnLeuAspSerPhe--HisThrLeuUlyeThr 527
QY      13698 TTTAAATTTTCTAGATGATGATTTGCTTGTATCTGTGAACACCAAGTTTCTCGCATG 13757
Db      528  LeuGlnUlyeGlyGlnUlyeAsnPhe11eCysSerCysGlnPheLeuSerPheThrGln-- 546
QY      13758 ATCAAGACCAAGACGACCTTCTGTGCAAGTT-----GAACGATGAGAA 13802
Db      547  -----GlnGlnGlnAlaLeuAlaVal1LeuUlyeAspTrpProAlaAenUlyeLeu 563
QY      13803 TGTGCAACACCTTCAATTAAGCAGGAGATGCTGCTGTGATTTGAATATCAC-- 13856
Db      564  CysAspSerProSerHisVal1ArgGlyGlnGlnVal1GlnAspVal1ArgLeuSerVal1Ser 583
QY      13857 ---TGTCAATGATTAAGACATCATTTGATGTCGTGCTGCTCAAGTGTGCTGTATGATCT 13913
Db      584  GlnCysHisArgThrAlaLeuVal1SerGlyMetCysCysAlaLeuPheLeuUlyeLeu 603
QY      13914 GTTGTAGACAGTCTGTCTATTAAGTTCTAT-----TTTCACTGATGCTTCTGTGCTGAG 13967
Db      604  LeuThrUlyeVal1LeuUlyeCysHisArgPheHisGlyLeuTrpUlyeMetUlyePheVal1 623
QY      13968 TGCATTAAGTAGTGATA-----GATGAAACATC--TATGATGCC 14006
Db      624  TrpLeuGlnAlaUlyeArgUlyeProArgUlyeAlaProSerArgAsn11eCysUlyeAspAla 643
QY      14007 TTTGTTTCTATCTCAACCCAGATGAGAGATGCTGTAAAGATGAGATGAGATTA 14066
Db      644  PheAsnSerUlyeSerGlnUlyeAspAla1eUlyeTrpAlaGlnUlyeAsnMetVal1GlnGlnUlye 663
QY      14067 GAAGAAAGGAGTCTCCATTTCAAGTCTGCTTCACTACAGAGATTTATTTCCGAGTGTG 14126
Db      664  GlnAsnPheAsnProProPheUlyeLeuUlyeCysUlyeHisUlyeAspPhe11eProGlyUlye 683
QY      14127 GCCATGCTGTCCCAACATCATCATGAAGTTTCCATTAAGAACCCAGAAAGTGATGTTGTG 14186
Db      684  Trp11eIleAspAsn11eIle--AspSer11eGlnUlyeSerHisUlyeThrVal1PheVal1 702

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QY      14187 GTGTCCAGACATTCATCCAGACCCGCTGATCTTGAATATGATGATGCTCAGACC 14246
Db      703  LeuSerGlnAsnPheVal1UlyeSerGlnUlyeTrpCysUlyeTyrlGlnUlyeAspPheSerHisPhe 722
QY      14247 TGGCAGTTTCTGACAGCTGTGCTGTATCATCTTCAATTTGCTTCTGCAAGAGTGAGAGAG 14306
Db      723  ArgLeuPheGlnGlnUlyeAsnAspAla1Ala1LeuUlyeLeuUlyeUlyePro11eGlnUlye 742
QY      14307 ACCCTGTCAAGGAGAG--GTGAGACTGTACCGGCTTCTCAGAGAAACATTTACCTG 14363
Db      743  LysAla11eProGlnUlyePheCysUlyeUlyeVal1LeuUlyeAsnThrUlyeTrpUlye 762
QY      14364 GAGTGGAGAGACAGTGTCTGTGGGCGGACATCTTGTGAGACAGTCAAGAAAGCCCTG 14423
Db      763  GluTrpProMetAspArgUlyeAlaGlnUlyeGlnUlyePheTrpVal1AsnUlyeArgAla1Ala1 782

RESULT 9
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; FILE REFERENCE: 3268, 1001-007
; CURRENT APPLICATION NUMBER: US/10/456, 947
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147, 447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291, 034
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-456-947-46

Alignment Scores:
Pred. No.: 1,24e-44 Length: 784
Score: 561.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.70% Indels: 219
Gaps: 38
DB:

US-09-396-985b-47 (1-18989) x US-10-456-947-46 (1-784)
QY      12246 ATCCAGACATTAAGATGGGCGCATATACAGGCTTAAGCCACTTCTTACTTAATTTG 12305
Db      88  11eAsnThr11eGlnUlyeAspSerPheSerSerUlyeUlyeSerUlyeUlyeAspLeu 107
QY      12306 ACAAGAAACCCATCCAGATTAAGCCCTGGAGCCCTTCTGAGATCAATGATTTACAG 12365
Db      108  SerUlyeAsnUlyeSerAsnLeuSerSerTrpPheUlyeProLeuSerSerLeuThr 127
QY      12366 AACCTG-----GTGCTGTGAGACAAAT 12389
Db      128  PheUlyeAsnLeuUlyeGlnAsnProUlyeTrpUlyeThrLeuUlyeGlnUlyeUlyePheSerHis 147
QY      12390 CTAGCATCTTGAAGAACTTCCCATTTGACATCTCAAACT----- 12431
Db      148  LeuThrUlyeUlyeGlnUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlye 167
QY      12432 -----TTGAAGAACTTAATGAGCTCAACATCTTATCCAA 12467
Db      168  LysAspPheAlaGlyLeuThrPheLeuGlnUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlyeUlye 187
QY      12468 TCTTTCAATTAACCTGATTTTCTAATCTGACCAATCTAAGACATTTGACCTTTCC 12527

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Db 188 SerTrgln---ProlySerLeuLeuSerIleGlnSerValSerIleLeuLeuHis 206
QY 12528 AGCAACAG-----ATTCAAAGATTATTATTC 12554
Db 207 MetLysGlnHisIleLeuLeuGlnIlePheValAspValIleSerSerValGluCys 226
QY 12555 ACAGACTGGGGGTTCATCATCAATGCCCCCTACTCATCTCTTTAGACTGTCCCTG 12614
Db 227 LeuGlnLeuArg-----AspThrAspLeu 234
QY 12615 AACCCATGACATT-----ATCCAAACAGTGCATTAAAGAAATTAGGCTTCATAG 12668
Db 235 AspThrPheHisPheSerGlnLeuSerThrGlnIleHisAsnSerLeu---IleLysLys 253
QY 12669 CTGACTTTAGAAAT-----AATTGATAGTGTTA---AATGTAATAAACTGT 12716
Db 254 PheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLysLeuLeu 273
QY 12717 -----ATTCAAGGTGGCTGGTTTAGAGTCCATGGTTGGTTGG-----GGA 12761
Db 274 AsnGlnIleSerGlnLysLeuGlnLeuGlnPheAspAspCysThrLeuAsnGlyValGly 293
QY 12762 GAATTGAAATGAGGAAAGCTTGAAAGTTTGAACAATCTGCTTAGAGGGCTGTGC 12821
Db 294 AsnPheArgIleSerAspAsnAspArgValIleAspProGlnLysValGln----- 310
QY 12822 AATTGACCATGAGAAATCCGATTAGCA-----TACTTAGACTACTACTCGATGAT 12875
Db 311 ThrLeuThrIleArgArgLeuHisIleProArgPheIleLeuPheIle---Asp 327
QY 12876 ATTATGACTATTATTATGTTTGAACAATGTTCTTCATTTCCCTGGTAGTGAGT 12935
Db 328 LeuSerThrLeuIleArgSerLeuThrGlnArgValLys-----ArgIleThr 342
QY 12936 ATTGAAGGGGTAAAGACTTTTCTTAATATTCGATGCGAACATTAGATTAGTTAAC 12995
Db 343 ValGlnAsnSerLysValPhe-----LeuValPro 352
QY 12996 TGTAATTGGACAGTTTCCACATTGAACCTCAAACTCTCAAAAGGCTTACTTCACT 13055
Db 353 CysLeuLeuSerGln----- 357
QY 13056 TCCAACAAAGGTGGAAATGCTTTTTCAGAGTGTATGCACAGCTTGAGTTCTAGAT 13115
Db 358 -----HisLeuLysSerLeuGlnLysLeuAsp 366
QY 13116 CTCAGTAGAAT-----GGCTTGAGTTTCAAAAGGTTGCTGTCTCAAAAGT 13160
Db 367 LeuSerGlnAsnLeuMetValGlnGlnIleLysIleLysAsnSerIleCys----- 382
QY 13161 GATTTTGGACACACAGCTTAAGTATTAGATTGAGCTTCAATGCTGTTATTACATG 13220
Db 383 GlnLysPheIleArgProSerLeuGlnIleThrLeuIleLeuLysArgIleAsn----- 397
QY 13221 AGTTCAAACTCTTGGGCTTAGACAACACTGAAACATGATTTCCAGACTTCCAAATTG 13280
Db 398 -----HisLeu-----AlaSerLeu 402
QY 13281 AAACAAATGAGTAGTTTTCAGATTCTTATCATCTGAGAAACCTCATTTACTGACAT 13340
Db 403 GlnLysThrGlnLys-----ThrLeuLeuThrLeuLysAsnLeuThrIleAspIle 420
QY 13341 TCTCATCTACACACCAAGTGTCTTCAATGGCATCTTCAATGGCTGTGTCAGATCTGAA 13400
Db 421 SerLys----- 422
QY 13401 GTCTTGAATAATGCTGGCAATTCTTTCAGAGAAATCTCTTCAGATATCTCAGAG 13460
Db 423 -----AsnSerPheHisSer-----MetProGlnIleCysGlnTrp 434
QY 13461 CTGAGAAACTTGACCTTCTGAGACCTCTCTCAGTGTCACTGAGACAGAGTTGCT----- 13514
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Db 435 ProGlnLysMetLysIleAsnLeuSerSerThrArgIleHisSerValThrGlyCys 454
QY 13515 -----CCACACAGATTAACTACTCTCAGTCTCAGGTTACTAAATATAGCCCAAC----- 13568
Db 455 IlePro-----LysThrLeuGlnIleLeuAspValSerAsnAsnAsn 468
QY 13569 -----AAGTTCTTTTCATTGGAT----- 13586
Db 469 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuValIleSerArgAsnLys 488
QY 13587 -----ACGTTTCT---TATAAGTCTGAACTCCCTCCAGGTTCTTGATTACAGTCTC 13637
Db 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLysIleSerArg 508
QY 13638 AATGCATATATGATCTTCCAAAACAGAACTACAGATTTTCCAAATAGCTGACTTTC 13697
Db 509 AsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe---HisThrLeuLysThr 527
QY 13698 TTAATCTTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13757
Db 528 LeuGlnAlaGlnLysAsnAsnPheIleCysSerCysGlnIleLeuLeuSerPheThrGln--- 546
QY 13758 ATCAAGACCAAGAGGAGCTTGTGTGAAGTT-----GAAAGAAATGAA 13802
Db 547 -----GlnGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTrpLeu 563
QY 13803 TGTGCAACACTTCAAGTAAAGACAGGATGCTGTGTGATGATGATGATGATGATGATGATG 13856
Db 564 CysAspSerProSerHisValArgGlnGlnGlnAlaGlnAspValArgLeuSerValSer 583
QY 13857 -----TGTCAGATGAAATGAACCATCATGATGATGATGATGATGATGATGATGATG 13913
Db 584 GluCysHisArgHisArgHisAlaLeuValSerGlnMetCysGlnAlaLeuPheLeuIleLeu 603
QY 13914 GTTGACAGTGTGTGTGTAAAGTTAT-----TTTCACTGATGCTTGTGTGCTGC 13967
Db 604 LeuThrGlnValLeuCysHisArgPheHisGlnLeuTrpIleMetLysMetMetTrpAla 623
QY 13968 TGCAATAAGTAGTAGA-----GTGAAAAATC---TATGATGCC 14006
Db 624 TrpLeuGlnAlaLysValLysProArgLysAlaProSerArgAsnIleCysLysAspAla 643
QY 14007 TTTGTTATCTACTCAAGCCAGATGAGGATGAGGATGAGGATGAGGATGAGGATGATGATG 14066
Db 644 PheValSerTrpSerGlnArgPheAlaTrpTrpAlaGlnAsnLeuMetValGlnGlnLeu 663
QY 14067 GAAGAGGGGTGCTCCATTTTCACTGCTGCTTCACTACAGAGACTTATTCGCGGTG 14126
Db 664 GlnAsnPheAsnProProPheLysLeuCysLeuHisIleLysArgAspPheIleProGlnLys 683
QY 14127 GCCATTGCTGCCAATCATCATCAATGAAGTTTCCATTAAGCCGAAGGATGTTGTG 14186
Db 684 TrpIleIleAspAsnIleIle---AspSerIleGlnLysSerHisLysThrValPheVal 702
QY 14187 GTGTCCAGCATCTTCAAGCCAGAGCCGCTGTGATCTTGAATATGATGATGCTCAGACC 14246
Db 703 LeuSerGlnAsnPheValLysSerGlnTrpCysLysTrpGlnLeuAspPheHisPhe 722
QY 14247 TGGCAGTTCTGAGAGCTGCTGTGTATCATCTTCAATGCTTCCGAGAGGTTGAGAG 14306
Db 723 ArgLeuPheGlnGlnAsnAsnAspAlaIleIleLeuLeuGlnIleGlnLys 742
QY 14307 ACCCTGCTCAGGACAG-----GTGAGCTGTACCGCTTCTCAGCAGAAACATTTACTG 14363
Db 743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThrTrpLeu 762
QY 14364 GAGTGGAGAGACAGTCTGCGGGGACATCTTCTGAGAGAGACTCAAGAAAGCCCTG 14423
Db 763 GluTrpProMetAspGlnAlaGlnArgGlnGlnPheTrpValAsnLeuArgAlaIle 782

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RESULT 10
 US-10-095-627-12
 ; Sequence 12, Application US/10095627

QY 13401 GTCTTGAAGATGGCTGCAATCTTTCCAGGAAAACTTCCTTCAGATATCTTCACAGAG 13460
 DB 423 -----AsnSerPheHisSer-----MetProGluThrCysGlnTrp 434
 QY 13461 CTGAGAAACTTGACCTTCCTGAGACTCTTCAGAGTCACTGAGACAGTGTCT----- 13514
 DB 435 ProGluysMetLysTrpLeuAsnLeuSerSerThrArgLysIleHisSerValThrGlyCys 454
 QY 13515 ---CCAACAGACATTTAACTCACTCTCCAGTCTTCAGGTAACATAATAGCACACAC--- 13568
 DB 455 IlePro-----LysThrLeuGluIleLeuAspValSerAsnAsnAsn 468
 QY 13569 ---AATCTTTTCATGTGAT----- 13586
 DB 469 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrLleSerArgAsnLys 488
 QY 13587 -----ACGTTTCCT---TATTAAGTGTGAACCTCCCTCCAGGTTCTTGATTAACAGTCTC 13637
 DB 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIleSerArg 508
 QY 13638 AATCACTAATAGACTCCAAAAACAGAACTACAGACTTTTCCAAAGTACTGACTTTC 13697
 DB 509 AsnAlaIleThrTrpPheSerLysGluLeuAspSerPhe---HisThrLeuLysThr 527
 QY 13698 TTTAATCTTACTCAGAACTTGCTGTGCTGTGTAACACACAGAGTTCTCTGCAATGC 13757
 DB 528 LeuGluAlaGlyGlyAsnAsnPheLleCysSerCysGluPheLeuSerPheThrGln--- 546
 QY 13758 ATCAAGACACAGAGCAGCTCTGTGTGAGAT-----GAAAGATGGA 13802
 DB 547 -----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTyrLeu 563
 QY 13803 TGTGCAACACTTTCAGATTAACAGGGCATGCGCTGCTGCAATTGAATATACCC----- 13856
 DB 564 CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSerValSer 583
 QY 13857 ---TGTGATGATTAAGCAACCATGATGTGGTGGTGGTCTCAGAGTGTGTGATGATCT 13913
 DB 584 GluLysHisArgThrAlaLeuValSerGlyMetCysValAlaLeuPheLeuLeuLeu 603
 QY 13914 GTTGTAGAGCTTGTGCTATTAAGTCTAT-----TTTCACTGATGCTTCTTGCTGGC 13967
 DB 604 LeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpTyrMetLysMetMetTrpAla 623
 QY 13968 TGCATTAAGTATGTGA-----GGTAAACATC---TATGATGCC 14006
 DB 624 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnLleCysTyrAspAla 643
 QY 14007 TTTGTATCTACTCAAGCCAGAGAGAGCTGGGTAAGGAATGAGCTAGTAAGATTTA 14066
 DB 644 PheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGlnGluLeu 663
 QY 14067 GAAGAAGGGGTGCTCCATTTCAAGTCTGCTCTCACTACAGAGACTTATTCGCGGTGC 14126
 DB 664 GluAsnPheAsnProProPheLysLeuLysLeuHisLysArgAspPheIleProGlyLys 683
 QY 14127 GCCATTGCTGCCAATATATCATGAAGTTTCCATAAAGCCGAAAGTGATTTGTTGG 14186
 DB 684 TrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrValPheVal 702
 QY 14187 GTGCCCAAGCACTTCACAGCCGCGGTGATCTTTGAATTAAGATTGCTCAGACC 14246
 DB 703 LeuSerGluAsnPheValLysSerGluTrpCysLysTyrGluLeuAspPheSerHisPhe 722
 QY 14247 TGGCAGTTTCTGACAGTCTGTGTGATCTTTCATCTTCACTGCAAGAGGTGAGAG 14306
 DB 723 ArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIleGluLys 742
 QY 14307 ACCCTGCTCAGGACGAG---GTGAGCTGTACCGCTTCTCAGACAGAACTTACCTG 14363
 DB 743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThrTyrLeu 762

QY 14364 GAGTGGAGAGACAGTGTCTGGGCGGACACTTCTTGAGACAGCACTCAGAAAAAGCCCTG 14423
 DB 763 GluTrpProMetAspGluAlaGlnArgGluGlyPheThrValAsnLeuArgAlaIle 782
 RESULT 11
 US-10-732-563-4
 ; Sequence 4, Application US/10732563
 ; Publication No. US20040132079A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gupta, Shalley K.
 ; APPLICANT: Ghosh, Tarun K.
 ; APPLICANT: Fink, Jason R.
 ; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
 ; FILE REFERENCE: 581830003
 ; CURRENT APPLICATION NUMBER: US/10/732,563
 ; CURRENT FILING DATE: 2003-12-10
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 784
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-10-732-563-4
 Alignment Scores:
 Pred. No.: 1.55e-44 Length: 784
 Score: 560.50 Matches: 220
 Percent Similarity: 41.59% Conservative: 121
 Best Local Similarity: 26.83% Mismatches: 260
 Query Match: 1.70% Indels: 219
 DB: Gaps: 38
 US-09-396-985b-47 (1-18989) x US-10-732-563-4 (1-784)
 QY 12246 ATCCAGCAATTAAGATGGGCGCATATACAGCTTAAGCCACTCTCTAATATATTG 12305
 DB 88 IleAsnThrIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnIleAsnLeu 107
 QY 12306 ACAGGAATCCCATCCAGACTTACCCCTGGAGACCTTTCTGAGTATCAAGTTTACG 12365
 DB 108 SerTyrAsnTyrLeuSerAsnLeuSerSerSerTrpPheLysProLysSerLeuThr 127
 QY 12366 AAGCTG-----GTGCTGTGAGACAAT 12389
 DB 128 PheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyGluThrSerLeuPheSerHis 147
 QY 12390 CTAGCATCTGTAGAACTTCCCATTCGACATCTCAAACT----- 12431
 DB 148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
 QY 12432 -----TTGAAGAATTAATGTGGCTCAATCTTATGCCA 12467
 DB 168 LysAspPheAlaGlyLeuThrPheLeuGlnGluLeuGluIleAspAlaSerAspLeuGln 187
 QY 12468 TCTTTAAATTAATCACTGAGTATTTTCTTAATCACTGACATTCAGACACTTGCCTCC 12527
 DB 188 SerTyrGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHis 206
 QY 12528 AGCAACAG-----ATTCAAGTATTAATGTC 12554
 DB 207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
 QY 12555 ACAGACTTGGGGGTTCATCAATCAAAATGCCCTACTCAATCTCTTTAGACTGCTCCCTG 12614
 DB 227 LeuGluLeuArg-----AspThrAspLeu 234
 QY 12615 AACCTATGAAGTT-----ATCCAAACAGGTGATTAAGAATTAAGCTTCAATAG 12668
 DB 235 AspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---IleLysLys 253
 QY 12669 CTGACTTAAGAAT-----AATTGATAGTTTA---AATGTAATGAATAACTGT 12716
 DB 254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273

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QY 12717 -----ATCAAGGTCTGGCTGGCTTTAGAAAGTCATGGTTTGGTTG-----GGA 12761
D 274 AsnGlnIleSerGlyLeuLeuGlnLeuGlnPheAspSerGlyThrLeuAsnGlyValGly 293
QY 12762 GAATTGAAATGAAGAAGAACTTGAAAGTTGCAAAATCTGCTTAGAGGGCTGTGC 12821
D 294 AsnPheArgIleSerAspAsnAspArgValIleAspProGlyLeuValGln----- 310
QY 12822 AATTGACCACTTGAAGAAATCCGATTAGCA-----TACTAGCTACTACCTGATGAT 12875
D 311 ThrLeuThrIleAspArgLeuHisIleProArgPheGlyLeuPheGly-----Asp 327
QY 12876 ATTTAGACTATTTATTTATGTTTGACAAGATGTTTCTTCATTTGCTGGTAGAGTGACT 12935
D 328 LeuSerThrLeuGlySerLeuThrGlnArgValys-----ArgIleThr 342
QY 12936 ATTGAAGGGTAAAGAACTTTCTTATATTTCCGATGGCAACATTAGAATTAGATTAAAC 12995
D 343 ValGlnSerSerGlyValPhe-----LeuValPro 352
QY 12996 TGTAAATTTGACACGTTTCCCACTTGAAACTCAATCTGCAAAAGGCTTACTTCACT 13055
D 353 CysLeuLeuSerGln----- 357
QY 13056 TCCAAACAAGGTGGGAATGTTTTTCAAGAGTTGATCTACCAAGCTTGAAGTTTCTGAT 13115
D 358 -----HisLeuGlySerLeuGlnGlyLeuAsp 366
QY 13116 CTCAGTAGAAAT-----GGCTGAGTTTCAAAGGTGCTGTCTTCAAAAGT 13160
D 367 LeuSerGlnLeuMetValGlnGlnGlyLeuGlyValSerGlnAsp----- 382
QY 13161 GATTTTGGGACACCAAGCTTAAATTTAGATTTAGATCTGAGCTTCATGGTTATTACCATG 13220
D 383 GlnAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
QY 13221 AGTTCAAACTTCTGGGCTTAGCAACTAGAACCTGATTTCCAGACTTCCAAATTTG 13280
D 398 -----HisLeu-----AlaSerLeu 402
QY 13281 AAACAAATGAGTGAATTTTCAAGTATCTCTATCACTGCAAAACCTCATTTACCTTGAAT 13340
D 403 GlnGlyThrGlnGly-----ThrLeuThrLeuGlyAsnLeuThrAsnIleAspIle 420
QY 13341 TCTCATACTCACACAGAGTTGCTTTCAATGAGCATTTCAATGCTGTCCAGTCTGAA 13400
D 421 SerGly----- 422
QY 13401 GTCTTGAATAATGGCTGGCAATTTCTTCCAGGAAATCTTCCAGATATCTTCACAGAG 13460
D 423 -----AsnSerPheHisSer-----MetProGlnThrCysGlnTrp 434
QY 13461 CTGAGAAACTTGACCTTCCGAGACTCTCTCAGTGTCACTGAGACAGTGTCT----- 13514
D 435 ProGlnGlyMetGlyGlyLeuAsnLeuSerSerThrArgIleHisSerValThrGlyCys 454
QY 13515 ---CCAACAGCATTTAACTCACTCTCCAGTCTCAGGATCAATATAGACCAAC--- 13568
D 455 IlePro-----LysThrLeuGlnIleLeuAspValSerAspAsn 468
QY 13569 ---AAGTCTTTTCAATGAT----- 13586
D 469 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuGlyLeuGlyThrIleSerArgAsnLys 488
QY 13587 -----ACGTTTCTT---TATTAAGTGTGAATCCCTCCAGGTTCTTGATTACAGTCTC 13637
D 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValIleGlyIleSerArg 508
QY 13638 AATCATATATGACTTCCAAAAACAGAACTCAAGCATTTTCCAAAGTGTGAGCTTTC 13697
D 509 AsnAlaIleThrThrPheSerGlyGlnLeuAspSerPhe---HisThrLeuGlyThr 527

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QY 13698 TTAATCTTACTCAGATGACTTTGCTGTGTAATGTAACACCAAGTTTCTSCAATGG 13757
D 528 LeuGlnAlaGlyGlyLeuAsnPheIleCysSerCysGlnPheLeuSerPheThrGln--- 546
QY 13758 ATGAGGACCAAGGCGAGCTTTGGTGAAGTT-----GACCAATGGAA 13802
D 547 -----GlnGlnGlnIleLeuAlaGlyValLeuIleAspTrpProAlaAsnGlyLeu 563
QY 13803 TGTGCAACACCTTCAGATTAAGACGAGCATGCTGTGCTGATGTTGAAATATACAC----- 13856
D 564 CysAspSerProSerIleValArgGlnGlnGlnValGlnAspValArgLeuSerValSer 583
QY 13857 ---TGTCAATGATTAAGACATCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13913
D 584 GlnCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuIleLeu 603
QY 13914 GTTGTACAGTTTGTGTGTATTAAGTTGAT-----TTTCACTGATGCTTTGTGTGTG 13967
D 604 LeuThrGlyValIleCysHisArgPheHisGlyLeuThrTrpGlyMetGlyMetMetTrpAla 623
QY 13968 TGCATAAAGTATGATGA-----GGTGAATAACATC---TATGATGSC 14006
D 624 TrpLeuGlnAlaGlySerGlyValProAlaGlyValAlaProSerArgAsnIleCysGlyAspAla 643
QY 14007 TTTGTTATCTACTCAAGCCAGATGAGCACTGGGTAAGAGATGAGCTAGTAAAGAAATTTA 14066
D 644 PheValSerGlySerGlnGlnAspAlaGlyTrpValGlnLeuMetValGlnGlnLeu 663
QY 14067 GAAGAAAGGGTCTGCTTCACTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14126
D 664 GlnAspPheAsnProGlyLeuGlyValCysValHisValArgAspPheIleProGlyLys 683
QY 14127 GCAATGTCTGCAACATCATCCATGAAGGTTTCCATTAAGGCGAAAGGATGTTGTGT 14186
D 684 TrpIleIleAspAsnIleIle---AspSerIleGlnGlySerIleGlyThrValPheVal 702
QY 14187 GTGTCCAGCACTTCACTCAAGACCCGCTGTGATCTTTGTAATAGATGATGTGTCAAGAC 14246
D 703 LeuSerGlnAsnPheValGlySerGlnTrpCysGlyGlyGlyLeuAspPheSerHisPhe 722
QY 14247 TGGCAGTTTGTGACAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14306
D 723 ArgLeuPheAspGlnAsnAsnAspAlaAlaIleLeuIleLeuLeuGlnGlnProIleGlnLys 742
QY 14307 ACCGTGCTACGAGCAGAG---GTGAGCTGTACCGCTTCTGACGAAACACTTACTCTG 14363
D 743 LysAlaIleProGlnArgPheCysGlyValLeuArgLysIleMetAsnThrGlyThrLeu 762
QY 14364 GAGTGGAGGACAGTGTCTGGGAGCGGACATCTTGTGAGAGCACTCAGAAAGCCCTG 14423
D 763 GlnTrpProMetAspArgIleAlaGlnArgGlnGlyPheThrValAsnLeuArgAlaIle 782

RESULT 12
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-10-732-796A-4
Alignment Scores:

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Qy 14067 GAAGAGGGGTGCTCCATTTTACGCTGTGCTTACTACAGACACTTATTCGCCGGTGTG 14126
Db 664 GluAsnProPheProPheLeuGluCysLeuHisIleuArgAspPheIleProGlyLys 683
Qy 14127 GCCATTGTCGACATCATCATGAGTTTCCATAAAGCCGAAGGTGATTTGTGTG 14186
Db 684 TrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisIleValPheVal 702
Qy 14187 GTGTCCCGACATTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTCACAGACC 14246
Db 703 LeuSerGluAsnProPheValLysSerGluTrpCysLysTyrGluLeuAspPheSerHisPhe 722
Qy 14247 TGGCAGTTTTCAGACAGTCGCTGTGTATCATTTTCATTTGCTTCGACAGAGTGGAGAG 14306
Db 723 ArgLeuPheAspGluAsnAsnAspAlaIleIleuIleLeuGluProIleGluLys 742
Qy 14307 ACCCTGCTCAGGACGACG--GTGAGCTGTACCGCTTCACACAGAACTTACTCTG 14363
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Qy 14364 GAGTGGAGAGCAGAGTCTGCTGGCGGACATCTTTCGAGACGACTCAGAAAGCCCTG 14423
Db 763 GluTrpProMetAspGluAlaGlnArgGluGluPheTrpValAsnLeuArgAlaIle 782

RESULT 13
US-10-741-600-1390
; Sequence 1390, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARILLI, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-741-600-1390

Alignment Scores:
Pred. No.: 1.55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.70% Indels: 219
DB: 17 Gaps: 38

US-09-396-985B-47 (1-18989) x US-10-741-600-1390 (1-784)
Qy 12246 ATCCAGACAATTGAAGATGGGACATATGAGCCCTTACACCACTTCTTACCTTAATATG 12305
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Qy 12306 ACAGAAACCCCATCCAGAGTTTAGCCCTGGGAGCCTTTTCGACATTCAGATTACAG 12365
Db 108 SerTyrAsnTyrLeuSerAsnLeuSerSerTrpPheLysProLeuSerSerLeuThr 127
Qy 12366 AAGCTG-----GTGCTGTGGAGACAAAT 12389
Db 128 PheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyGluThrSerLeuPheSerHis 147
Qy 12390 CTAGATCTCTAGAGAACTTCCCATTTGGACATCTCAAAACT-----12431
Db 148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
Qy 12432 -----TTGAAGAAGCTTAATGTGGCTCACAACTTATCCA 12467
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Db 168 LysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAspLeuGln 187
Qy 12468 TCTTTCAAAATTAACCTGAGATTTTTCATATCTACCAATCTAGACACTTGGACCTTCC 12527
Db 188 SerTyrGlu--ProLysSerLeuLysSerIleGlnAsnValSerHisIleuLeuHis 206
Qy 12528 AGCAACAG-----ATTCAAAGTATTTATTCG 12554
Db 207 MetLysGlnHisIleLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
Qy 12555 ACAGATCTGGGAGTTTCATCAATGACCCCTTACATCTCTTTAGACCTGTCCCTG 12614
Db 227 LeuGluLeuArg-----AspThrAspLeu 234
Qy 12615 AACCCATTAAGACTTT-----ATCCAAACAGTGTCATTTAAAGAAATTAAGCTTCATAG 12668
Db 235 AspThrPheHisAspSerGluLeuSerThrGlyThrAsnSerLeu--IleLysLys 253
Qy 12669 CTGACTTTAAGAAAT-----AATTTGATAGTTTA--AATGTAATGAAGAACTGT 12716
Db 254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
Qy 12717 -----ATTCAGAGTCTGCTGGCTTTAGAGTCATCTGTTGGTTCTG-----GGA 12761
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Qy 12762 GAATTGAAAATGAGAAACTTGAAAGCTTGACAAATCTGCTCTAGAGGCGCTGTGC 12821
Db 294 AsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu-----310
Qy 12822 AATTTGACCTTGAAGAAATTCGATTAGCA-----TACTTAGACTACTACCTGATGAT 12875
Db 311 ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr-----Asp 327
Qy 12876 ATTATGACTTAATTAATGTTTGACAAATGTTTCTTCATTTTCCCTGAGTGTGACT 12935
Db 328 LeuSerThrLeuTyrSerLeuThrGluArgValLys-----ArgIleThr 342
Qy 12936 ATTGAAGGGGTAAAGACTTTTCTTAATATTCGATGGCAACTTGAATTAAGTTAAC 12995
Db 343 ValGluAsnSerLysValPhe-----LeuValPro 352
Qy 12996 TGTAATTTGAGACGTTTCCACATTTGAATCTCAAACTCTCAAAAGCTTACTTCACT 13055
Db 353 CysLeuLeuSerGln-----357
Qy 13056 TCCAAACAAAGTGGAGATGCTTTTCAGAAATTGATCTACCAAGCCTTGAATTCTAGAT 13115
Db 358 -----HisLeuLysSerLeuGluTyrLeuAsp 366
Qy 13116 CTCAGTGAAT-----GGCTGAGTTTCAAAAGTCTGTTCTCAAAAGT 13160
Db 367 LeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys-----382
Qy 13161 GATTTTGGACACACCAAGCTTAAGTATTTAGATCTGAGCTTCATAGGTGTTATTACATG 13220
Db 383 GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn-----397
Qy 13221 AGTTCAAACTTTGGCTTAGAACAATACTGAATTCGATTTCCAGATTCCAATTTG 13280
Db 398 -----HisLeu-----AlaSerLeu 402
Qy 13281 AAACAAATGAGTAGTTTTCAGATTTCTATCTACCTAGAAACCTCATTTACCTTGACATT 13340
Db 403 GluTyrThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIleAspIle 420
Qy 13341 TCTCATACTCACACAGAGTTGCTTCAATGGCATCTCAATGGCTGTGCAAGCTCGAA 13400
Db 421 SerLys-----422
Qy 13401 GTCTTGAAGAAATGCTGGCAATTTCTTTCAGAGAAACTTCTTCAGATATCTTCACAGAG 13460
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QY      13515 ---CCAAGACATTTAACTCACTCTCCAGTCTTCAGTACTTAATATGAGCCACAAC--- 13568
Db      455 IlePro-----LysThrLeuGluIleLeuAspValSerAsnAsnAsn 468
QY      13569 ---AAGTTCTTTGATTGGAT----- 13586
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QY      13587 -----ACGTTTCTT---TATTAAGTGTGAACTCCCTCCAGGTTTCTTGATTAAAGTCTC 13637
Db      489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuYsIleSerArg 508
QY      13638 AATCACAATAATGACTTCCAAAAAACAAGAACTACAGCAATTTCCAGTAGTCTGCTTTC 13697
Db      509 AsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---HisThrLeuLysThr 527
QY      13698 TTTAAATCTTACTCAAAATGACTTGTCTGTACTGTGTAACAACAAGTTCTTCGCAATGG 13757
Db      528 LeuGlnIaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThrGln--- 546
QY      13758 ATCAGAGACCAAGGACGCTTGTGGAGATT-----GAAAGAAATGGA 13802
Db      547 -----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTrpLeu 563
QY      13803 TGTGCAACACCTTCAAGATTAAGCAGCATGCTGCTGAGATTGGAATATCAAC----- 13856
Db      564 CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValaGluLeuSerValSer 583
QY      13857 ---TGTCAATGAATAAGACCATCATTTGTTGTGTGTCGCTCTCACTGTGCTTGAATACT 13913
Db      584 GluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuIleLeu 603
QY      13914 GTTGAGACAGTTCTGGTCTAATAGTTCTAT-----TTTCACTGATGCTTCTTGCTGGC 13967
Db      604 LeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpYrMetLysMetMetTrpAla 623
QY      13968 TGCATAAGATGATGATGA-----GATGAAGATC---TATGATGCC 14006
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QY      14007 TTTGTTATCTACTCAAGCCAGATGAGACTGGGTAAAGAACTAGTAAGAAATTTA 14066
Db      644 PheValSerTrpSerGluArgAspAlaIleTrpValGlnAsnLeuMetValGlnGluLeu 663
QY      14067 GAAGAAGGGGTGCTCATTTCACTTTCGCTTCTCACTACAGACATTTATCCGGGTG 14126
Db      664 GluAsnAspLeuProPheLysLeuCysLeuHisLysArgAspPheIleProGlyLys 683
QY      14127 GCCATCTCTGCAACATCATTCATGAAGGTTTCCATAAAGCCGAAGTGATGTTGTG 14186
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QY      14187 GTGTCCAGACATTCATCAAGAGCCGCTGTGTATCTTTGAATATGAGATTGCTCAGACC 14246
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QY      14247 TGGCAGTTTCTGAGCACTGCTGCTGATATCATTTCTTCTGCTGCAAGAGTGGAGAG 14306
Db      723 ArgLeuAspLeuAspGluAsnAspAlaAlaIleLeuIleLeuGluProIleGluLys 742
QY      14307 ACCCTGTACAGCAGCAG---GTGAGCTGTACCGCTTCTCAGCAGAAACATTACTCTG 14363
Db      743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnTrpLysThrTrpLeu 762
QY      14364 GAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGACGACTCAGAAAAAGCCCTG 14423
Db      763 GluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaAlaIle 782

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RESULT 14
US-10-741-600-1391
; Sequence 1391, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0601499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1391
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1391

Alignment Scores:
Pred. No.: 1,55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1,70% Indels: 219
DB: 17 Gaps: 38

US-09-396-985b-47 (1-18989) x US-10-741-600-1391 (1-784)
QY      12246 ATCCAGACATTTGAAGATGGGGCATATCAGAGCCATTAAGCACTCTTACCTTAATATG 12305
Db      88 IleAsnThrIleGluGlnAspSerSerSerLeuGluHisLeuAspLeu 107
QY      12306 ACAAGAAACCCATCCAGACTTTAGCCCTGGAGACCTTTCTGACATCAAGTTTACAG 12365
Db      108 SerTrpAsnTrpLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
QY      12366 AAGCTG-----GTGCTGTGGACAAAT 12389
Db      128 PheLeuAsnLeuLeuGluAsnProGlyTrpThrLeuGlyGluThrSerLeuPheSerHis 147
QY      12390 CTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACT----- 12431
Db      148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
QY      12432 -----TTGAAGAAGCTTAATGTGGCTCAAACTTTATCCAA 12467
Db      168 LysAspPheAlaGlyLeuThrPheLeuGluGlnLeuGluIleAspAlaSerAspLeuGln 187
QY      12468 TCTTTCAAAATTACCTGAGATTTTCTTATCTGACCAATCTTAAGACATTTGACCTTTCC 12527
Db      188 SerTrpGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuHis 206
QY      12528 AGCAACAG-----ATTCAAAGTATTATTGC 12554
Db      207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValHisTrpSerSerValGluCys 226
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Db      227 LeuGluLeuArg-----AspThrAspLeu 234
QY      12615 AACCTTATGAACTTT-----ATCCAAACAGGTGATTAAGAATAATGAGCTTCATAG 12668
Db      235 AspThrPheHisAspSerGluLeuSerThrGlyGluThrAsnSerLeu---IleLysLys 253
QY      12669 CTGACTTTAAGAAAT-----AATTGATGAGTTTA---AATGTAATGAAGAACTGT 12716
Db      254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
QY      12717 -----ATTCAAGATGTGCTGCTGTGATTAAGATCCATCGTTGGTCTG-----GGA 12761
Db      274 AsnGlnIleSerIleLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly 293

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QY 12762 GAATTGAAATGAGGAAGAACTTGAAAGATTTGACAAATCGTGTCTAGAGGGCTGTGC 12821
 DB 294 AsnProMetArgLysAspSerPheValIleLeuProGluValGlu----- 310
 QY 12822 AATTGACCACTGAGAAATTCGATAGCA-----TACTTGAAGTACTACCTCGATGAT 12875
 DB 311 ThrLeuThrIleArgGluHisIleProArgPheThrLeuPhe-----Asp 327
 QY 12876 AATTATGACTTATTTATTTGTTGACAAATGTTCTTCATTTCCCTGGAGAGTGACT 12935
 DB 328 LeuSerThrLeuThrLeuThrGluArgValLys-----ArgIleThr 342
 QY 12936 AATTGAAAGGTAAGAAAGCTTTCTTATATTTGCGATGCAACATTTAGATTTAGTTAAC 12995
 DB 343 ValGluAsnSerLysValPhe-----LeuValPro 352
 QY 12996 TGTAAATTTGACAGTTTCCCACTTGAACTCAAAATCTCTCAAAAGCTTACTTTGACT 13055
 DB 353 CysLeuLeuSerGln----- 357
 QY 13056 TCCAAACAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTTGAGTTTATGAT 13115
 DB 358 -----HisLeuLysSerLeuGluLysLeuAsp 366
 QY 13116 CTCAGTAGAAT-----GGCTTGAAGTTTCAAAAGGTTCTGTCTCAAAAGT 13160
 DB 367 LeuSerGluAsnLeuMetValGluGluLysLeuLysAsnSerAlaCys----- 382
 QY 13161 GATTTTGGGACAAACAGCTTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTATACCATG 13220
 DB 383 GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgLysAsn----- 397
 QY 13221 AGTTCAAACTTTCTGGGCTTAGAACAACACTAGAACATGTGATTTCCAGATTCCAATTTG 13280
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 US-10-145-014-23
 Sequence 23, Application US/10145014
 Publication No. US20020168755A1
 GENERAL INFORMATION:
 APPLICANT: Daille, Barbara
 APPLICANT: Fan, Xuedong
 APPLICANT: Lundell, Daniel
 APPLICANT: Lunn, Charles A.
 APPLICANT: Tenn, Jimmy C.
 APPLICANT: Zavodny, Paul J.
 TITLE OF INVENTION: Mammalian TNF-alpha Convertases
 FILE REFERENCE: J06010D
 CURRENT APPLICATION NUMBER: US/10/145,014
 CURRENT FILING DATE: 2002-05-14
 PRIOR APPLICATION NUMBER: 09/982,308
 PRIOR FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: 09/156,163
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 08/889,909
 PRIOR FILING DATE: 1997-07-10
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Job time : 903 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 1865 Seconds
(without alignments)
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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 5629608

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

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2	2591	3.0	799	14	US-09-950-041-8	Sequence 8, App1
3	2591	3.0	799	14	US-10-128-166-7	Sequence 7, App1
4	2591	3.0	799	16	US-10-732-563-8	Sequence 8, App1
5	2591	3.0	799	16	US-10-732-563-8	Sequence 8, App1
6	575.5	0.7	641	16	US-10-408-765A-181	Sequence 181, App
7	571.5	0.7	956	14	US-10-000-256A-153	Sequence 153, App
8	572.5	0.7	1275	14	US-10-025-201-3	Sequence 3, App1
9	568.5	0.7	1010	14	US-10-050-882-80	Sequence 80, App1
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13	548	0.6	1032	14	US-10-272-502B-31	Sequence 31, App1
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16	541.5	0.6	240	15	US-10-094-749-2471	Sequence 2471, App
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ALIGNMENTS

RESULT 1
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Sequence 26, Application US/09950041
Publication No. US2003032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Kock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kaestlein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: EX0724X1
CURRENT APPLICATION NUMBER: US/09/950, 041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728, 540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207, 558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073, 363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044, 293

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; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-950-041-26

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Best Local Similarity: 61.81% Mismatches: 171
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QY 39494 GCATTTGTGATCTACGTGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39553
Db 674 AlaPheValIleTyrSerSerGlnAspGlnAspTyrValAlaGlnGlnLeuValLysAsn 693
QY 39554 TTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39613
Db 694 LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGly 713
QY 39614 GTAGCCATTGCTGCAACATCATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39673
Db 714 ValAlaIleAlaAlaAlaAlaIleIleHisGlnGlyPheHisIleYrGlnValIleVal 733
QY 39674 GTAGTGTCTAGACATTTATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39733
Db 734 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnIleValAlaGln 753
QY 39734 ACAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39793
Db 754 ThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 773
QY 39794 AAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39853
Db 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrIleLeu 793
QY 39854 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39913
Db 794 GlnTyrGlnAspSerValLeuGlyArgHisIlePheThrArgLeuArgLysAlaLeu 813
QY 39914 TTGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 39946
Db 814 LeuAspGlyLysSerTyrAsnProGlnGlyThr 824

RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaetelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DK0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212

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; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conserves: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2.98% Indels: 6
DB: 10 Gaps: 4

US-09-396-985b-48 (1-50000) x US-09-950-041-8 (1-799)

QY 37685 TTTTTCAGCAAAAATACATATTTGATCTTTTCCCATAGTGTGAATTTGA 37744
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QY 37745 ACAATTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 37804
Db 52 ThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisIleSerThrLeuIleThrGly 71
QY 37805 AACCTATTCAGAGATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 37864
Db 72 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerCylYeuSerSerLeuGlnLysLeu 91
QY 37865 GTGGCTGTGAGACAAATTTGGCTCTCTAGAAAGCTTCCTATTGGACAGCTTATACC 37924
Db 92 ValAlaValGlnThrAsnLeuAlaSerLeuGlnAspPheProIleGlyHisLeuLysThr 111
QY 37925 TTTAAGAACTCAATGTGGCTGACAAATTTATATCATTTCCGTGAAGTTACCTGATATTT 37984
Db 112 LeuLysGlnLeuAsnValAlaHisIleAsnLeuIleGlnSerPheLysLeuProGlyTyrPhe 131
QY 37985 TCCATCTGACGAGACCTAGTACATGTGATCTTTTATATCATATTTCAACTATTACT 38044
Db 132 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyr 151
QY 38045 GTCAAGACCTTACAGTTTCTACGTGAATAATCCAAAGTCAATCTCTTTAGACAGTCT 38104
Db 152 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 171
QY 38105 TTGAACCCATGTGACTTATTCATTAAGACCAAGACCTTCAGGAGATTAAGCTCCATGAAC 38164
Db 172 LeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGlnIleArgLysHisIleLeu 191
QY 38165 ACTCTAAGAGATATTTATATAGCTCAATATATATGAAAATTGCTTCAAACTGGCT 38224
Db 192 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 211
QY 38225 GGTTTACAGCTCATGTGCTTGTGAGAAATTTAAGATGAAAGAAATTCGAAATT 38284
Db 212 GlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnLysLeuGlnLys 231
QY 38285 TTGAACCCCTCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 38344
Db 232 PheAspLysSerAlaLeuGlnGlyLysCysAsnLeuThrIleGlnGlnPheArgLeuAla 251
QY 38345 TATACAAATGATTTTTCAGATGATTTTAAAG---TTCATTTGCTTGGGAAATGTTCT 38401
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QY 38402 GCATGTCTCTGACAGTGTATCTATATAATATCTGAAGATGTTCTTAAACATTTCAA 38461
Db 272 SerPheSerLeuValSerValThrIleGlnArgValLysAspPheSerTyrAsnPheGly 291

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Db 292 TrpIlnHsIleuGluIleuValaAsnCysIlySerHegIyGlnPheProthIleuIlySer 311
QY 38522 TTTCTTAAAGTTGACTTAACTATGAAACAAGGGCTCTACGTTTAAAAAAGTGGCC 38581
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Db 312 SerIleuYsArgIleuThrPheThrSerAsnIlyGlnAenAlaPheSerGlnValaAsp 331
QY 38582 CTACCAAGTTCACGTAATCTAGTACTTATGTAAGAAATGACCTGACCTTACGTTGCTGT 38641
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Db 332 LeuProSerIleuGluPheLeuAspIleuSerArgAsnGlyLeuSerPheIlyGlyCysCys 351
QY 38642 TCTTATCTGATTTGGGAACAACAAGCCTGAGACCTTGAACCTGACCTTCAATGAGTGGC 38701
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Db 352 SerGlnSerAspIleuGlyThrThrSerIleuYsTrIleuAspIleuSerPheAsnGlyVal 371
QY 38702 ATCATATAGTGGCCAAATTTCAATGAGGCTGTAGAAAGCTGACGACACTTGATTTTCAGAC 38761
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Db 372 IleThrMetSerSerAsnPheLeuGlyLeuGlnGlnIleuGlnIlnIleuAspPheGlnHis 391
QY 38762 TCTTACTTAAAGGGTCAACAAGATTTCTACGCTTCTTATCCCTTGAAGCTACTTAC 38821
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Db 392 SerAsnIleuYsGlnMetSerGlnPheSerValaPheLeuSerIleuAspAsnIleuIlyTr 411
QY 38822 CTTGACATCTCTTACTTAAACCAACAATGACTTCGATGATATTTCTTGAGCTTGAC 38881
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Db 412 LeuAspIleuSerHisIleuHisIleuThrArgValaAlaPheAsnGlyIlePheAsnGlyLeuSer 431
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Db 432 SerIleuGlnValaIleuYsMetAlaGlyAsnSerPheGlnGlnIleuAsnIleuProAspIle 451
QY 38942 TTTGCAAAACACAACAACTTACATCTCTGATCTTTTAAATGTCATTTGGAACAATA 39001
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Db 452 PheThrGluIleuAspGlnIleuThrPheLeuAspIleuSerGlnCysGlnIleuGlnIleu 471
QY 39002 TCTTGGGGGGTATTGACACCTCCATGACTTCAATTTAAATATGAGTCACACAAT 39061
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Db 472 SerProthIleuAsnSerIleuSerSerIleuGlnIleuAsnMetSerHisAsnAsn 491
QY 39062 CTATGTTTGGATTTCCCATTTATTAACAAGCTGTATTCCTCAGACACTTGTGATTC 39121
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QY 39122 AGTTTCAATCCGATGACACATCT---AAAGAAATACGCAACATTTCCAAAGCTTA 39178
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Db 512 SerIleuAsnHisIleuMetThrSerIlyGlnIleuGlnIlnIleuPheProSerIleu 531
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Db 532 AlaPheLeuAsnIleuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheIleu 551
QY 39239 CAGTGGGTCAAGAAACAGACAGAGTCTTGGTGAATGTTTGAACAATGACATGTGGACA 39298
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QY 39299 CCTGTAAGAGATTAACCTCTGATGTTGATTTTATTAATTTCTACCTGTATATATGAC 39358
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Db 572 ProSerAspIlyGlnIlyMetProValaIleuSerIleu---AsnIleuThrCysGlnMetAsn 590
QY 39359 AAGCAATCATCAGTGTGTGACGTGATGATGATGATGATGATGATGATGATGATGATGATG 39418
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Db 591 LysThrIleuIleuGlyValaSerValaIleuSerValaIleuValaIleuValaIleuVala 610
QY 39419 ATATATCACTTCTATTTTCAACCTGATCTTATTTGCTGGCTGTAAAGTATACAGACAGGA 39478
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Db 611 ValIlyIlyAspPheIlyPheHisIleuMetIleuAsnIleuGlyCysIleuYsGlyArgGly 630
QY 39479 GAAAGCATATGATGATGATTTGTGATCTACTGATGATGATGATGATGATGATGATGATG 39538
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Db 631 GlnAsnIleuYsArgAspAlaPheValaIleuYsSerSerGlnAspGlnAspTrpValaArgAsn 650
QY 39539 GAGCTGTAAAGAAATTTAGAAAGAGAGTGGCCCGCTTTCACCTTGCCCTTCACTACAGA 39598
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Db 651 GlnIleuValaIlyAsnIleuGlnIleuGlyValaProProPheGlnIleuCysIleuHisTrpArg 670
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QY 39719 TATGAGATTTCTCAAAATGAGCATGCTTCTGAGACCGCTCTGACATCATCTTCAATGTC 39778
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Db 711 TyrGlnIleuIleuGlnIleuThrGlnPheIleuSerSerArgAlaIleuIleuPheIleuVal 730
QY 39779 CTTGAGAAAGTTTGAAGAATCCCTGCTGAGGACACAGTGAATTTGATGCGCTTCTTAC 39838
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Db 731 LeuGlnIlyValaIleuYsThrIleuIleuAspGlnGlnIleuValaGlnIleuYsArgIleuLeuSer 750
QY 39839 AGAAACACTTACCTGGAAATGAGAGACAATCTCTGGGGAGAGACATCTTCTGAGAGAGA 39898
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Db 751 ArgAsnThrIlyIleuGlnIleuTrpGlnAspSerValaIleuGlyArgHisIleuPheTrpArg 770
QY 39899 CTTAAAAATGCCCTATTGATGATGAAAAACCTCGAATCTTGAGCAACA 39946
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Db 771 LeuArgIlyAlaIleuIleuAspGlyIlySerTrpAsnProGlnIlyThr 786

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US2003007279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OR INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-128-166-7

Alignment Scores:
Score: No.: 4,97e-191 Length: 799
Percent Similarity: 79.76% Matches: 508
Best Local Similarity: 67.20% Conservative: 95
Query Match: 2.98% Mismatches: 147
DB: 14 Indels: 6
Gaps: 4

US-09-396-985b-48 (1-50000) x US-10-128-166-7 (1-799)
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QY 37745 ACAATTGAACAAGAGATGGCATGGCTTACACACCTCTCAACTTGAATGATGACAGGA 37804
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Db 72 AsnProIleuIleuIleuIleuAlaIleuGlyAlaPheSerGlyIleuSerIleuGlnIlySer 91
QY 37865 GTGGCTGTGAGACAAATATTTGCTCTTGAAGAAAGCTTCCATTTGAGACCTTATTAAC 37924
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FILE REFERENCE: 58183W0003
CURRENT APPLICATION NUMBER: US/10/732,563
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 799
TYPE: PR1
ORGANISM: Homo sapiens
US-10-732-563-8

Alignment Scores:
Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2,98% Indels: 6
DB: 16 Gaps: 4

US-09-396-985B-48 (1-50000) x US-10-732-563-8 (1-799)

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QY 37745 ACAATTGAGACAGCAAGGATGGCATGGCTTACACACACCTCGAAACTTGATCTGACAGGA 37804
D 52 ThrIleGluAspGlyAlaTyrGlnSerLeuSerThrIleLeuThrGly 71
QY 37805 AACCTATCCAGAGTTTTCGCCAGAGTTTCTCTGACTACAGAGTTTGAAGATCTG 37864
D 72 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLeu 91
QY 37865 GTGGCTGTGGAGCAAAATTTGGCTCTTAGAAAGCTTCCCTATTGGACACTTATACC 37924
D 92 ValAlaValGluThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuLeuThr 111
QY 37925 TTAAGAAACTCAATGTGGCTCACAAATTTTATACATCTCTGAATGTTACCTGATATTT 37984
D 112 LeuIleuGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheLeuProGluTyrPhe 131
QY 37985 TTCAATCTGACGAACCTATGATCATGTGGATCTTTCTTAACTATATTCAACTATTA 38044
D 132 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyr 151
QY 38045 GTCAACGACTTACAGATTTCTACGTGAAATTCACAGCAATCTCTCTTAGACATGCT 38104
D 152 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 171
QY 38105 TTGAACCAATTTGACTTCAATCAAGACCAAGCCTTTCAGGGAATTAAGCTCCATGAAC 38164
D 172 LeuAsnProMetAsnPheIleGlnProGlyAlaPheLeuGluIleArgLeuHisLysLeu 191
QY 38165 ACTCTAAGAGGTAATTTTATAGCTCAATATATATGAATAAAGCTTGCCTTCAAAAGCTGCT 38224
D 192 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 211
QY 38225 GGTTCACGTCCTCATCGGTGATCTTGGAGAGATTTAAAGATGAAGAAGATCTGAAATT 38284
D 212 GlyLeuGlnValHisArgLeuValLeuGlnGluPheArgAsnGlnGlyAlaSerLeuGlnLys 231
QY 38285 TTGAACCTCTATATGAGGAAGGACTATGTAGTGAACATTTAGATGAGTTAGAGTTACA 38344
D 232 PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeuAla 251
QY 38345 TATACCAATGATTTTTCAGATGATTTGTAG--TTCCATTTGCTGGCGAATTTTCT 38401
D 252 TyrLeuAspLysTyrTyrLeuAspAspIleIleLeuAspLeuPheAsnCySLeuThrAsnValSer 271
QY 38402 GCAATGCTCTGGCAGGCTGTATTAATAATATCTAGAAAGATTTCTTAAACATTTGCAA 38461
D 272 SerPheSerLeuValSerValThrIleGlnArgValLysAspPheSerTyrAsnPheGly 291
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QY 38462 TGGCAATCCTTATCATATATGATGCACTTAAGCAGTTTCCAACTCTGATCTAACCC 38521
D 292 TrrGlnHisLeuGlnLeuValAsnCySlyPheGlyGlnPheProThrLeuLysLeuLys 311
QY 38522 TTTCTTAAAGTTTGACTTTTAACTATGACAAAGGCTTATCACTTTTAAAGTGGCC 38581
D 312 SerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnValAsp 331
QY 38582 CTACCAAGTCTGACATATCTTAGTGAAGAAAGCACTGAGCTTATAGGTGGTGT 38641
D 332 LeuProSerLeuGluPheLeuAspLeuSerAsnArgLysLeuSerPheLysGlyCyS 351
QY 38642 TCTTATCTGATTTGGGACAAACAGCTGAGACACTTACAGCTCAAGCTTCAATGGTGCC 38701
D 352 SerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyVal 371
QY 38702 ATCATTTAGAGTCCAAATTTATGAGGCTTGAAGAAGCTGACAGACCTGGATTTTCAGCAC 38761
D 372 IleThrMetSerSerAsnPheLeuGlnGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHis 391
QY 38762 TCTACTTAAAGGCGTCAAGAAATCTGACGCTTCTTATCCCTGAAAAGCTACTTAC 38821
D 392 SerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTyr 411
QY 38822 CTTGACATCTCTTATATCAACCAAAATGACTTGATGATATTTCTTGCGCTTGACC 38881
D 412 LeuAspLysSerThrIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 431
QY 38882 AGTCTCAACATTTAAATGCGTGGCAATTTCTTCAAGACAAACACCTTTCAATGTC 38941
D 432 SerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnProAspIle 451
QY 38942 TTTGCAAAACAAACAACTTGACATCTCCGAGTCTTTCAATGTCAAATGTC 39001
D 452 PheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCySLeuGlnLeu 471
QY 39002 TCTTGCGGGGTATTTGACACCTCCATAGACTTCAATTAATTAATGATGTCACAAAT 39061
D 472 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 491
QY 39062 CTATGTTTGGATTCATCCATTTATACCAAGCTGATTTCCCTGACGACTTTGATTGC 39121
D 492 PhePheSerLeuAspThrPheProTyrLysCySLeuAsnSerLeuGlnValLeuAspTyr 511
QY 39122 AGTTTCAATCGCATAGACATCT--AAAGAAATTCGCAACATTTCCAAAGAGCTA 39178
D 512 SerLeuAsnHisIleMetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeu 531
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D 532 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCySerThrCySLeuHisGlnSerPheLeu 551
QY 39239 CAGTGGTCAAGACAGAAAGAGTCTTGGTGAATTTGAACAAATGACATGTGCAACA 39298
D 552 GlnThrLysAspGlnArgGlnLeuValGlnValGlnArgMetGlnCySAlaThr 571
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D 572 ProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCySLeuMetAsn 590
QY 39359 AAGACATCATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39418
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QY 39419 ATATACACTTATATTTTCACTTGATATCTTATGCTGGCTGTAAAGTAACAGAGAGA 39478
D 611 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
QY 39479 GAAAGCATCTATATGATGATTTGTGATCTACTCGATCGAATGAGATGAGCTGGGTGAAGAA 39538
D 631 GluAsnLysTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyrValArgAsn 650
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Db 651 GtLeuValLysAsnLeuGluGluValProPheGlnLeuCyLeuHisTyrArg 670
Qy 39599 GACTTATTCCTGGTGGTCCCATTCCTCCCAATCATTCAGAGAGGCTTCCACAGAGC 39658
Db 671 AspPheLeuProGlyValAlaLeuAlaAsnLeuLeuHisGluGlyPheHisTyrSer 690
Qy 39659 CGAAGGTTATTTGGTGTAGTGTCTAGACATTTATTAGAGCCGTTGGTGTATCTTAA 39718
Db 691 ArgLysValIleValValSerGlnHisPheIleGlnSerHisTyrGlyPheGln 710
Qy 39719 TATGAGATTGCTCAAAACATGCGAGTTCTTGACAGCCGCTCTGGCATCTTCATTTC 39778
Db 711 TyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
Qy 39779 CTGAGAAAGTTGAGAAATCCCTGCTGAGGAGCAGCGGTGGAATTGTATCGCTTTCAGC 39838
Db 731 LeuGlnLysValIleGluLysThrLeuLeuArgGlnGlnValIleGluLysTyrArgLeuLeuSer 750
Qy 39839 AGAAGACCTGCTGGAATGGAGAGCAATCTCTGGGAGGACATCTTCTGGAGAGA 39898
Db 751 ArgAsnThrTyrLeuGluTrpGluAspSerValLeuGlyArgHisIlePheTrpArgArg 770
Qy 39899 CTTAAAGATGCCCTATTGGATGAAAAGCTCGAATCTTGAGCAAAACA 39946
Db 771 LeuArgLysValIleLeuLeuAspGlyLysSerTrpAsnProGluGlyThr 786

RESULT 5

US-10-732-796A-8
Sequence 8, Application US/10732796A
Publication No. US20040197865A1

GENERAL INFORMATION:

APPLICANT: Gupta, Shalley K.
APPLICANT: Ghosh, Tatum K.
TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
FILE REFERENCE: 58182US004
CURRENT APPLICATION NUMBER: US/10/732,796A
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 799
TYPE: PR1
ORGANISM: Homo sapiens
US-10-732-796A-8

Alignment Scores:

Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2.98% Indels: 6
Gaps: 4

US-09-396-985B-48 (1-50000) x US-10-732-796A-8 (1-799)

Qy 37685 TTTTTCGCAAAATACATATTTGTAATCTTTGGCCATAGGTGTAATTTGA 37744
Db 35 PheSerPheProGluLeuGlnValLeuAspLeuSer-----ArgCysGluIleGln 51
Qy 37745 ACAATTGAGACAGGATGCGATGCGTTACACACCTCTCAAACTTGATCTGACAGGA 37804
Db 52 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 71
Qy 37805 AACCTATCCAGAGTTTTCCTCCAGAGAGTTCTCTGACTAGACAGTTTAGAGATCTG 37864
Db 72 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 91
Qy 37865 GTGGCTGTGGAGCAAAATTTGGCTCTTACAAAGCTTCCCTATTGAGACGTTATTAAC 37924
Db 92 ValAlaValGluThrAsnLeuAlaSerLeuGlnLysAsnProIleGlyHisLeuLysThr 111

Qy 37925 TTAAGAACTCATGTGGCTGCACAAATTTATACATCTCTGTAACTTACGTCAATATTT 37984
Db 112 LeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPhe 131
Qy 37985 TCCAACTGAGCAACCTAGTACATGTGGATCTTTCTTAACTATATATTCAACTTAACT 38044
Db 132 SerAsnLeuThrAsnLeuGluHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyr 151
Qy 38045 GTCACACATCTTACGTTTCTACGAGAAATCCACAACTCAATCTCTCTTATAGACATGCT 38104
Db 152 CysThrAspLeuAspValLeuHisGlnMetProLeuAsnLeuSerLeuAspLeuSer 171
Qy 38105 TTGAACCCAAATTTGACTTCAATCAAGACCAAGCTTTCAGGAAATTAAGTCCAGAACTG 38164
Db 172 LeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleAlaGluLeuHisLysLeu 191
Qy 38165 ACTCTAAGAGTAAATTTTAAATAGCTCAATATATATGAAAATCTGCTTCAAACTGGCT 38224
Db 192 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 211
Qy 38225 GCTTTACAGTCCCTCGGTTGATCTTGGGAGAAATTTAAAGTAAAGAAATCTGGAATT 38284
Db 212 GlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGluLys 231
Qy 38285 TTGAACCTCTCATCATGAGAAAGACTATGTAGATGTGACCAATGTGAGTTCAAGTTAA 38344
Db 232 PheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeuAla 251
Qy 38345 TATACAAATGATTTTTCAGATGATATTTGTTAAG--TTCCATTGCTTGGCGAATGTTCT 38401
Db 252 TyrLeuAspLysTyrTyrLeuAspAspIleIleAspLeuPheAsnLysCysLeuThrAsnValSer 271
Qy 38402 GCAATGCTCTGGCAGGTGTATCTAATTAATATCTAAGAAATGTTCTTAAACATTTCAA 38461
Db 272 SerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPheGly 291
Qy 38462 TGGCAATCTCTATCATCATTTAGATGTGCAACTTAAGGAGTTTCCAACTCGATCTACCC 38521
Db 292 TrpGlnHisLeuGluLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeuLys 311
Qy 38522 TTTCTTAAAGTTTGACTTTAATCATATGAACAAAGGCTCTACGTTTAAAGAGTGCC 38581
Db 312 SerLeuLysArgLeuThrPheThrSerAsnLysGlyValAsnAlaPheSerGluValAsp 331
Qy 38582 CTACCAAGTCTCAGACTATCTAGATCTTAGTGAATTCATGACCTGAGCTTATGCTGCTGT 38641
Db 332 LeuProSerLeuGluPheLeuAspLeuSerArgAsnLysLeuSerPheLysGlyCys 351
Qy 38642 TCTTATCTGATTTGGGACAAACAGCCTGAGACACTTAGACCTTCAATAGTGCC 38701
Db 352 SerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyVal 371
Qy 38702 ATCATTTAGAGTCCCAATTTTCATGGGTCTAGAAAGCTGACGACCTGATTTTCACAC 38761
Db 372 IleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGluHisLeuAspPheGlnHis 391
Qy 38762 TCTACTTAAAGAGGTCACAGAAATTTCTAGCGTTCTTATCCCTGTAAGAAAGCTTATAC 38821
Db 392 SerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAspLeuIleTyr 411
Qy 38822 CTTGACATCTCTTATACACCAAAATGACTGATGATGATGATTTATTTCTGGCTGACC 38881
Db 412 LeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 431
Qy 38882 AGTCTCAACACATTTAAATGCTGCGCAATCTTTCAAGAACACACCTTTCAATATGTC 38941
Db 432 SerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGlnLysPheLeuProAspIle 451
Qy 38942 TTTGCAAAACCAACAAATCTGACATTCCTGATCTTTCTAAAGTCAATTTGAAACAAATA 39001
Db 452 PheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnGlnLeuGluGlnLeu 471
Qy 39002 TCTTGGGGGTATTTGACACCTCCATAGACTTCAATTATTAATATGAGTCAACAAAT 39061

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Db 472 SerProthralAlpheanSerLeuSerLeuInValLeuAnMetSerHisAAsn 491
Qy 39062 CTATGTTTGGATTCATCCATTAACAGCTGATTCCTTCAGACATCTTGATTC 39121
Db 492 PhePheSerLeuAptRhrPheProTyrLeuCySeuLeuSerLeuGlnValLeuAptTyr 511
Qy 39122 AGTTTCATCCGATGAGACATCT--AAAGAAATACCTGCAATTTTCCAAAGCTA 39178
Db 512 SerLeuAnHisTlleMetThrSerLeuValSerGlnLeuGlnHisPheProSerLeu 531
Qy 39179 GCCTTCTTCATCTTACTAACAATTCCTGCTGTATGTATGTGAACATCAAGAAATTCCTG 39238
Db 532 AlAlpheuAnLeuThrGlnAnAsPheAlaCyThrCySeuGlnHisGlnSerPheLeu 551
Qy 39239 CAGTGGGTCAGAAAGACAGACAGCTTCTGGTGAATGTGAACAATGACATGTGCACA 39298
Db 552 GlnTrrPheLeuValSerGlnAnArgGlnLeuValGlnValGlnArgMetGlnCyAlaThr 571
Qy 39299 CCTGTAGAGATGAAATACCTCCTTAGTGTGATTTTAATATGTAACCTGTATATGTAC 39358
Db 572 ProSerAspLeuValGlnGlyMetProValLeuSerLeu--Asn1LeuThrCySeuGlnMetAsn 590
Qy 39359 AAGCAATCATCAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 39418
Db 591 LysThrTlleLeuGlnValSerValLeuSerValLeuValValSerValAlaAlaValLeu 610
Qy 39419 ATATACCACTTCTATTTTACCTGATTAATTTGCTGGCTGTAAAGTACAGACAGAGA 39478
Db 611 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCyS1LeuValGlyAlaArgGly 630
Qy 39479 GAAAGCATCTATGATGATTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 39538
Db 631 GlnAnTlleTyrAsPheAlaPheVal1LeuTyrSerSerGlnAsPheGlnAsPheTrrValArgAsn 650
Qy 39539 GAGCTGTAAAGAAATTTGAGAAAGAGAGTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 39598
Db 651 GluLeuValLysAnLeuGlnGlnGlyAlaProPhePheGlnLeuCySeuLeuHisTyrArg 670
Qy 39599 GACTTATTCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 39658
Db 671 AspPheTleProGlnValAla1leAla1AnTlle1leHisGlnGlyPheHisLysSer 690
Qy 39659 CGAAGGTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 39718
Db 691 ArgLysVal1leValValSerGlnHisPhe1leGlnSerArgTrrCyS1lePheGln 710
Qy 39719 TATGATTTGCTCAACATGACAGTTCCTGAGCAGCCGCTGCGATCATCTTCATTTGTC 39778
Db 711 TyrGlnTlleAlaGlnThrTrrPheLeuSerSerArgAlaGlyTllePhe1leVal 730
Qy 39779 CTTCAGAAAGTTGAGAAAGTCCCTGTGTGAGCAGCAGGTTGAATGTATGCGCTTTCAGC 39838
Db 731 LeuGlnLysVal1GlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
Qy 39839 AGAAACACCTTCCTGAGATGAGAGAGACATCTTCGAGAGAGACATCTTCGAGAGAGA 39898
Db 751 ArgAnThrTrrLysGlnTrrPheGlnAsPheSerValLeuGlnLysArgHis1lePheTrrPheArg 770
Qy 39899 CTTAAAAATGCCCTATTTGATGAGAAAGCCTCGATCTTCGAGCAACAA 39946
Db 771 LeuArgLysAlaTlleLeuAsPhePolLysSerTrrPheAnProGlnGlyThr 786

RESULT 6
; Sequence 181, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
```

```
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ. ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-181

Alignment Scores:
Pred. No.: 4,81e-34 Length: 641
Score: 575.50 Matches: 110
Percent Similarity: 72.73% Conservative: 34
Best Local Similarity: 55.56% Mismatches: 53
Query Match: 0.66% Indels: 2
DB: 16 Gaps: 1

US-09-396-985b-48 (1-50000) x US-10-408-765A-181 (1-641)
Qy 36378 ATTGAAATATGGGGTACAGAACTAAAGAAATTCCTCACTGAGGAATGATGACT 36319
Db 435 TlleLysTrrPheAlaLysAsPheClnAnArgHisPheSerLysGlnSrrPheTrrAlaAla 454
Qy 36318 GAAAGTACCTAAATAAATGTTTACATCTTATGATCATCAGGAAATGCAATCAAAACA 36259
Db 455 LysLysHisMetLysLysCySeuSerSerSerLeuAla1leArgGlnMetGlnTlleTrr 474
Qy 36258 ACCCTGATTTCCATCTTCACACAGCAGTCAAGATGACTTAAGTCAAAAATCTAATGACAGC 36199
Db 475 ThMetArgTrrHisLysTrrProValArgMetAla1leTlleLysSerGlyAsnAsn 494
Qy 36198 AGATGCTCCGAGAGA-TGTAGAGAGAGAGAACCTCTCCATGCTGCGAGAACTGTAA 36140
Db 495 ArgGlyTrrPheGlnLysGlnGlyGlnTlleGlyThrLeuLeuHisCySrrPrrAsPheCyS1Lys 514
Qy 36139 CTGATTAACCACTCTGAAATGCAATGATTTGTGTGCTCTCAGAAATTTGACATGTACTA 36080
Db 515 LeuValGlnProLeuTrrPrrLysSerValTrrArgPheLeuArgSrrLeuGlnTlle 534
Qy 36079 CTTGAGAGTCCAGCATACCATCTTCAGGCAAAATATCCAGATAT--GCTTCACTTGT 36023
Db 535 ProPheAsPrrAla1leProLeuLeuGlyTlleTrrProAnAsPrrTrrLysSerCyS1Lys 554
Qy 36022 AATPAGACACATGCTCTACTATGTTCAATGACAGTTTATTTAATPAGCAGATGCTTG 35963
Db 555 TyrLysAsPrrHisCySrrHisArgMetPhe1leAlaAlaLeuPheThrTlleAlaLysThrTrr 574
Qy 35962 AAAGAACTGATGTCTCTCAACAGAAATGAGATCAAAAATATGTGATCATTTGCACA 35903
Db 575 AsnGlnProLysCySrrHisArgMetTlleAsPrrTlleLysLysMetTrrHisTlleTrr 594
Qy 35902 GTGAGTACTTATGACGATTAATAAACAAGTGAATCTATGACATTTCTTGAAGCAATGAATG 35843
Db 595 MetGlnLysTrrAlaAlaTlleLysAsnAsPrrLysPheMetSerPheValGlyThrTrrMet 614
Qy 35842 GACCTGAGGAGGACATCATCTGAGTGAAGTAAACCAGTCATMAAAGAAAGACACAT 35789
Db 615 LysLeuGlnThrTlleTlleLeuSerLysLeuSerGlnGlnLysThrLysHis 632

RESULT 7
; Sequence 153, Application US/10000256A
; Publication No. US2003003985A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yungming
; APPLICANT: Recipon, Hervey
; APPLICANT: Chen, Sel-Yu
```


FILE REFERENCE:	P2038P1
CURRENT APPLICATION NUMBER:	US/10/050,882
CURRENT FILING DATE:	2002-01-18
PRIOR APPLICATION NUMBER:	09/661,453
PRIOR FILING DATE:	2000-09-13
PRIOR APPLICATION NUMBER:	PCT/US00/06783
PRIOR FILING DATE:	2000-03-16
PRIOR APPLICATION NUMBER:	60/125,055
PRIOR FILING DATE:	1999-03-18
NUMBER OF SEQ ID NOS:	156
SOFTWARE:	Patentin Ver. 2.0
SEQ ID NO 80	
LENGTH:	1010
TYPE:	PR1
ORGANISM:	Homo sapiens
FEATURE:	
NAME/KEY:	SITE
LOCATION:	(125)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(104)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(194)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(362)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(525)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(643)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(649)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(656)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(660)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(731)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(770)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(777)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(790)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(800)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(825)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(987)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(996)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
NAME/KEY:	SITE
LOCATION:	(1003)
OTHER INFORMATION:	Xaa equals any of the naturally occurring L-amino acids
US-10-050-882-80	
Alignment Scores:	

Pred. No.:	2e-33	Length:	1010
Score:	568.50	Matches:	109
Percent Similarity:	71.72%	Conservative:	33
Best Local Similarity:	55.05%	Mismatches:	55
Query Match:	0.66%	Indels:	2
DB:	14	Gaps:	1

US-09-396-985B-48 (1-50000) x US-10-050-882-80 (1-1010)

QY	36378	ATTGAAATATGGGGTACAGAACTAAAGAAAGAAATTTCTCACTGAGAGATACCTGAATGACT	36319
DB	804	lelylsytrp alalsyapmctaa cgh snpserlysg uabp lelyr aa a	823
QY	36318	GAAGAGTAAAGAAATTTTAAACATGCTTACATCATAGGAAATGAAATCAAAACA	36259
DB	824	LyS**H smctlysyb CyS ser Ser Ser le a a le a g u w et c n le y st tr	843
QY	36258	ACCTGATATTCACACTTCACACAGCAGACAGATGATAGATGAAATCAAGTACAGC	36199
DB	844	Th n e c t g T y n h e u t t p r o v a l a g m e a l e l e y l y s e r c l y s n e n	863
QY	36198	AGATGCTCGCAAGA-TGTAGAAGAGAGAGAAACACTTCTCATTTGCTGGCAGACTGTAA	36140
DB	864	Arg Cy e r t p a g l y c y s g l u n l e g l y t n e u n h e c y e r t p a s p Cy b s	883
QY	36139	CTGATATTAACCACTCTCGAAATCAAGTTTGGTGGTCTTCAGAAATTTGCACTGGACTA	36080
DB	884	Le u a l n p r o e u t p l y s e r a l t p a g p h e l e a g a s p l e u e u l e	903
QY	36079	CCTAGAGTACAGAAATACACATCCAGAGCAAAATATTCACAGATGAT---GCTTCACCTTGT	36023
DB	904	P r o h e a s p r o a l e p r o l e u e u g l y l e y t p r o l y a s p r y t y s e r Cy b s	923
QY	36022	AATAGAGACATAGCTCTACTATGTTCATAGCAGTTTATTTATAATAGCCAGATGCTTG	35963
DB	924	Ty t y a s p h r Cy t n t a g m e t p h e a l a l e u p h e t t l e a l y s t t p	943
QY	35962	AAAGACCTTAGTGTCCTTCCCTACAGAGAAATGATACAAAATAAGTACATTTCACA	35903
DB	944	A s n l n p r o l y s C y s p r o t h e t l e a s p t p l e y l y e w e t t p h s l e y t n t	963
QY	35902	GTGAGTACTATGAGAGCTATTAATAACAGATGATCTATGACATTTTATGACCAATGATG	35843
DB	964	W e t g u t y t y a l a a l e y l y a s a p g l p h e w e s e r h e v a l y t n t p w e t	983
QY	35842	GACCTGAGGAGCATCTCTGATGAGGTAAACCCAGCTCATTAAGAGAGACAT	35789
DB	984	Ly s le u g u a ** e l e l e u s e r y l e u s e r c l n ** G l y s t h r y s h s	1001

RESULT 10

US-10-800-322-34

/ Sequence 34, Application US/10800322

/ Publication No. US20050053967A1

/ GENERAL INFORMATION:

/ APPLICANT: MEDIMOLECULAR PTY LTD

/ TITLE OF INVENTION: NOVEL MARKERS AND USES THEREOF

/ FILE REFERENCE: 2558321/TDO

/ CURRENT APPLICATION NUMBER: US/10/800,322

/ CURRENT FILING DATE: 2004-03-12

/ PRIOR APPLICATION NUMBER: US 60/322228

/ PRIOR FILING DATE: 2001-09-14

/ NUMBER OF SEQ ID NOS: 338

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 34

/ LENGTH: 1275

/ TYPE: PRT

/ ORGANISM: mammalian

US-10-800-322-34

Alignment Scores:

Pred. No.:	3.12e-33	Length:	1275
Score:	567.50	Matches:	108
Percent Similarity:	72.73%	Conservative:	36

[illegible][illegible]

Oy		36022	AATPAGACACAGCCTCTACTATGTCATGACGGTTTATTATAATACCAGA-----	35963
Db		1180	Tyrttysaphrtycstrhtiswmetphellalaaleuphetrrllledglubrgleugly	1199
Oy		35968	-----TGCTTGAAGAACCTCATGTGTCCTCAACAGAGAAATGCATTACAAMAA	35921
Db		1200	ThrasnProlyshtrhtpranglnPrplyscysprothrmellamspTrlleyelsys	1219
Oy		35920	ATATGTGACATTGSCACAGTGGAGTACTATGACGTAATTAAAAACGTGAATCTATGACA	35861
Db		1220	MetrPhlsilerTyrtThmetGluryTYZALAlallelysbnmludluPhemeter	1239
Oy		35860	TTCTTCAGCAAAATGAAGACCTGGAGGGCATGATCCTGAGAGGTAAACCGATCATPA	35801
Db		1240	PhevalglthrtrhpmetcluyelulllelleuseusryeusergInglugn	1259
Oy		35800	AAGAAGACAGAT 35789	
Db		1260	Lyrthrlyshls 1263	
RESULT 12				
		US-09-954-987B-192		
		/ Sequence 192, Application US/09954987B		
		/ Publication No. US20030104523A1		
		/ GENERAL INFORMATION:		
		/ APPLICANT: Stefan Bauer		
		/ APPLICANT: Grayson B. Lipford		
		/ TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF		
		/ TITLE OF INVENTION: CPG-BASED IMMUNO-AGONIST/ANTAGONIST		
		/ FILE REFERENCE: C1041/7016 (AMS)		
		/ CURRENT APPLICATION NUMBER: US/09/954,987B		
		/ PRIOR FILING DATE: 2001-09-17		
		/ PRIOR APPLICATION NUMBER: US 60/233,035		
		/ PRIOR FILING DATE: 2000-09-15		
		/ PRIOR APPLICATION NUMBER: US 60/263,657		
		/ PRIOR FILING DATE: 2001-01-23		
		/ PRIOR APPLICATION NUMBER: US 60/291,726		
		/ PRIOR FILING DATE: 2001-05-17		
		/ PRIOR APPLICATION NUMBER: US 60/300,210		
		/ PRIOR FILING DATE: 2001-06-22		
		/ NUMBER OF SEQ ID NOS: 230		
		/ SOFTWARE: FastSeq for Windows Version 3.0		
		/ SEQ ID NO 192		
		/ LENGTH: 1032		
		/ TYPE: PRT		
		/ ORGANISM: Mus musculus		
		US-09-954-987B-192		
Alignment Scores:				
		Pred. No.: 1,31e-32		length: 1032
		Score: 548.00		Matches: 219
		Percent Similarity: 42.89%		Conservative: 149
		Gest Local Similarity: 25.52%		Mismatches: 298
		Query Match: 0.63%		Indels: 192
		DB: 10		Gaps: 35
		US-09-396-985B-48 (1-50000) x US-09-954-987B-192 (1-1032)		
Oy		37721	TTTTGCCCATGAGTGTGAATTTGAACAATTTGAAGACAGGATGGCATGGCTTACACAC	37780
Db		223	PheuserSerenalalylsllemetAdanilleThrGlnIuhpRheylsglyeuGIuaen	242
Oy		37781	CTCTCAAACTTGATTACTGACAGAGAAAC-----	37807
Db		243	LeuthrleueuapRleuSerGlyAcysProlatCystrYrAnAlaProPheProcys	262
Oy		37808	---CCATCCAGAGATTTTCC-----	37849
Db		263	ThrpocysylsvgluabenserSelleihieilPheProleuAlahedInserleutnr	282
Oy		37850	AGTTTAGAATCTGTGTGCTGTGGAGACAAAATTGGCCTCTCTGAAAAGCTTCCCTATT	37909

Db	283	GlnLeuLeuTyrLeuAsnLeuSerSerThrSerLeuArgThrIleProSerThrTrpPhe	302
Oy	37910	GGACAGCTTATAACCTTTAAAGAAACCAATGTGGCTCACAATTTT---ATACATTCTGT	37966
Db	303	GlnAsnLeuSerAsnLeuLeuArgIleuThrIleuThrIleuGlnPheAsnTyrLeuValGlnIle	322
Oy	37967	AACTTACCTGCATATTTTTCACATCTGCAGCAACCTGACATGACATGTCGATCTTTCTATAC	38026
Db	323	AlaSerGlyAlaPheLeuThrLysLeuProSerIleuGlnIleLeuAspLeuSerPheAsn	342
Oy	38027	-----TATATGCAACTATATACCTGC---AACGACCTTACAGTTTCTACGT	38068
Db	343	PheGlnTyrLeuGlnTyrLeuGlnPheIleAsnIleSerSerAsnPheSerIleuArg	362
Oy	38069	GAATAATCCAAAGCTCAATCTC-----	38089
Db	363	SerLeuLysLeuThrLeuThrIleuArgGlyTyrValPheArgGluLeuLysLeuHisPhe	382
Oy	38090	-----	38119
Db	383	GlnHisLeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIleAsnHisLeuGlu	402
Oy	38120	TTGATTTCAAGACCAAGCTCTTTCAGGGAAT---AAGCTTCATGACATGACCTTAAGAGT	38176
Db	403	LysIleAspPheLysAlaPheGlnAsnPheSerLysLeuAspValIleTyrLeuSerGly	422
Oy	38177	AATTTTAATAGCTCAATTAATTAAGAAACTTCCTTCAAACTGGCTGGTTTACAGCTC	38236
Db	423	AsnArgIleAlaSerValLeuAspGlyThr-----	432
Oy	38237	CATCGGTGATCTTGGGAGAATTTAAAGATGAAGAAAGATCTGGAAATTTTGAACCTCT	38296
Db	433	-----AspTyrSerSerTrpArgAsn---ArgLeuArgLysProLeu	445
Oy	38297	ATCATGAAGAGCTATGTGATGACCATGTGATGAGTTGAGGTTTAACATATACAAATGAT	38356
Db	446	SerThrAspAsp-----AspGlnPheAsp---ProHisValAsnHisPhe	458
Oy	38357	TTT-----TCAGATGATATTGTTAAGTTCCATGCTGGCGCAATGTTCTGCAATGCT	38410
Db	459	TyrHisSerThrLysProLeuIleLysProGlnCysThrAlaTyrGlyLysAlaLeuAsp	478
Oy	38411	CTGGCAGGTGATCTTAAATAATCTACAGAAGATGTTCCATTAATTCGAAAGGCAATCC	38470
Db	479	Leu-----SerLeuAsnAsnIlePheIleGlyLysSer---GlnPheGlnGly	494
Oy	38471	TTATCATCATTTAGATGTCAACTTAAAGACGTTTCCAACTGTGATCACTTCTTAA	38530
Db	495	PheGlnAspIleAlaCys-----	500
Oy	38531	AGTTGACTTAACTATGAACAAGGCTCTATACAGTTTAAAAAGTG-----GCC	38581
Db	501	-----LeuAsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGluPheSerSer	519
Oy	38582	CTAACCAAGTCTGAGCTATCATGATCTTAAGNAAATGACCTGAGCTTGTAGTGTGCTGT	38641
Db	520	MetProHisIleLysTyrIleuAspLeuThrAsnAsnArgLeuAspPheAspAsnAsn	539
Oy	38642	TCTTATTTCTGATTTGGAAACAAACAGCTGAGACACTTAAAGCTTACAGCTTCAATGATGCC	38701
Db	540	AlaPheSerAspLeu-----HisAspLeuGlnValLeuAspLeuSerHisAsnAlaHis	557
Oy	38702	ATCATTTATGATGCCAAT-----TTATGGGTTTAAAGAGCTG	38740
Db	558	TyrPheSerIleAlaGlyValThrHisArgLeuGlyPheIleGlnAsnLeuIleAsnLeu	577
Oy	38741	CAGACACTGGATTTTACGACCTCTACTTTAAAAAGGCTACAGAA-----	38785
Db	578	ArgValLeuAsnLeuSerHisAsnGlyIleTyrThrLeuThrGlnGluSerGluLeuLys	597
Oy	38785	-----	38785

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Db      598 SerIleSerLeuValGluLeuValPheSerGluValAsnArgLeuAspHisLeuTrpAsnAla 617
Qy      38786 -----TTCTGAGCGTTTATCCCTGAAAGACTTATCTTGACATC 38830
Db      618 AsnArgGluValYrTrpSerIlePheLeuSerLeuGlnAsnLeuIleArgLeuAspLeu 637
Qy      38831 TCTTATACTAACACCAAAATGACTCGATGATATTTCTTGCGCTTG--ACCAAGCTTC 38887
Db      638 SerIyrAsnAsnLeuGlnGlnIleProAsnGluAlaPheLeuAsnLeuProGlnSerLeu 657
Qy      38888 AACACATTAAAAAGCGCTGGCAATTTCT-----TTCAAGACAAACCCCTTCAAAATGC 38941
Db      658 GlnGluLeuLeuIleSerGluValAsnLeuArgPheAsnTrpIleLeuGlnIlyr 677
Qy      38942 TTTCGAAACACAAACAACTTACATTCCTGATCTTTTAAATGATGCAATGGAACAAATA 39001
Db      678 Phe-----ProIleValHisLeuLeuAspLeuSerIleArgAsnGluLeuTrpPheLeu 694
Qy      39002 TCTTGGGGGATATTGACACCCCTGATGACTCAATTAATTAATGATGATGATGATGATGAT 39061
Db      695 ProAsnCysLeuSerIyrPheAlaHisSerLeuGlnIlyrLeuLeuLeuSerHisAsnHis 714
Qy      39062 CTATGTTTGTGGATGATCCCATTAATTAACAGCTGATTTCCCTGACAGACTTGTGATTC 39121
Db      715 PheSerHisLeuProSerGluPheLeuSerGluAlaArgAsnLeuValHisLeuAspLeu 734
Qy      39122 AGTTTCATGCGCATAGAG--ACATCTAAAGGAATACGCAACATTTTCCAAAG--AGT 39175
Db      735 SerPheAsnTrpIleValMetIleAsnLeuSerLeuGlnIlyrValMetLeuTrpAsn 754
Qy      39176 CTACGCTTCTTCAATCTTACTACAAATCTTCTGCTGATATGCAATCAACAAATTC 39235
Db      755 LeuSerIleLeuGluLeuHisGluValAsnTrpPheAspCysTrpCysAspIleSerAspPhe 774
Qy      39236 CTGACAGTGGCTCAAGAAACAGACGAGCTC-----TTGGTGAATGTTGAACAA 39283
Db      775 ArgSerTrpLeuAspGluAsnLeuAsnIleTrpIleProValLeuValAsnVal----- 792
Qy      39284 ATGACATGTGCAACACCGTGAAGATGAATACCTCTGATGTTGATTTTAATTAATTC 39343
Db      793 ---IleCysSerAsnProGluValAspGlnLeuValSerLeuIleMetSerLeuAspLeuThr 811
Qy      39344 ACCTGTATATATGTAACAAGCAATCATCAGTGTGATGATGATGATGATGATGATGATGATGAT 39403
Db      812 ThrCysValSerAspTrpIleAlaValLeuPheLeuThrPheLeuThrSer 831
Qy      39404 ACTGTA-----GCATTTCTGATATACAC-----TTCTATTTT 39436
Db      832 MetValMetLeuAlaIleValHisIleValPheTrpValTrpPheIleTrp 851
Qy      39437 CACCTG-----ATACTTATGCTGCGCTGTAAGAAAGTACAGCAAGAGAAAGATCTAT 39490
Db      852 HisMetCysSerAlaValLeuValGluTrpArgTrpSerSerTrpSerGlnTrpPheTrp 871
Qy      39491 GATGCAATTTGATGATCTGAGTCAAGAT-----GAGCACTGGGTGAGAAATGAG 39541
Db      872 AspIleArgTrpIleSerTrpAspTrpLeuAspAlaSerValTrpAspTrpValIleAsnGlu 891
Qy      39542 CTGCTAAAGATTTTGAAGAAAGAGTCCCGC--TTTCACTCTGCTGCTTCACTACAGA 39598
Db      892 LeuArgTrpHisLeuGlnGluSerGluAspSerValLeuLeuValCysLeuGlnGluArg 911
Qy      39599 GACTTATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39658
Db      912 AspTrpAspProGluLeuProIleIleAspAsnLeuMetGln---SerIleAsnGlnSer 930
Qy      39659 CGAAGGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39718
Db      931 LysArgTrpIlePheValLeuThrLysLysTrp----- 941
Qy      39719 TATAGATGCTCAACAGCACTGCTGAGC----- 39751
Db      942 -----AlaLysSerTrpAsnPheThrAlaPheTrpLeuAlaLeuGlnArgLeu 958

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Qy      39752 -----AGCCGCTGCGATCATCTTCAATTTCTTGAGAGTTTGAGAACTCCCTG 39802
Db      959 MetAspGluAsnMetAspValIleIlePheIleLeuLeuGlnProValLeuGln----- 976
Qy      39803 CTGAGGAGCAGGATGGAATTTGATTCGCTTTTACAGAAAACCTTACCTGGAATGGAG 39862
Db      977 TyrSerGlnTrpLeuArgLeuArgGlnArgIleCysLysSerSerIleLeuGlnTrpPro 996
Qy      39863 GACAACTCTCTGGGAGAGCACATCTTCTGAGAGAACTTAAATAGCCCTATTG 39916
Db      997 AsnAsnProValAlaGluAsnLeuPheTrpGlnSerLeuLysAsnValValLeu 1014

RESULT 13
US-10-272-502A-31
: Sequence 31, Application US/10272502A
: Publication No. US20030139364A1
: GENERAL INFORMATION:
: APPLICANT: Krieg, Arthur M.
: APPLICANT: Schetter, Christian
: APPLICANT: Bratzler, Robert L.
: APPLICANT: Volmer, Jorg
: APPLICANT: Bauer, Stefan
: APPLICANT: Jurk, Marion
: TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
: FILE REFERENCE: C01039.70065 US
: CURRENT APPLICATION NUMBER: US/10/272.502A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/329,208
: PRIOR FILING DATE: 2001-10-12
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 31
: LENGTH: 1032
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-272-502A-31

Alignment Scores:
Pred. No.: 1,31e-32 Length: 1032
Score: 548.00 Matches: 219
Percent Similarity: 42.89% Conservative: 149
Best Local Similarity: 25.52% Mismatches: 298
Query Match: 0.63% Indels: 192
DB: 14 Gaps: 35

US-09-396-985B-48 (1-50000) x US-10-272-502A-31 (1-1032)
Qy      37721 TTGGCCCATAGGTGTAATTTGAACAATTTGAAGACAGGACGCTTACACAC 37780
Db      223 PheLeuSerAsnAlaLysIleMetAsnIleThrGlnIleAspPheLysGluLeuValAsn 242
Qy      37781 CTCTCAAACTTGATCTGACAGGAAC----- 37807
Db      243 LeuThrLeuLeuAspLeuSerGluValAsnCysProArgCysTrpTrpAsnAlaProPheProCys 262
Qy      37808 ---CTATCCAGAGTTTTC-----CCAGAAATTTCTCTGAGCTTACA 37849
Db      263 ThrProCysLeuValGluAsnSerSerIleHisIleIleProLeuAlaPheGlnSerLeuThr 282
Qy      37850 AGTTTGAAGAACTGTGCGCTGAGAGAAATTTGGCCCTCTAGAAAGCTTCCCATAT 37909
Db      283 GlnLeuLeuTrpLeuAsnLeuSerSerTrpSerLeuArgTrpIleProSerTrpTrpPhe 302
Qy      37910 GACAGCTTATTAACCTTAAAGAACTCAATGTGCTCACAAATTT--ATACTTCCTGT 37966
Db      303 GluAsnLeuSerAsnLeuLysGluLeuHisLeuGlnPheAsnTrpTrpValGlnGluIle 322
Qy      37967 AAGTTACCTGCATATTTTTCATCTGACGAACTTGTATACCTTGTGATCTTTTATTAAC 38026
Db      323 AlaSerGluAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAspLeuSerPheAsn 342

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[illegible]

Db	658	GlInGluLeuLeuLeuLeuSerGlyLeuValSLeuArgPhePheAsnTrpThrLeuLeuGlnTyr	677
QY	38942	TTTGCAAAACAAACAACAACTGGACATTTCTGGATCTTTCTTAATATGTCATGGAACAATAA	39001
Db	678	Phe-----ProHisLeuHisLeuLeuAspLeuSerArgAsnGluLeuTyrPheLeu	694
QY	39002	TCCTGGGGGGATTGTCACCCCTCCATGACTTCAATTATTAATATGAGTCACAACAAT	39061
Db	695	ProAsnCySerLeuSerLysPheAlaHisSerLeuGlnThrLeuLeuLeuSerHisAsnHis	714
QY	39062	CTATTTGTTTGGATTCATCCCATTTTAACACAGCTGTATTCCTCCAGACCTGTGATTTC	39121
Db	715	PheSerHisLeuProSerGlyPheLeuSerGlnAlaArgAsnLeuValHisLeuAspLeu	734
QY	39122	AGTTTCATGCGCATAGAG--ACATCTGTAAGAGAACTAGTCAACAATTTTCAAG--AGT	39175
Db	735	SerPheAsnThrIleLysMetIleAsnLysSerLeuGlnThrIleLysMetLysThrAsn	754
QY	39176	CTAGCCTTCTTCATCTTACTTAACAATTCTGTTCCTGTATATGTAACATCAGAAATTC	39235
Db	755	LeuSerIleLeuGlnLeuHisGlyAsnTyrPheAspCysThrCysAspThrLeuSerAspPhe	774
QY	39236	CTGCAGTGGGTCAAGAAACAGAAAGCACTTC-----TTGGTGAATGTGAAACA	39288
Db	775	ArgSerTrpLeuAspGlyAsnLeuAsnIleThrIleProLysLeuValAsnVal-----	792
QY	39284	ATGACATGTGCAACACCTGTAGATGATGATACCTCTTAGTGTGGATTATTAATATCT	39343
Db	793	---IleCysSerAsnProGlyAspGlnLysSerLysSerIleMetSerLeuAspLeuThr	811
QY	39344	ACCTGTATATATGACAAAGACAATCATCATCAGTGTGTCAGTGTCACTGTGATGTGTATCC	39403
Db	812	ThrCysValSerAspThrThrAlaAlaValLeuPhePheLeuThrPheLeuThrThrSer	831
QY	39404	ACTGTA-----GATTTCGATATATACC-----TTCTATTTT	39436
Db	832	MetValMetLeuAlaAlaLeuValHisHisLeuPheTyrTrpAspValTrpPheIleTyr	851
QY	39437	CACCTG-----ATACTTATGCTGGCTGTGTAAGAAAGTACAGAGAGAAAGACATCTAT	39490
Db	852	HisMetCysSerAlaLysLeuLysGlyTyrArgThrSerSerThrSerGlnThrPheTyr	871
QY	39491	GATGCATTTGTGATCTACTCGATCAGAAAT-----GAGGACTGGGTGAGAAATGAG	39541
Db	872	AspIleTyrIleSerTyrAspThrLysAspAlaSerValThrAspTrpValIleAsnGln	891
QY	39542	CTGTAAAGAAATTATGAAGAAGAGTCCCGC-----TTTCACTCTGCTTCACTACACA	39599
Db	892	LeuArgTyrHisLeuGlnGlnSerGluAspLysSerValLeuLeuCysLeuGlnGluAsp	911
QY	39599	GACTTTATCTCGTGTAGCATTGCTGCGCAACATCATCAGAGAAAGCTTCCACAGAGC	39658
Db	912	AspTrpAspProGlyLeuProIleIleAspAsnMetGln---SerIleAsnGlnSer	930
QY	39659	CGGAAGTTATTGTGATGATGTCTAGACACTTATTACAGCCGTTGCTGTATCTTTGAA	39718
Db	931	LysLysThrIlePheValLeuThrLysLysTyr-----	941
QY	39719	TATGAGATTGCTCAACAATGGCACTTCTGAC-----	39753
Db	942	---AlaLysSerTrpAsnPheLysThrAlaPheTyrLeuAlaLeuGlnArgLeu	958
QY	39752	-----AGCGCTCGGAGATCATCTTATGCTTGTGAGAAGGTGAGAGTCCCG	39802
Db	959	MetAspGlnAsnMetAspValIleIlePheIleLeuLeuGlnProValLeuGln-----	976
QY	39803	CTGAGCAGACAGGTGATGTATTCGCTTTTATGACAGAAACACTTACCTGATGATGGAG	39863
Db	977	TyrSerGlnTyrLeuArgLeuArgGlnArgIleCysLysSerSerIleLeuGlnTrpPro	996
QY	39863	GACAATCTCTGGGGAGGACATCTTGTGAGAAAGACTTAAAAATGCCCTATTG	39916

Db 997 AsnAsnProlysaIaGluAsnLeuPheTrpGlnSerLeuIysAsnValIaIleu 1014

RESULT 14
US-10-407-952-32
Sequence 32, Application US/10407952
Publication No. US20030232074A1
GENERAL INFORMATION:
APPLICANT: Lipford, Grayson
APPLICANT: Bauer, Stefan
TITLE OF INVENTION: Immunostimulatory G, U-Containing Oligoribonucleotides
FILE REFERENCE: C01041.70037.US
CURRENT APPLICATION NUMBER: US/10/407,952
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/421,966
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 60/370,515
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-10-407-952-32

Alignment Scores:
Pred. No.: 1,31e-32 Length: 1032
Score: 548.00 Matches: 219
Percent Similarity: 42.89% Conservative: 149
Best Local Similarity: 25.52% Mismatches: 192
Query Match: 0.63% Indels: 192
Gaps: 35

US-09-396-985b-48 (1-50000) x US-10-407-952-32 (1-1032)

Qy 37721 TTGCCCCATAGCTGTGAATTAAGAAACAATTGAAGACAGAGCGATGCGTTACACCAC 37780
Db 223 PheIuSerAenAlaIysIleMeIaenIleThrgInIuAepHeIySglYleuGluAen 242
Qy 37781 CTCGCAACTGTGATACGACAGCAAC----- 37807
Db 243 LeuThrIeulAenAepIeSerGlyAsnCyProArgCyStryrAenAlaProPheProCys 262
Qy 37808 ---CCTATCCAGAGTTTTC-----CCAGAGAGTTTCTCGACTACA 37849
Db 263 ThrProCyIysGluAenSerSerIleHisIleHisProIeAlaApeGlnSerLeuThr 282
Qy 37850 AGTTAGAGATCTGTGGCTGTGGAGACAAATTTGCGCTCTAGAAAGCTTCCCTATT 37909
Db 283 GlnIeulAenIyrlAenAenIeSerSerThrSerIeulAenThrlIeProSerThrTrpPhe 302
Qy 37910 GGACAGCTTAATACCTTAAGAAACTCAATGTGCTCACAATTT---ATACATTCCTGT 37966
Db 303 GluAenIeulAenIyrlAenIeSerSerIleHisIleHisProIeAlaApeGlnSerLeuThr 322
Qy 37967 AAGTACCTGATATTTTCCAAATCTGACGAACTAGACATGAGATCTTCTATTAAC 38026
Db 323 AlaSerGlyAlaPheLeuThrlYleuProSerLeuGlnIleAenAepIeSerPheAsn 342
Qy 38027 ---TATATCAACTATTAAGTCTC---AAGCACTTAAGTTTCTAGT 38068
Db 343 PheGlnIyrlYlsGluYrlAenGlnPheIleAsnIleSerSerAenPheSerIyLeuArg 362
Qy 38069 GAAATTCACAAAGCATCTC----- 38089
Db 363 SerLeuIySylAenIleAenIyGlyYrIvalPheArgIuIeulYylYlsHisPhe 382
Qy 38090 ---TCTTACAGATGCTTTGAACCAATGAC 38119
Db 383 GluHisIeulGlnSerLeuProAsnLeuAlaThrIleAenIeulGlyIleAsnPhelIleGlu 402
Qy 38120 TTCAATTCAGACCAAGCTTTCAAGGAAT---AAGCTTCATGAATGACTTAAAGAGT 38176
Db 38120 TTCAATTCAGACCAAGCTTTCAAGGAAT---AAGCTTCATGAATGACTTAAAGAGT 38176

Db 403 LysIleAspPheIySaIaPheGlnAsnPheSerIySleuAspValIleYrIleuSerGly 422
Qy 38177 AATTTAATAGCTCAATATATATGAAACTTGCTGAAAACCGGCTGTTACAGTC 38236
Db 423 AsnArgIleAlaSerValIeAspGlyThr----- 432
Qy 38237 CATCGTTGATCTTGGAGAAATTTAAAGATGAAAGATCTGAAATTTTGAACCTCT 38296
Db 433 -----AspIySerSerTrpArgAsn---ArgIeArgIyProIeU 445
Qy 38297 ATCATGAGAGCATATGATGACCATTTGATGATGATGATGATGATGATGATGATGAT 38356
Db 446 SerThrAspAsp-----AspIuPheAsp---ProHisValAsnPhe 458
Qy 38357 TTT-----TCAGATGATATTTGAATTCATTCATTCATTCATTCATTCATTCATTCAT 38410
Db 459 TyrHisSerThrIySylProIeIleIySylProGlnIySerThrlAlYrIySylAenAsp 478
Qy 38411 CTGGCAGGTGATATTAATAATATCTGAAGATGCTTCAACATTTCAATGCAATCC 38470
Db 479 Leu-----SerIeAenAenIlePheIleIleGlySer---GlnPheGlnGly 494
Qy 38471 TTATCAATCATTTAGATGCACTTAAGACAGTTTCAACTGTGATCACTTCTTAA 38530
Db 495 PheGlnAspIleAlaCys----- 500
Qy 38531 AGTTGACTTAACTATGACAAAGGCTATACGTTTAAAGAGG-----GCC 38581
Db 501 ---LeuAsnIeulSerPheAenAlaAenThrGlnValPheAsnGlyThrGluPheSerSer 519
Qy 38582 CTACCAAGTCTCACTATCTAGATCTTATGAGAAATGACATGATGATGATGATGATGATGAT 38641
Db 520 MetProHisIleIySylYrlAenAepIeThrAsnAsnArgIeAsnPheAspAsnAsn 539
Qy 38642 TCTTATTCGATTTGGGACAAACAGCTGAGACACTTAACCTCAGCTTCAATGTCGCC 38701
Db 540 AlaPheSerAspLeu-----HisAspLeuGluValIeAspIeulSerHisAsnAlHis 557
Qy 38702 ATCATTTAGAGTGCAT-----TTCAATGCTCTAGAAAGACTG 38740
Db 558 TyrPheSerIleAlaGlyValThrlHisArgLeuGlyPheIleGlnAenIleAenLeu 577
Qy 38741 CAGCAGCTGATTTTGCAGACTCTACTTAAAGAGCTCAGACA----- 38785
Db 578 ArgValIeAsnIeulSerHisAsnGlyIleYrThrlIeulThrgIuIuSerGluLeuIys 597
Qy 38785 ----- 38785
Db 598 SerIleSerLeuIySglIeulAenIyPheSerGlyAsnArgIeAsnHisIleuTrpAsnAla 617
Qy 38786 -----TTCACAGGCTTATTCCTTGAAGAAAGTACTTACCTTGACATC 38830
Db 618 AsnAspGlyIyStryrIlePheIySerIeulGlnAsnIleArgIeAspLeu 637
Qy 38831 TCTTATCTAACAACAATTTGACTGATGATATTTCTTGAGCTTG---ACCAAGCTC 38887
Db 638 SerIyAsnAsnIeulGlnIleProAsnGlyAlaPheIeAsnIeulProGlnSerLeu 657
Qy 38888 AACACATTAATAATGCTGCAATTC-----TTCAAGACAAACACCTTCAATGTC 38941
Db 658 GlnGluIeulAenIeSerGlyAenIySylAenIyPheAsnIlePheIleGlnIy 677
Qy 38942 TTTCGAAACACAAACCTTGACATTCCTGATCTTCTTAATGTCAAATGGAACAATA 39001
Db 678 Phe-----ProHisIeulHisIleuIeAspIeulSerIyAsnGlnIeulYrPheIeU 694
Qy 39002 TCTTGGGGGATATTTGACACCTTCATAGACTTCAATTAATTAATGATGACCAACAT 39061
Db 695 ProAsnCySleuSerIySylPheAlaHisSerIeulGlnThrlIeulAenIeulSerHis 714
Qy 39062 CTATGTTTGGATTCATCCATTAATACAGACTGATATTCCTCAGACACTTGTGATGC 39121
Db 715 PheSerHisIeulProSerGlyPheIeulSerGluAlaArgAsnIeulValHisIeulAepLeu 734

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QY 39122 AGTTCAATGCGATAGAG---ACATCTAAGGAATACGTCAACATTTTCCAAAG---AGT 39175
D 735 SerpheanhrilleyMetileasnlysserserleuglnhrLysMetLysrthAsn 754
QY 39176 CTACCCCTTCCTCAATCTTACTACAAATTCCTGCTGTATGTAATGCAATCAGAAATTC 39235
D 755 LeuserileleuGluehniGlyAsnhrYrheaprcystrhCyabpilleseAspPhe 774
QY 39236 CTGCACTGGCTCAAGAACAGACAGACAGTTC-----TTGGTGAATGTTGAACAA 39283
D 775 ArgsertrileuaprgluasnleuasnillethrilleproulyleuValAsnVal----- 792
QY 39284 ATGACATGTGCAACACCTGTAGATGAATGATGATCTCTTAAAGTGAATTTAAATATCT 39343
D 793 ---ileCyserAsnProglyAspelnlysserlysserilleMetSerleuAspLeuthr 811
QY 39344 ACCTGTATATATGTACAAACAATCATCATGTCAGTGTGTCAGTGTGATGTCATCC 39403
D 812 ThrCyseValserAspThrThrAlaValleuPhePheLeuthrPheLeuthrThrSer 831
QY 39404 ACTGTA-----GCATTTCTGATATACCA-----TTCTATTTT 39436
D 832 MetValMetleuAlaAlaValValHisHisleupheryrtrpAspValtrpPheilleYr 851
QY 39437 CACCTG-----ATACTATGTGCTGCTGTAAGAAAGTACAGCAGAGAGAAAGCATCTAT 39490
D 852 HisMetCyseSerAlaLysleuLysGlyYrYrthrSerSerThrSerGlnThrPheYr 871
QY 39491 GATCATATTGTGATCTACTGTCAGTCAAGAT-----GAGACCTGGGTGAGAAATGAG 39541
D 872 AspAlaYrIleSerYrAspThrLysAspAlaSerValThrAspTrpValilleAsnGlu 891
QY 39542 CTGCTAAGAAATTTTGAAGAAGAGAGTCCCGC---TTTCACTTCCTGCTTCACTACGA 39598
D 892 LeuArgYrHisleuGluGluSerGluAspLysSerValleuLeuCyseLugluGluArg 911
QY 39599 GACCTTATTCCTGGTGGCCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 39658
D 912 AspTrpAspProglyLeuProilleleAspAsnleuMetGln---SerilleAsnGlnSer 930
QY 39659 CGGAAGTATATGTGTCAGTGTCTAGACACTTATTCAGACCGTGTGTATCTTTGAA 39718
D 931 LysLysThrIlePheValleuThrLysLysYr----- 941
QY 39719 TATGATGTCCTCAAAACATGCGAGTTTCTGAGC----- 39751
D 942 -----AlaLysSertrpAsnPhelythrAlaPheYrLeuAlaLeuGlnArgLeu 958
QY 39752 -----AGCCGCTGCGGACATCTTCATTTGCTTGAAGAGTTGAGAGCCCTG 39802
D 959 MetAspGluAsnMetAspValillelePheilleuLeuGluProValleuGln----- 976
QY 39803 CTGAGCAGACAGTGGAAATGTATGACCTTCTTACAGAAAACCTTACCTGGAATGGAG 39862
D 977 TyrsertGlnYrleuArgleuArgGlnArgIleCyseLysSerSerilleleuGlnTrpPro 996
QY 39863 GACATCTCTGCGGAGGACATCTTCTGAGAGAGACTTAAATGCCCTTATG 39916
D 997 AsnAsnProlysaIaGluAsnleuPheTrpGlnSerleuYsaAsnValValleu 1014

RESULT 15
US-10-415-615-3
; Sequence 3, Application US/10415615
; Publication No. US20040101943A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LU, Yan
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: GANDHI, Ameena R.
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APPLICANT: HAFALIA, April J.A.
; APPLICANT: LAL, Preeti G.
; TITLE OR INVENTION: NUCLEIC ACID MODIFICATION ENZYMES
; FILE REFERENCE: PI-0280 USN
; CURRENT APPLICATION NUMBER: US/10/415, 615
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: PCT/US01/46301
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/245,458
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/255,107
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 1274
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1258887CD1
US-10-415-615-3

Alignment Scores:
Pred. No.: 3,47e-32 Length: 1274
Score: 551.50 Matches: 106
Percent Similarity: 69.61% Conservative: 36
Best Local Similarity: 51.96% Mismatches: 61
Query Match: 0.64% Indels: 2
DB: Gaps: 1

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QY 36318 GAAAGACCTCAAAAAAATGTTTAACTCTTGTGTCATGAGGAAATGCAAAATCAAAACA 36259
D 1088 AsnArgHisMetLysLysCyseSerSerleuValAlaYrGluMetGlnIleYstr 1107
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QY 36079 CTGAGAGTCCAGCAATACCACTCCAGAGCAAAATATCCAGATGAT--GCTTCACTTGT 36023
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D 1228 MetGluYrYrAlaAlaIleLysAsnAspGluPheMetSerPheValArgThrTrpMet 1247
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Db 1268 PheSerLeuIle 1271

Search completed: March 30, 2005, 15:34:07
Job time : 4042 secs

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4	2726	45.9	799	16	US-10-732-563-8
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6	609	10.2	661	13	US-10-114-893-10
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12	575	9.7	1032	15	US-10-407-952-32
13	559	9.4	1050	10	US-09-954-987B-175
14	559	9.4	1050	14	US-10-272-502A-22
15	559	9.4	1050	15	US-10-407-952-26
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? PRIOR FILING DATE: 1997-05-07
? PRIOR APPLICATION NUMBER: 60/072,212
? PRIOR FILING DATE: 1998-01-22
? PRIOR APPLICATION NUMBER: 60/076,947
? PRIOR FILING DATE: 1998-03-05
? NUMBER OF SEQ ID NOS: 45
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 26
? LENGTH: 837
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-950-041-26

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Alignment Scores:

Pred. No.:	2,45e-262	Length:	837
Score:	284.00	Matches:	558
Percent Similarity:	80.10%	Conservative:	114
Best Local Similarity:	66.51%	Mismatches:	159
Query Match:	47.85%	Indels:	8
DB:	10	Gaps:	6

US-09-396-985B-5 (1-3395) X US-09-950-041-26 (1-837)

QY	263	ATGCGTCCTTGAACTGGCGCGGGAGCTGTAACTAGGATGGT---	TTGCTTTCCGCGCG	319	
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QY	320	AGACGAGAACTTGAAATCCCTGCAATGAGGACTTCCCTAATATTAACCTACCAATGCATG		379	
Db	21	ArgProGlnSerT	rgGluProCysValGluVal---	ProAleni1eThrTyrGlnCysMet	39
QY	380	GATCAAGAACTCAGCAAAATCCCTTCATGACATCCCTTATTGAAACCAAACTTAGTCTG		439	
Db	40	GluIeuAsnPheTyrLys1LeuProAspAsnLeuProPheSerThrLysAsnLeuAspLeu		59	
QY	440	AGCTTCAACCCCTGGAAGCTTTAAGAAAGCTATAGCTTCAACCAATTTCTCAAACTTCAG		499	
Db	60	SerPheAsnProLeuAlaArgHisLeuGlnYserTyrSerPhePheSerPheProGluIeuGln		79	
QY	500	TGCGTCGATTTATCCAGGCTGTGAATTTGACAATTTGAAAGACAAGGCAATGCGATGGCTTA		559	
Db	80	ValIeuAspLeuSerArgCysGlu1IleGlnThrTrileGluAspArgLysAlaTyrGlnSerLeu		99	
QY	560	AACCAAGCTTCAACCTTGGTACTACAGGAAACCTATCAAGAGTCTTTCCCGAGAACT		619	
Db	100	SerHisLeuSerThrLeu1IleLeuThrTrileuAsnPro1IleGlnSerLeuAlaLeuGlnLysAla		119	
QY	620	TTTTTGGACATCAACAAATTTAGAGAAATGTGGCTGTGGAGACAAATAATGACCTGTCTA		679	
Db	120	PheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSerIeu		139	
QY	680	GAGGATTTCCAAATTTGACAGACTTATATCTTTAAAGAACTAATGTGGCTCATATCTTT		739	
Db	140	GluAsnPhePro1IleGlyHisLeuLysThrIleuLysGlyLeuAsnValAlaHisValIeu		159	
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QY	800	TTTTCTTATCACTATATTCAAACTATTTCTGTGCAAGAGCACTTACAGTTCTCACTGAAAT		859	
Db	180	LeuSerSerAsnLys1IleGlnSerTrileTyrCysThrAspLeuArgValLeuHisGlnMet		199	
QY	860	CCCCAAGTCATCTCTCTTTAGACTGTGCTTTAAACCCCAATTTGACTCCATTCMAAGCCCA		919	
Db	200	ProIleuAsnLeuLeuSerLeuAspLeuSerLeuAsnProMetAsnPhe1IleGlnProGly		219	
QY	920	GCTTTTCAAGGAATTAAGGCTCCATCAATTTGACTTAAAGAAAGTAATTTTAAATAGGCTCAAT		979	
Db	220	AlaPheLysGlu1IleArgLeuHisLysLysLeuThrLeuAlaGluAsnPheAspSerLeuAsn		239	
QY	980	GTACTGAAATATGTGCTTCAAAACATGACTGGTTTACATGTCCATCGGTTGATCTTGGGA		1039	

Db	240	ValMetLysrhrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly	252
Qy	1040	GAATTAAAGAAATGAAGAAATCTGGAAAGTTTGGACCGTTCTGTCAATGAAAGACTATGC	1099
Db	260	GluPheArgAnsgnGluGlyAsnLeuGlnLysPheAspSerAlaLeuGlnGlyLeuCys	279
Qy	1100	AATGTGACATGTGATGAGTTCAAGTTTAAACATATATAAATCATTTTTCAGATGATATTAT	1159
Db	280	AsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspPheIle	299
Qy	1160	AATCTC---AATTCCTTGGCAAAATATTTTCGAAATGCTTTTCAAGCTGTACATATATAA	1216
Db	300	AspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu	319
Qy	1217	CACATGACAGATGTTCTTAGCGATTTCGAAATGGCAATCCTTATCATCATTTAGATGTCA	1276
Db	320	ArgValLysAspPheSerTyrAsnPheGlyTyrGlnIleSerLeuGluLeuValAsnGlyLys	339
Qy	1277	CTTAAAGCTTTCCAAAGCTGAGCTTACCTTTTCTTAAAGTTGAGATTTTAACTACCAAC	1336
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Qy	1337	AGAGAGATATACACTTTGGTCAGTTGGCTGTGCTGGCAAGTCTCAGATATCTAGATCTAG	1396
Db	360	LysIleGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeuSer	379
Qy	1397	AGAATGCGCATGAGCTTTAGAGTTTGGCTGTCTTATTTCTGATTTTGGACAAACAACTG	1456
Db	380	ArgAnsgnLysLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu	399
Qy	1457	AAGTATCTTAACCTCAGCTTTCATATGATGTATCTATAGATGGCACTTACATGGGTCTA	1516
Db	400	LysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu	419
Qy	1517	GAGAGCGTGAATATCTGCACTTTCACACATCCCACTTAAAAAGGACAGAAATTTCTCA	1576
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Qy	1577	GTTGTTCTTATCTTGTGAAAACTTCTTACCTTGACATCTTCTTCACTAAATCCAAAAAT	1636
Db	440	ValPheLeuSerLeuAlaArgAnLeuIleLysTyrLeuAspIleSerHisThrHisIleThrArgVal	459
Qy	1637	GACTTTGATGGCATATTTCTTGACCTGATCAGTCTCAACACTTTAAAAATGGCTGGCAAT	1696
Db	460	AlaPheAnsgnLysIlePheAnsgnLysLeuSerSerLeuGluValLeuLysMetAlaGlyAsn	479
Qy	1697	TCTTTCAAGACACACCCCTTCAAATGTCCTTTCAACAACAAACAACTTAAACTTCCTG	1756
Db	480	SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAnLeuThrPheLeu	499
Qy	1757	GATCTTTTGAATGCCAACTGGAACAGATATCTAGGGGGGATATTGACACACTTACAGA	1816
Db	500	AspLeuSerGlnGlyGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSer	519
Qy	1817	CTCCAGTTATTAACATGAGTCAACAACACTGTTTCTGGATTCATCCATTTATAA	1876
Db	520	LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrLys	539
Qy	1877	CAGCTGTACTCCCTCAGGACTCTTGATTTGACGTTTCAATGSCATAGAGACATCC---AAA	1933
Db	540	CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysLys	559
Qy	1934	GGAAATCTGCAAACTTTTCCAAAGAGTTCAGCCGTTCTTCAATCTGACTTAATATTCTGT	1993
Db	560	GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe	579
Db	580	AlaCysThrCysGlyHisAsnGlnSerPheLeuGlnIleThrLysAspGlnArgGlnLeuLeu	599
Qy	1994	GCTTGATATGTGAATACAGAAATTTCTTGACGTGGGTCAAGACGACAAAGAAATGTTCTG	2053
Db	600	ValGlnValGlnGlyAsnMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu	619

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OY      2114 GATTTCAGAAATCCACCTGTTATATTAACAAGACATATACACAGATGTCGGTGCAGT 2173
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Db      620 SerIeu-----AsnIleIthrCysGlnMetCnluysThrIleIleGlyValSerValIeuSer 638
OY      2174 GTGCTTGTGTAGACCACTGTAGACATTTCTGTATATACCACTTCTATTTTCACTGATACTT 2233
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Db      639 ValIeuValValSerIeuValAlaValIeuValTyrLysPheTyrPheIleIeuMetIeu 658
OY      2224 ATTGTGGCTGTAAAAAGTATACAGCAGAGAGAAAACATCTATGATGCATTTGTGATCTAC 2293
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Db      659 LeuAlaGlyCysIleLysTyrIolYargGlyCnluAsnIleTyrAspAlaPheValIleTyr 678
OY      2294 TCGAGCCAGAAATGAGACACTGGGTGGAACAACGAGCTGTAAAGAAATTTAGAAAGAGAGCTG 2353
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Db      679 SerSerGlnAspGluAspTyrValAlaArgAsnGluIeuValLysAsnIeuGluGluValAl 698
OY      2354 CCCCCGCTTTCAGCTTTCCTTCATTATACAGGAACTTTATTCCTGTGTAGCCATTTCTGCC 2413
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Db      699 ProPhePheGlnIeuCysLeuHisIeTyrIaArgAspPheIleProGlyValAlaIleAla 718
OY      2414 AACATCATCCAGAAAGCGCTTCACAAAGACCGGAAAGTTATTTGSGTGTCTTACAGAC 2473
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Db      719 AsnIleIleHisGluGlyIlePheHisLysSerArgLysValIleValValValSerGlnHis 738
OY      2474 TTATATCCAGACCCGTTGGTGTATCTTTGAATATGATGATTCCTCAGACATGCGACGTTCTG 2533
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Db      739 PheIleGlnSerArgTyrCysIleIlePheGluTyrGluIleAlaGlnThrTyrGlnPheIeu 758
OY      2534 AGTACCGCGCTCTGCGCATCATCTTCACTTCTGCTTGAGAAAGTGAGAGACTCTTGCTGAGG 2593
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Db      759 SerSerArgAlaGlyIleIleIlePheIleValIeuGlnLysValGluTyrThrIeuLysArg 778
OY      2594 CAGCAGGTGCGAAATGTATATCGCTTCTTGACGAAACACATCCTCGATGGAGAGACAT 2653
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OY      2654 GCTCTGGAGAGGACATCTTCTGAGAGAGACTCAAAAAAGCCCTGTTGATGTAAAAACC 2713
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Db      799 ValIeuGlyArgHisIleIlePheTyrArgIeuArgLysAlaIleuLysPseLysSer 818
OY      2714 TTGAATCCAGAT-----GAAACATCAGAGAGAAAGACAGAAAGCAACACTTGG 2761
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RESULT 2
US-09-950-041-8
/ Sequence 8, Application US/09950041
/ Publication No. US20030032090A1
/ GENERAL INFORMATION:
/ APPLICANT: Hardiman, Gerard T.
/ APPLICANT: Rock, Fernando L.
/ APPLICANT: Bazan, J. Fernando
/ APPLICANT: Kastelein, Robert A.
/ APPLICANT: Ho, Stephen W.K.
/ APPLICANT: Liu, Yong-Jun
/ TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DWO724XK1
/ CURRENT APPLICATION NUMBER: US/09/950,041
/ CURRENT FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: 09/728,540
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 60/207,558
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 09/073,363
/ PRIOR FILING DATE: 1999-06-05
/ PRIOR APPLICATION NUMBER: 60/044,293
/ PRIOR FILING DATE: 1997-05-07
/ PRIOR APPLICATION NUMBER: 60/072,212
/ PRIOR FILING DATE: 1998-01-22
/ PRIOR APPLICATION NUMBER: 60/076,947
/ PRIOR FILING DATE: 1998-03-05
/ NUMBER OF SEQ ID NOS: 45

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[illegible]

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Oy 1274 CATCTTAAGCCCTTTCCAAAGCTGAGTCTACCTTTCTTAAAGATTGGACCTTAATGAC 1333
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Oy 1334 AACGAGAGGATATCAGCTTTGGTCAGTGGCTCTGCCAATCTCAGATATCATGATCTT 1393
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Db 321 AsnYsGlyAlaAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
Oy 1394 AGTGAAGATGCCATGAGCTTTAGAGTGTCTGTTCTTATCTGATTTTGAACAAACAC 1453
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Oy 1454 CTGAAGTATCTTAAGACCTCAGCTTCATAGTGTCTCATCTGATAGTGCACCTTCATGGGT 1513
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Db 361 LeuYsTrYleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhelGly 380
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Db 381 LeuGlnGlnLeuGlnHsleuAspPheGlnHsSerAsnLeuYsGlnMetSerGluPhe 400
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Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuYMetAlaGly 440
Oy 1694 AATCTTTCAAGACAAACACCTTTCAAAATGCTTTAACAACAAACAAACTTAAACATTC 1753
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Db 501 LysCySLeuAsnSerLeuGlnValLeuAspTrYSerLeuAsnHsIleMetThrSerLys 520
Oy 1931 AAAGGAATACTGCAACATTTTCCAAAGAGCTAGCCGCTTCAATCTGATTAATATATCT 1990
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 521 LysGlnGlnLeuGlnHsPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
Oy 1991 GTTGCTGTATATGTAATATACAAATTTCTTGACGTGGGTCAAGGACCAAGAAATGTT 2050
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 541 PheAlaCySThrCySglnHsIleGlnSerPheLeuGlnTrpIleYsAspGlnArgGlnLeu 560
Oy 2051 TTGGTGATGTGGAACAATGAATATGTCATCACTTAAGACATGAAAGCCCTCCCTGGTG 2110
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 561 LeuValGluValGlnArgMetGlnCySAlaThrProSerAspLysGlnGlyMetProVal 580
Oy 2111 TTGATTTTACGAATTCACCTGTTATATATACAGATCATATCAGTATCGGTGGTGC 2170
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 581 LeuSerLeu---AsnIleThrCySglnMetCAsnYsThrIleIleGlyValSerValLeu 599
Oy 2171 AGTGTGCTTGTGTAGCACTGTAGCACTTTCTGATATACCACTTATTTTCACTGATTA 2230
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 600 SerValLeuValIleSerValIleValAlaValLeuValTrYLysPheTrYPheHisLeuMet 619
Oy 2231 CTATATGTGGCTGTAAAAAGTACAGCAGAGAAAGACATCTATGATGCACTTTGTATC 2290
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 620 LeuLeuAlaGlyCySAlaLeuTrYTrYArgGlyGlnAsnIleTrYAspAlaPheValIle 639
Oy 2291 TACTGACCCAGAAATGAGGACTGGGTGAGAAACGAGCTGTGTAAAGATTTTGAAGAAAGA 2350

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Db 640 TyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValYsAsnLeuGlnGly 659
Oy 2351 GTGCCCCGCTTTACGCTTTGCCCTTCATTTACAGGACCTTATTTCTGCTGATGACCATTTGCT 2410
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 660 ValProProGlnGlnLeuCySLeuHsTrYArgAspPheIleProGlyValAlaIleAla 679
Oy 2411 GCCAATCATCTCAAGGAGGCTTCCAAAGACCCGGAAGATTTATGTTGGTGGTGTCTAGA 2470
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 680 AlaAsnIleIleHsGlnGlyPheHsLysSerArgLysValIleValValSerGln 699
Oy 2471 CACTTTATCCAGAGCCGCTGTGTATCTTTGAATATGATGATTCCTCAGACATGGCACTTT 2530
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 700 HisPheIleGlnSerArgTrpCySlePheGlnTrYGlnIleAlaGlnThrTrpGlnPhe 719
Oy 2531 CTGAGTACGCCGCTCTGCATCATCTTCACTTGTCTTGAGAAAGTGGAGAAAGTCTTCCTG 2590
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 720 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnYsValGlnYsThrLeu 739
Oy 2591 AGGACAGAGGTGCAATGTATGCTTCTTACGAGAAACATCACTCCAGTGGAGAGAC 2650
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 740 ArgGlnGlnValGlnLeuTrYArgLeuLeuSerArgAsnThrTrYLeuGlnTrpGlnAsp 759
Oy 2651 AATGCTCTGGAGAGGACATCTTCTGAGAGAGCTCAAAAAGCCCTGTTGATGAGAAA 2710
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 760 SerValLeuGlnArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLys 779
Oy 2711 GCCTTGAAATCCAGAT-----GAAACATCAGAGGAGAAACAAAGCAAGCAACTTTG 2761
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 780 SerTrpAsnProGlnGlyThrValGlyThrGlyCySAsnTrpGlnIleAlaThrSerIle 799

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US2003007279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Alignment Scores:
Pred. No.: 4,63e-251 Length: 799
Score: 2726.00 Matches: 532
Percent Simlarity: 80.38% Conservative: 111
Best Local Simlarity: 66.50% Mismatches: 151
Query Match: 45.87% Indels: 6
DB: 14 Gaps: 4

US-09-396-985B-5 (1-3395) x US-10-128-166-7 (1-799)
Oy 377 ATGATACAGAAATCTCAGCAAAATCCCTCAAGACATCCCTTATTAACCAAGAACTGAT 436
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Db 1 MetGlnLeuAsnPheTrYLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
Oy 437 CTGAGCTTCAACCCCTGAGATCTTAAAGACTATGCTTCAACATTTCTCAACTT 496
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 21 LeuSerPheAsnProLeuAlaGlnHsleuGlySerTrYSerPhePheSerPheProGlnLeu 40
Oy 497 CAGTGGCTGATTTATTCACAGTGTGAATTTGAGACAAATTTGAGACAAAGCATGGCATGGC 556
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 41 GlnValLeuAspLeuSerArgCySglnIleGlnThrIleGlnAspGlyAlaTrYGlnSer 60

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557 TTAACGACGCTCTCAACCTGGTACTGACAGAAACCCATCAAGATTTCCTCCAGCA 616
 61 LeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
 617 AGTTTTCGTGACCTAACAAATTTAGAGAATCTGTGGCTGTGGAGACAAAATGACCTCT 676
 81 AlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuLaser 100
 677 CTAGAGGTTTCCATATTCGACAGCTTATTCCTTAAAGAACTTAAATGGCTCATAT 736
 101 LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
 737 CTATATACATCTTAAAGTGGCTGAATATTTTCTATATTCGACAAACCTGAACATGTTG 796
 121 LeuIleGlnSerPheLeuLeuProGluThrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
 797 GATCTTTCTTAACTATATTCAAACATATTTCTGTCAAGAGCTTACAGTTTCTACGTGA 856
 141 AspLeuSerSerAsnLysIleGlnSerIleThrCysThrAspLeuArgValLeuHisGln 160
 857 AATCCCAAGTCATCTCTCTTAAAGCTGTCTTAAACCCATGAGTCCATTCAGACC 916
 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
 917 CAAGCTTTCAGGGAATAGGCTCCATGATTAATGACTTAAAGATTTTAAATGAGCTCA 976
 181 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLysAlaGlnAsnPheSerLeu 200
 977 AATGACTGAAATATGTGCTTCAAAACATGACTGTGTTTACATGTCCATCGGTGATCTTG 1036
 201 AsnValMetLysThrCysIleGlnIleuLysGluLeuGluValHisArgLeuValLeu 220
 1037 GGAGATTTTAAATGAAAGAAATCTGGAAGATTTCACCGTCTGTATGGAAGAGATA 1096
 221 GlyIleuPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGlnGlyLeu 240
 1097 TGCATGAGACATGATGAGTTCAGGTTTAAATATTAATCAATTTTTCAGATGATTT 1156
 241 CysAsnLeuThrIleGluGlnPheArgLeuAlaThrLysLeuAspIleThrLeuAspIle 260
 1157 TATATATCTC--AATGTGCTTGCAAAATATTTCTGCATGTCTTTCACAGGTGTAATATA 1213
 261 IleAspLeuPheAsnCysLeuThrAsnValSerPheSerLeuValSerValThrIle 280
 1214 AAAACATACGACATGTTCTTACGAGTTCGAAATGCGCATCTTATCATATTAATGATGT 1273
 281 GluArgValLysAspPheSerLysAsnGlyThrGlnHisLeuGluLeuValAsnLys 300
 1274 CATCTTAAGCTTTTCCAAAGCTGACTACCTTTTCTTAAAGTTGAGCTTAACTAC 1333
 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 1334 AACAGAGAGATATACGCTTGTCTCAAGTGTGCTGCGCAAGTTCAGATATCTAGATCTT 1393
 321 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
 1394 AGTGAAGATGCCATGAGCTTTAGAGTTCGTGTTCTTATTTCTGATTTTGAACAAACAC 1453
 341 SerArgAsnGlyLeuSerPheLysGlyCysSerSerGlnSerAspPheGlyThrThrSer 360
 1454 CTGAAGTACTGAAGCTCAGCTTCAATGCTGTCATCCGATGAGTCCCACTTATAGGCT 1513
 361 LeuLysThrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuLys 380
 1514 CTGAAGAGCTGATATCTGAGCTTTCAGACTCCATTTTAAAGAAAGTCAAGAAATTC 1573
 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
 1574 TCAGTGTCTTATCTCTTGAAGAACTTTTACCTTGAACATCTCTTAACTATTAACCAA 1633
 401 SerValPheLeuSerLeuArgAsnLeuIleThrLeuAspIleSerHisThrHisThrArg 420

1634 ATTGACTTTCAGGACATATTTCTTGCGTTGATGACTCTCAACATTTAAAGATGGCTGC 1693
 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
 1694 AATCTTTCAAGAACAAACACCTTTTCAATGCTTTTCAACAAACAAACAACTTAACTTC 1753
 441 AsnSerPheGlnGluAsnProPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
 1754 CTGATCTTTCTAAATGCGCAACCTGAAACAGATATCTAGGGGGGATTTGACACCTGAC 1813
 461 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeu 480
 1814 AGACTCCAGTATTAACATGAGTCAACAACCTACTGTTTCTGATCCATCCATTTAT 1873
 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProThr 500
 1874 AAACAGCTGATCTCCCTGAGACTTGTGATTCGAGTTCAATGCGCATGAGACATCC-- 1930
 501 LysCysLeuAsnSerLeuGlnValLeuAspLysSerLeuAsnHisIleMetThrSerLys 520
 1931 AAAGAAATACGCAACATTTTCCAAAGCTGACCGCTTTCATCTGACATTAATTTCT 1990
 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 1991 GTTGCTGTATATGTGAATATCAGAAATTTCTGACAGTGGGTCAAGACCAAGAAATGTTTC 2050
 541 PheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnIleThrLysValArgGlnLeu 560
 2051 TTGGGAATGTTGAACAAATGAATGTGCATCACTTAATGACATGAAGGCTCCCTGCTG 2110
 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
 2111 TTGATTTTACGATTCACCTGTTATATATACAGACTATCAATCACTATTCGCTGCTC 2170
 581 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 599
 2171 AGTGTCTGTGTGAGACCTAGTGTGACTTTCTGATATACCACTTATTTTCACTGATA 2230
 600 SerValLeuValValSerValValAlaValLeuValLysThrPheThrPheHisLeuMet 619
 2231 CTATTCCTGCTGTGTAAGAAAGTACAGACAGAGAGAGAAACATCTATGATTCATTTGATC 2290
 620 LeuLeuAlaGlyCysIleLysThrGlyArgGlyGluAsnIleThrArgAlaPheValIle 639
 2291 TACTCGACCAAGATGAGAGCTGGGTGAGAAACAGAGCTGTGTAAGATTTTGAAGAGAGA 2350
 640 TyrSerSerGlnAspGluAspThrValArgAsnGluLeuValLysAsnLeuGlnGly 659
 2351 GTGCGCCGCTTTCAGCTTGTGCTTATTAACAGGACTTTATTCCTGGTGTAGCATTGCT 2410
 660 ValProProPheGlnLeuCysValLeuHisLysThrArgAspPheIleProGlyValAlaIleAla 679
 2411 GCGAATCATTCAGAAAGGCTTCCACAAAGCCGGAAGCTTATTTGGTGGTGTGAGA 2470
 680 AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValAlaValSerGln 699
 2471 CACTTTATCCAGAGCGCTGTGATCTTGAATATAGAGTGTGTCAGACATGCGACTTT 2530
 700 HisPheIleGlnSerArgThrCysIlePheGluIleGluIleAlaGlnIleThrGlnPhe 719
 2531 CTGAGTAGCGGCTGTGACATCTTATTCATTTGCTTGTAGAAAGTGAAGAGTCTTGTCTG 2590
 720 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeu 739
 2591 AGGCGAGAGGTGAATGTATTCGCTTTTACAGAAACATTCCTGAGTGGAGAGAC 2650
 740 ArgGlnGlnValGluLeuThrArgLeuLeuSerArgAsnThrThrLysGluIleThrGluAsp 759
 2651 AATGCTGTGGGAGGCACTTTCTGAGAGAACTCAAAAAGCCCTGTGTGAGAGAAA 2710
 760 SerValLeuGlyArgHisIlePheThrArgArgLeuArgValAlaLeuAspGlyLys 779
 2711 GCCTTGATTCAGAT-----GAAACATTCAGAGGAAACAAAGCAACAACTTTG 2761

[illegible]

QY	977	AAAGTACGAAATATGAGCCCTTCAAAAACAGACGTTTACATGGCCATCGGTTACCTTG	1036
Db	201	AsnValMetCysThrCysGlnGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu	220
QY	1037	GGAGAATTTAAAAATGAAAGAAATCTGGAAAGTTTTCAGCCGTTCTGTCATGGAAGACTA	1096
Db	221	GlyGlnIuHeArbAnsglnGlyAnLeuGlnIuLysPheAspLysSerAlaLeuGlnGlyLeu	240
QY	1097	TGCAGTGTGACGATGTGATGAGTTCAAGTTAACATATATTAATCACTTTTTCAGATGATATT	1156
Db	241	CysAsnLeuThrIleGlnGlnPheArgLeuAlaGlyLeuAspTrpTrpLeuAspAspIle	260
QY	1157	TATTAATCTC--AATTGCTTGGCAAAATATTTCGAAATGCTTTTCAACAGGTGTCATATTA	1213
Db	261	IleAspLeuPheAsnGlyLeuThrAsnValSerPheSerLeuValSerValThrIle	280
QY	1214	AAACACATPACGACAGATGTCTTACGACATTTTCAAAATGGCAATCTTATCATTCATGATAGT	1273
Db	281	GlnArgValLysAspPheSerTrpAsnPheGlyTrpIleHisLeuGlnLeuValAsnGly	300
QY	1274	CATCTTAAGCCTTTTCCAAAGCTGAGTCTACTTTTCTTAAAGTTGACTTAACTAC	1333
Db	301	LysPheGlnGlyAsnProThrLeuLysLeuSerLeuLysArgLeuThrPheThrSer	320
QY	1334	AACGACAGACATATACACTTTTGGCTACATTTGGCTCTGCGCAAGCTCCACATATCTAGATCTT	1393
Db	321	AsnLysGlnGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnLysLeuAspLeu	340
QY	1394	AGTGAATATGCGCATGACCTTTAGAGTGTGCTGTTCTTATTTCTGATTTTGGAAACAACAC	1453
Db	341	SerTrpAsnGlnLysSerPheLysGlyCysCysSerIleAsnAspPheGlnGlyThrThrSer	360
QY	1454	CTGAAGTACTTGAACCTCAAGCTTCAATGTGTCTATCTGTAGTGGCCAACTTCAATGGGT	1513
Db	361	LeuLysTrpLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly	380
QY	1514	CTAAGAAGCTGGAAATACCTGACATTTTCAGACATCTCCACTTAAAAAAGTCACAGAAATTC	1573
Db	381	LeuGlnIuLeuGlnIuHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe	400
QY	1574	TCAGTGTCTTATCTCTGAAAACTCTTTTACCTTACATCTGTTCACATTAATACCAAA	1633
Db	401	SerValPheLeuSerLysLeuArgAsnLeuIleTrpLeuAspIleSerHisThrHisThrArg	420
QY	1634	ATTGACTTTTATGACATATTTCTTGGCTTGATCTACGTCTCAACACTTAAAAATGGCTGC	1693
Db	421	ValAlaPheAsnGlnLysLeuAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly	440
QY	1694	AATTCTTTCAAGACACACACCTTTCAAAATGCTCTTTCACAAACACAACTTAAACATTC	1753
Db	441	AsnSerPheGlnGlnAsnPheLeuProAspAlaPheThrGlnLeuArgAsnLeuThrPhe	460
QY	1754	CTGATCTTTCTTAATGCGCACTGGAAACAGATATCTAGGGGGGTATTTGACACACTCTAC	1813
Db	461	LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer	480
QY	1814	AGACTCCAGTATTAACATGACTGACACACACTTACTGTCTTCTGATCCATCCATTAAT	1873
Db	481	SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProGly	500
QY	1874	AAACAGCTGTACTCCCTCAGGACTCTTGATGTGCAGTTTCAATGCGCATPAGACATCC--	1930
Db	501	LysCysLeuAsnSerLeuGlnValLeuAspTrpTrpSerLeuAsnHisIleMetThrSerLys	520
QY	1931	AAAGGAATPACTGCAACATTTTCCAAAGTCTACGCGCTTCATCTGACATTAATTAATCT	1990
Db	521	LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	540
QY	1991	GTTCTCTGTATATGTAATACAAATTTCTTGCAGTGGGCTCAAGACGACAGAAATGTTTC	2050
Db	541	PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleTrpLysAspGlnArgGlnLeu	560
QY	2051	TTGGTGAATGTTGAAACAATGAAATGTGCATACCTATPAGCATGAAGGCTCCCTGGTG	2110

[illegible]

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QY	437	CTGAGCTTCACACCCCTGAGAAAGATCTTAAAGAACTTAAGCTTCACCAATTTCTCAACTT	496
Db	21	LeuSerPheAsnProLeuArgItyLeuGlySerTyrSerPhePheSerPheProGluLeu	40
QY	497	CAGTGGCTGCAATTTATCCAGGTGTGAAATTTAGACAAATTTGAAGACAAGCAATGGCATGGC	556
Db	41	GlnValLeuAspLeuSerPheArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer	60
QY	557	TTAAACCAAGCTCTCAACCTGGGTAATGACAGAAACCCATCAAGAGCTTTTCCCAAGA	616
Db	61	LeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuGly	80
QY	617	AGTTTTCTGACATCAACAAATTTAGAACATCTGTAGCTGTGTGAGACAAAAATGACCTGT	676
Db	81	AlaPheSerGlyLeuSerSerLeuGlnIlySerValAlaValGluThrAsnLeuAlaSer	100
QY	677	CTAAGAGGTTTCCATATTGACAGCTTATATCTTAAAGAACTAAATGTGCTCATAT	736
Db	101	LeuGluAsnPheProIleGlyHisLeuTyrThrLeuLysGluLeuAsnValAlaHisAsn	120
QY	737	CTTATACATCCCTTAAATGGCTGGAATATTTTCTTAATCTGACAAACCTAGAACATGTG	796
Db	121	LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu	140
QY	797	GATCTTTCTTAACTATATTCATATTCAACTATTTCTGTCAAAAGCTACAGTTTCTACGTGA	856
Db	141	AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln	160
QY	857	AATCCCAAGTCATCTCTCTTTAGACCTGTCTTTAAACCAATGATGATCCATTCAGCC	916
Db	161	MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro	180
QY	917	CAAGCCTTCAAGGGAATTAGGCTCCATGAATTTGACTCTTAGAAGAAATTTTAATAGTCA	976
Db	181	GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuAspGluAsnHisPheSerLeu	200
QY	977	AATGACTGAAATATGTGCTTCAAAACATGACCTGGTTTACATGTCATGCTGTGATCTTG	1033
Db	201	AsnValMetLysThrCysIleGlnIlyLeuAlaGlyLeuGluValHisArgLeuValLeu	220
QY	1037	GGAGAAATTTAAAAATGAAAGAAATCTGGAAAGTTTGAACCGTTGTCTCATGGAAGACATA	1099
Db	221	GlyIleuPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu	240
QY	1097	TGCAATGTGAGACATTTGAGAGTTTCAAGTTTACATATATATTAATCATATTTTCAATGATAT	1155
Db	241	CysAsnLeuThrIleGluGlnPheArgLeuAlaTyrLeuAspLysTyrItyLeuAspIle	260
QY	1157	TATATATCTC--AATTTGCTGGCAAAATATTTTCTGCAAGTCTTTTCAAGAGTATACATATA	1211
Db	261	IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	280
QY	1214	AAACACATAGACAGATGTTCTTAGACATTTCAAAATGGCAATCTTATTCATCATTTAGATGT	1277
Db	281	GluArgValLysAspPheSerTyrLysAsnPheGluTyrGlnHisLeuGluIleValLysCys	300
QY	1274	CATCTTAAAGCTTTTCCAAAGCTAGTACCTTTTCTTAAAGTTTGAAGCTTTTAACTAC	1333
Db	301	LysPheGluGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer	320
QY	1334	AAACAGAGATATCAGCTTTGTCTAGTGGCTGCGCAAGTCCAGATCTCAGATTTAGATCTT	1399
Db	321	AsnLysGluGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu	340
QY	1394	AGTGAATAATGCCATGAGCTTTTAGAGGTGTCTGTTTATTTGATTTTGAACAAACAAC	1455

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Db      341 SerArgenGlyLeuSerPheGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Qy      1454 CTGAAGTACTTAAGCCTCAGCTTCAATGGTGTCTCCTGATGATGCCAATCTTAGGCT 1513
Db      361 LeuYSYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuGly 380
Qy      1514 CTGAAGAGCTGGAATACCTGAGCTTTCAGACCTCCACTTAAATAAAAGGTCAAGAAATTC 1573
Db      381 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuGlnMetSerGluPhe 400
Qy      1574 TCAGTGTCTTATCTTGTGAAAACTTCTTACCTTGACATCTTTACACTTAATACCAA 1633
Db      401 SerValPheLeuSerLeuArgAsnLeuIleTyrrLeuAspIleSerHisThrHisArg 420
Qy      1634 ATTGACTTGTATGCAATTTCTTGCGTGTATCACTCAACACTTTAAATAAGCTGGC 1693
Db      421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuYsMetAlaGly 440
Qy      1694 AATTCTTTCAAGACACACCTTCAATGTCTTTAACAACACAACTTAACATTC 1753
Db      441 AsnSerPheGlnGlnHisPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 460
Qy      1754 CTGATCTTTTAAATGCGCACTGGAAACAGATATCTAGGGGGTATTGACACACTTAC 1813
Db      461 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 480
Qy      1814 AGACTCCAGTTATTAAATGATAGTCACAAACCTACTGTTCTTGAGTCCATCCCATAT 1873
Db      481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProTyrr 500
Qy      1874 AAACAGCGTACTACCTCAGACACTTGTATGTCAGTTTCAATCGCATGAGACATCC--- 1930
Db      501 LysCysLeuAsnSerLeuGlnValLeuAspTyrrSerLeuAsnHisIleMetThrSerLys 520
Qy      1931 AAAGAAATATCTGAACATTTTCCAAAGATAGCCGCTTCAATCTGACTAATATTC 1990
Db      521 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
Qy      1991 GTTGCTGTATATGTAATATCAAAATTTCTTGAGTGGGTCAAGAGCCAGAAATGTC 2050
Db      541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 560
Qy      2051 TTGGTAATGTTGAACAATGAATGTCATCACTCACTATAGACATGAAGCCCTCCCTGGTG 2110
Db      561 LeuValGlnValGlnArgMetGlnCysAlaIleThrProSerAspTyrrGlnGlyMetProVal 580
Qy      2111 TTGATTTTACGAATTCACCTGTATATATACAAGACTATATCAATGATGATCGGTGCT 2170
Db      581 LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 599
Qy      2171 AGTGTGCTGTGGTGGTACCACTGTAGCAATTTCTGATATACCACTTATTTTCACTGATA 2230
Db      600 SerValLeuValIleValSerValAlaValLeuValTyrrLysPheTyrrPheHisLeuMet 619
Qy      2231 CTATATGCTGGGTGTAATAAGTACAGAGAGAGAAACATCTATAGCATGATTTGTGATC 2290
Db      620 LeuLeuAlaGlyCysIleLeuTyrrGlyTyrrGlyValAsnIleTyrrAspAlaPheValIle 639
Qy      2291 TACTGAGCCAGATAGAGACTGGGTGAGAAACGAGCTGTAAAGATTTAGAAAGAGA 2350
Db      640 TyrrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 659
Qy      2351 GTGCCCGCTTACACTTGGCTTCTTATTAACAGGACTTATTCCTGTGTAGCCATTTGCT 2410
Db      660 ValProPhePheGlnLeuCysLeuHisTyrrArgAspPheIleProGlyValAlaIleAla 679
Qy      2411 GCGAATCATCATCAGAAAGGCTTCCACAAGAGCCGGAAGTATATGTGGTGTCTTGA 2470
Db      680 AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGln 699
Qy      2471 CACTTATTCAGAGCCGTGTGTATCTTTGAATATGAGATTTCTCAGACATGGCAGTTT 2530

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Db      700 HisPheIleGlnSerArgTyrrCysIlePheGlnTyrrGlnIleAlaGlnThrTrpGlnPhe 719
Qy      2531 CTAGATAGCCGCTGGGCATCATCTTGCCTTGAGAAAGTGAGAGTCTTGCTG 2590
Db      720 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeu 739
Qy      2591 AGGACAGAGCTCGAATTTGATTCGCTTCTTACGAGAAACCTACCTGAGTGGAGAC 2650
Db      740 ArgGlnGlnValGlnLeuTyrrArgLeuLeuSerArgAsnThrTyrrLeuGlnTyrrGlnAsp 759
Qy      2651 AATGCTTGGGAGGCGCATCTTCTGAGAAAGACTCAAAAAGCCCTGTGATGAGAAA 2710
Db      760 SerValLeuValArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLys 779
Qy      2711 GCCTTGAATCCAGAT-----GAAACATCAGAGAGAAAGAACAGAACCAACTTTG 2761
Db      780 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799

RESULT 6
US-10-114-893-10
; Sequence 10. Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Metberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OR INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Alignment Scores:
Pred. No.: 1,25e-48 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conserved: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
DB: Gaps: 21

US-09-396-985b-5 (1-3395) x US-10-114-893-10 (1-661)
Qy      208 TACAGTTGTCGATGCTTT-----CTCAGGCGCTCCGCTGCTGCAGAAATGCCAG 258
Db      3 PheAspValSerCysPhePheTrpValValLeuPheSerAlaGlyCysLys----- 19
Qy      259 GATATGCTCTCTTGTGATCGTGGAGCTCTGATCATGCGATGTTCCTTCTGCTGCT 318
Db      20 -----ValIleThrSerTrpAspGln-Met----- 27
Qy      319 GAGACGAGAAAGCTTGAATCCCTGCATAGAGGTACTTCTTAATATTACTTACCAATGCAT 378
Db      28 -----CysIleGlnLysGlnAlaAsnLysThrTyrrAsnCysGln 40
Qy      379 GGATCAGAAATCTCAGAAATCCCTCATGACATCCCTTATTCACCAAGAACTTGAATCT 438

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Db 40 uasnleuglyleuSerGIuileProaspThrleuProasnThrtrglnpheleuGIuPh 60
 QY 439 GAGCTTCAACCCCTGAAGATCTTTAAGAGCTATAGTTCACCAATTTCTCAACACTTCA 498
 Db 60 eSerPheasnPhleuProthrIleHisasnrgThrPheSertrgIeuMetAsnleuTh 80
 QY 499 GTGGCTGATTTATTCAGAGTGTGAATTTAGACAATTGAGACAAGGATGGCTT 558
 Db 80 rPheleuaspLeuThrtrgCysglnIleasnTrpIleHisglnaspThrPheGlnSerHI 100
 QY 559 AAACAGCTCTCAACCTTGTGACTGACAGAAACCTTCAAGAGTTTCCCGACGAG 618
 Db 100 sHisglnleuSerThrleuValleuThrGlyAsnProleuIlePheMetAlaGluThrSe 120
 QY 619 TTTTCTGACATAACAATTTAGAGAAATCTGGCTGGCTGGAGACAATAATGACCTCT 678
 Db 120 rIeuasnGlyProlySerleuLyHisleuPheleuIleGlnThrGlyIleSerAsnle 140
 QY 679 AGAGGCTTTCATATTGACAGCTTATATCTTAAAGAACTAAATGTGCTCATATCT 738
 Db 140 uGluPheIleProValHisasnleuGIuasnleuGlnSerleuYrleuGlySerAsnHI 160
 QY 739 TATACATCTCTTAACTGCTGAAATTTTCTAATCTGACAAACCTTGAACATGTGGA 798
 Db 160 sIleSerSerIleLyaspPhePro--AlaArgAsnleuLyValleuAs 179
 QY 799 TCTTCTTATTAATTAATTTCAACTATTTCTGTAAGACTTACAGTTTCTACGTGAAA 858
 Db 179 rPheGlnAsnAsnAlaIleHisrYrIleSerArgIuaspMetArgSerleuGIuGln- 198
 QY 859 TCCCAACATCAATCTCTTGTAGACCTGTCTTAAACCAATTAATGATCTCATCAAGCCA 918
 Db 199 ----AlaIleasnleuSerleuAsnPhenAsnGlyAsnAsnVallysglyIleGluLeuGI 217
 QY 919 AGCCTTTCAGGGAATTAGGCTCCATGAATTGACTCTAAGAGTAATTTAATAGCTCAA 978
 Db 217 yAlaPheaspSerThrValPheGlnSerleu-----AsnPhelgIyGluThrPr 233
 QY 979 TGTACTGAATGTGCTTCAAAAACATGACGTGTTATCATGTCATGCGTGTGATCTGGG 1038
 Db 233 oAsnleuSerValIlePheasnGlyleuGlnAsnSerThrtrglnSerleuTrpLeuGI 253
 QY 1039 AGAATTTAAATGAAGAAATCTGAAATCTGAAAGTTTACGCTGTCATGAGAGACTAT 1098
 Db 253 yThrPheGlnaspIleaspasp---GluaspIleSerSerIleMetleuLysglyLeuCy 272
 QY 1099 CAATGTGACATGATGATGAGTTTACATATATTAATCAATTTTTCAGAT--GATAT 1155
 Db 272 sGluMetSerValGlnSerleuAsnleuGlnGlu--HisArgPheSeraspIleSerSe 291
 QY 1156 TTATATCTCAATGCTTGGCAATATTTTGCATATGCTTTCACAGGTGACATATTA 1215
 Db 291 rThrThrPheGlnCysPheThrGlnleuGlnleuAsnleuSpLeuThrAlaThrIleleuLy 311
 QY 1216 ACACATGACAGATGCTTCAAGCAATTTCAAAATGCAATCTTATCAATCATTTAGA 1270
 Db 311 s-----GlyleuProSerGlyMetLyS-----GlyleuAsnleuLeuLySlySle 326
 QY 1271 -----TGTACTTAAAGCT-----TTTCCAAA 1293
 Db 326 uValleuSerValAsnHisPheaspGlnleuCyGlnIleSerAlaAlaAsnPheProSe 346
 QY 1294 GCTGAGTCTACCTTTTCTTAAAGTTGACATTAACTAACCAACAGAGAGATACAGCTT 1353
 Db 346 rLeuThrHisleuYrIleArgGly-----AsnVallySlySerHisleuGlyVa 363
 QY 1354 TGGTCAGTTG--GCTGTGCAAGTCTCAAGATATCTAGATCTTGAAGATGCCATGAG 1410
 Db 363 lGlyCysleuGlnlyleuGlyAsnleuGlnThrleuAsnleuSerHisAsnAlaIleGI 383
 QY 1411 CTTTAAAGGTTGCTGTCTTATTTCTGATTTTGAACAAACCAACTGAAGATCTTAAAGCT 1470
 Db 383 uAlaSeraspCysSerleuGlnleuLyAsnleuSerHisleuGlnThrleuAsnle 403

QY 1471 CAGCTCAATGCTGTCATC---CTGATGAGTCCCACTTCAAGGATCTAAGAGACTGA 1527
 Db 403 uSerHisAsnGlnProleuGlyleuGlnSerGlnAlaPheleuSlyCysProGlnleuGI 423
 QY 1528 ATACCTGAGCTTTCAGACATCTCCACTTTAAAAAAGTCAACAGAAATTCAGATGTTCTTATC 1587
 Db 423 uLeuLeuaspLeuAlaPheThrArgLeuHisIleAsnAlaProGlnSerProPheGlnAs 443
 QY 1588 TCTTGAAGAACTTTCTTCACTGACATCTCTTACATATACCAAAATTTGACTTGATGG 1647
 Db 443 nLeuHisPheleuGlnValleuAsnleuThrTyCysPheleuaspThrSerAsnGlnHI 463
 QY 1648 CATATTTCTGGCTGATGACTGACATCTTAAATGAGTGGCTGCAATTTCTTCAAGA 1707
 Db 463 sIleuLeuAlaGlyleuProValleuAsnGlnHisleuAsnleuSlyAsnHisPheGlnAs 483
 QY 1708 CAACACCTT-----TCAATGTCTTTCACAAACAAACAAACTTAAACATTCCTGATCT 1761
 Db 483 rGlyThrIleThrLyThrAsnleuGlnThrValGlySerleuGlnValleuIlele 503
 QY 1762 TTTTAAATGCCAAGTGAACAGATATTTAGAGGGGTATTGACACACTTACAGACTTCA 1821
 Db 503 uSerSerCysGlyleuLeuSerIleaspGlnGlnAlaPheHisSerleuGlyLyMetSe 523
 QY 1822 GTTATTAACATGAGTCAACAAACCTACTG-----TTTCTGATGCA---TCCCAATTA 1872
 Db 523 rHisValAsnleuSerHisAsnSerleuThrCysAspSerIleaspSerleuSerHisle 543
 QY 1873 TAAACAGCTGTACTCCTCAGACACTTGTATGAGATTTCAATGCAATGACATGACATCCAA 1932
 Db 543 uLyGlyIleTy-----LeuAsnleuAlaAlaAsnSerIleAsnIleIleSe 559
 QY 1933 AGGAATCTGCACACTTTTCCAAAGAGTCAAGCGTCTTCAATGACTATATTTCTGT 1992
 Db 559 rProArgleuLeuProIleleuSerGlnGlnSerThrIleAsnleuSerHisAsnProle 579
 QY 1993 TGTCTATATATGCAATATGCAATTTCTGACGTGGGTCAAGGACCAAGAAATGTTCTT 2052
 Db 579 uAspCysThrCysSerAsnIleHisPheleuThrTrpYrlyAsnleuHislySlySle 599
 QY 2053 GGTGAATGTTGAACAAATGAAATGTGTCATCACTTATGACATGAAAGCCTCCCTGATTT 2112
 Db 599 uGlnGlySerGlnGlnThrThrCysAlaAsnPropSerleuArglyVallySleuSe 619
 QY 2113 GGAATTTACGAATTC-----ACCTGTATATATACAAAGCTATCATAGTCT 2160
 Db 619 rAspVallyleuSerCysGlyIleThrAlaIleGlyIlePhePheleuIleValPhele 639
 QY 2161 ATGGGTGTCAGTGTGCTTGTGGAGACCTGTAGCATTTCTGATATACCACTTATTT 2220
 Db 639 uLeuLeuAlaIleleuLeuPhePheAlaVallySlyrleuLeuArgTrpLySlyrGI 659
 QY 2221 TCACCTG 2227
 Db 659 nHisIle 661

RESULT 7
 US-10-038-854-134
 / Sequence 134, Application US/10038854
 / Publication No. US20040022781A1
 GENERAL INFORMATION:
 / APPLICANT: Spytek, Kimberly A
 / APPLICANT: LI, LI
 / APPLICANT: Wolenc, Adam R
 / APPLICANT: Vernecl, Corine
 / APPLICANT: Riesen, Andrew J
 / APPLICANT: Liu, Xiaohong
 / APPLICANT: Malyankar, Uriel M
 / APPLICANT: Shinkets, Richard A
 / APPLICANT: Tcherven, Velizar
 / APPLICANT: Spaderna, Steven K
 / APPLICANT: Gorman, Linda

```

/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Gusev, Vladimir Y
/ APPLICANT: Gangolli, Beha A
/ APPLICANT: Guo, Xiaojia S
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Raateili, Luca
/ APPLICANT: Caeman, Stacie J
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Burges, Catherine E
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Gunther, Erik
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millet, Isabelle
/ APPLICANT: MacDougall, John R
/ TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-230
/ CURRENT APPLICATION NUMBER: US/10/038, 854
/ PRIOR FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: 60/256, 928
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR APPLICATION NUMBER: 60/259, 415
/ PRIOR FILING DATE: 2001-01-02
/ PRIOR APPLICATION NUMBER: 60/259, 785
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: 60/269, 814
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/279, 832
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/279, 833
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/279, 863
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/283, 889
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284, 447
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/286, 683
/ PRIOR FILING DATE: 2001-04-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 411
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 134
/ LENGTH: 661
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-038-854-134

Alignment Scores:
Pred. No.: 1,25e-48 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conservative: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
Gaps: 21
DB: 15

US-09-396-985b-5 (1-3395) x US-10-038-854-134 (1-661)
QY 208 TACAGTTCGATGCTTT-----CTCAGGCGCTCCGCTGCTGTCAGAAATGCCAG 258
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QY 3 PheAspValSerCysPhePheTrpValValLeuPheSerAlaGlyCysIys----- 19
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 259 GATATGCTCTCTTGATCTGGCTGGATCTGATCATCGCATTTGCTCTTCTGCT 318
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 319 GAGACGAGAGCTTGAATCCCTGATGAGGACTTCTTATATTAACCTACATGAT 378
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 28 -----CysIleGluIlyGluAlaAsnIlyThrIysAsnCysG 40
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 379 GGATCAGAAATCTCAGCAAAATCCTTCATGACATCCCTTATTCACCAAGAACTGATCT 438
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

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Db 40 uAenLeuGlyLeuSerGluIleProAspThrLeuProAsnThrThrGluPheLeuGluP 60
QY 439 GAGCTTCAACCCCTGAAGATCTTAAGAGCTATAGCTTACCAACAAATTTCCACAACTTCA 498
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QY 60 eSerPheAsnPheLeuProThrIleHisAsnArgThrPheSerArgLeuMetAsnLeuTh 80
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QY 499 GTGGCTGATTTATTCAGAGTGTGAAATTTAGACAAATTTAGACAGAGCATGGCTT 558
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 80 rPheLeuAspLeuThrArgCysGlnIleAsnTrpIleHisGluAspThrPheGlnSerH 100
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 559 AAACAGCTCTCAACCTTGGTACTGACAGAAACCTTATCAAGAGTTTTCACAGAGAG 618
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QY 100 sHisGlnLeuSerThrLeuValLeuThrGlyAsnProLeuIlePheMetIleGluThrSe 120
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QY 619 TTTTCTGAGCTAACAAATTTAGAAATCTGGGCTGGGAGACAAATAAGTCACTCTCT 678
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QY 120 rLeuAsnGlyProlSerLeuIlyshIleuPheLeuIleGlnThrGlyIleSerIsh 140
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 679 AGAGGCTTTCATATTTGACAGCTTATATCTTAAAGAACTAAATGTGCTCATATCT 738
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 140 uGluPheIleProValHisAsnLeuGluAsnLeuGluSerLeuThrLeuGlySerAsnH 160
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 739 TATACATCTCTTAAAGTGGCTGAATATTTTCTAATCTGACAAACCTTACAAATGTGGA 798
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 160 sIleSerSerIleIlySerPheProlSerPhePro--AlaArgAsnLeuIlyValLeuAs 179
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 799 TCCTTCTTATACATATTTCAAACTATTTCTGCAAGAACTTACAGTTTCTAGTGAAA 858
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 179 rPheGlnAsnAsnAlaIleHisGlyrIleSerArgIlyAspMetArgSerLeuGluGln-- 198
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 859 TCCCAAGCTCAATCTCTTAAAGCTGTGCTTAAACCCATTAAGTACTCCATTCAGGCCA 918
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 199 -----AlaIleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValIlyGlyIleGlu 217
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 919 AGCTTTACAGGAAATTAAGCTCCATGAATTAATGACTTCAAGAAATTTTATAGCTAAA 978
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 217 yAlaPheAspSerThrValPheGlnSerLeu-----AsnPheGlyGlyThrPr 233
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 979 TGATCTGAATAATGGCTTCAAAAATGATGCTTTATACATGTCATCGATGCTGATCTGGG 1038
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QY 233 oAsnLeuSerValIlePheAsnGlyLeuGlnAsnSerThrThrGlnSerLeuThrPleuGl 253
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1039 AGAATTTAAATAATGAAGAATCTGAAAGTTTGAACGTTCTGTCTGATGAGAGCATAG 1098
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QY 253 yThrThrPheGluAspIleAspAsp---GluAspIleSerSerAlaMetLeuIlyGlyLeuCy 272
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1099 CAATGAGCATGTGATGAGTTCAGGTTTACATATTAATCAATTTTCAAT--GATAT 1155
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 272 sGluMetSerValGluSerLeuAsnLeuGlnGlu--HisArgPheSerArgIleSerSe 291
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1156 TTATTAATCTCAATTTCTGGCAAAATATTTCTGCAATGTCTTCAAGGCTGATCATATAA 1215
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 291 rThrThrPheGlnCysPheThrGlnLeuGlnGluLeuAspLeuThrAlaThrIshLeuLy 311
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1216 ACAATAGCAGATGTTCTTGAAGCATTTCAATGAGCAATCTTCAATCATTAAGA----- 1270
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 311 s-----GlyLeuProSerGlyMetIys-----GlyLeuAsnLeuLeuIlyshIle 326
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1271 -----TGTCACTTAAGCT-----TTTCCAAA 1293
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 326 uValLeuSerValAsnHisPheAspGlnLeuCyGlnIleSerAlaIleAsnPheProSe 346
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1294 GCTGAGCTACCTTTTCTTAAAGTTGAGCTTAACTGACCAACAGAGAGATACCTT 1353
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 346 rLeuThrHisLeuIlyThrIleArgIly-----AsnValIlyshIlyLeuHisIlyeGlyVa 363
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1354 TGGTCAAGT---GCTTGCACAGTCTCAGATATCTTGAATCTTATAGTAAGATGCAAG 1410
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 363 lGlyCyLeuGlnIlyshIlyshIlyshIlyshIlyshIlyshIlyshIlyshIlyshI 383
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 1411 CTTTAAAGTGTGCTGTTCTTATTTCTGATTTTGAACAACAACCTGAGTACTTGAACCT 1470
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 383 uAlaSerAspCyCysSerLeuGlnLeuIlyshIlyshIlyshIlyshIlyshIlyshIlysh 403
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

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Db 70 AsnThrThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIle 89
 QY 527 GAGCAATTGAGACCAAGCATGGCATGGCTTAAACCAAGCTTCAACCTTGGTACTGACA 586
 Db 90 TyrTrpIleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
 QY 587 GGAACCTATACAGAGTTTTCACAGAGATTTTTCAGAGATTTTTCAGATTTTTCAGAGAT 646
 Db 110 AlaAsnProLeuIlePheMetAlaGluThrAlaLeuSerGlyProIlyAlaLeuIlyHis 129
 QY 647 CTGGTGGCTGGAGACAAAATGACCTCTAGAGGTTTCCATATTGACACGCTTATA 706
 Db 130 LeuPhePheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnIly 149
 QY 707 TCCTTAAGAACTTAATGGCTCATATATCTTATCTTCTTAAAGTCCGGAATAT 766
 Db 150 ThrLeuGluSerLeuTyrLeuGlySerAsnHisIleSerSerIleIlyLeuProIlyGly 169
 QY 767 TTTTCTATCTGACAAACCTAGAAACATGGTATCTTTCTTATATCTATATCAACTAT 826
 Db 170 PheProThr---GluIlySleuIlyValIleuAspPheGlnAsnAsnAlaIleHisTyrIleu 188
 QY 827 TCTGTCAAGACTTACAGTTTCTACGTGAAAATCCCAAGTCAATCTCTTTAGACCTG 886
 Db 189 SerIlySgluAspMetSerSerLeuGlnIle----AlaThrAsnLeuSerLeuAsnLeu 206
 QY 887 TCTTTAAACCAATTGACTCCATTCAGACCCAGCTTTCAGGAAATTAGGCTCCATGAA 946
 Db 207 AsnIlyAsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSer 226
 QY 947 TTGACTCTAGAGATTTTATATAGCTCAATATGATGAAATGGTGCCTTCAAAACAT 1006
 Db 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuValIlePheIlySglIyLeu 242
 QY 1007 ACTGGTTACATGTCATCGGTGATCTTGGAGAAATTTAAAGAAAGCAATCTGGAA 1066
 Db 243 LysAsnSerThrIleGlnSerLeuTrpLeuGlyThrPheGln---AspMetAspAspIly 261
 QY 1067 AGTTTGAACGTTCTGTATGAGAGATATGCAATGAGCATTTGATGAGTCAAGTTA 1126
 Db 262 AspIleSerProAlaValPheGluIlyLeuCysGluMetSerValGluSerIleAsnLeu 281
 QY 1127 ACATATATAATCAATTTTTCAGATGATATTTAATCAATTTTTCAGATGATTTTCT 1186
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 QY 1187 GCAATGTCTTTCACAGGTGATCATATTAACAACATAGACAGAT----- 1228
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 QY 1229 -----GTTCTTAGGCAATTTCAATGGCAATCTTATCATATCATTAAGATGT 1273
 Db 322 ThrLeuIlySlySleuValLeuSerAlaAsnIlySspPheGluAsnLeu-----Cys 337
 QY 1274 CATCTTAAGCCT-----TTTCCAAAGCTGAGTCTTACCTTTCTTAAAGTTGACTTTA 1327
 Db 338 GlnIleSerAlaSerAsnPheProSerLeuThrHisLeuSerIleIlyGly----- 354
 QY 1328 ACTACCAACAGAGAGATATACGTTTGGTACGTTGGCT---CTGCCAAGTCTCAGATAT 1384
 Db 355 AsnThrIlySargLeuGlnIleuGlyThrGlyCysLeuGluAsnLeuGluAsnLeuArgIly 374
 QY 1385 CTAGATCTTATGAAATGCCATGAGCTTATAGAGTGGTCTGTTCTTATTCGATTTTGA 1444
 Db 375 LeuAspLeuSerHisAspAspIleGluThrSerAspCysCysAsnLeuGlnLeuArgAsn 394
 QY 1445 ACAAAACAACTGATCTAGACTTACCTCAGCTTCAATGGTGCATC---CTAGTGGTCC 1501
 Db 395 LeuSerHisLeuGlnSerLeuAsnLeuSerIlyArgGluProLeuSerLeuIlyThrGlu 414
 QY 1502 AACTTCATGGGTCTTGAAGAGCTGGAATACCTGCACTTTCAGCACTTCAATTAAGAAAG 1561
 Db 415 AlaPheIlySgluIlyCysProGlnLeuGluIleuLeuAspLeuAlaPheThrArgLeuIlyVal 434

QY 1562 CTCACAGAAATTCACAGTGTCTTATCTTTGAAAACTTTTATACCTTGACATCTCTTAC 1621
 Db 435 LysAspAlaGlnSerProPheGlnAsnLeuHisLeuLeuIlyValIleuAsnLeuSerHis 454
 QY 1622 ACTAATATCAAAATTTGATTTGATGCAATATTTCTTGGCTTGTATGATGATCAACTTTA 1681
 Db 455 SerLeuLeuAspIleSerSerGlnIleuPheAspGlyLeuProAlaLeuGlnHisLeu 474
 QY 1682 AAAATGGCTGGCAATTTCTTCAAGACACACCTT-----TCAATGTCTTACAAAC 1735
 Db 475 AsnLeuGlnIlyAsnHisPheProIlySgluAsnIleGlnIlyThrAsnSerLeuGlnThr 494
 QY 1736 ACAAAACAACTTCAATCTCGATCTTCTTAAAGGCCAATGGCAACGATATCTAGGGGG 1795
 Db 495 LeuGlyArgLeuGluIleuValLeuSerPheCysAspLeuSerSerIleAspGlnHis 514
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 Db 535 SerSerIleGluAlaLeuSerHisLeuIlyGlyIleTyr-----LeuAsnLeu 550
 QY 1907 AGTTTCAATGCAATGAGACATCCAAAGAAATCTGCAACATTTTCCAAAGATCTAGCC 1966
 Db 551 AlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleLeuSerGlnIlyArg 570
 QY 1967 GTCTTCAATGCAATATATTTCTGTGCTTGTATATGTAATATGCAATTTCTTTCAG 2026
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 Db 591 TrpTyrSgluSmetGlnIlyLeuGluAspThrGluAspThrIleuCysGluAsnPro 610
 QY 2087 ATGACATGAAGGCTCCCTGGTGGATTTTATGCAATTCACACTGTAT----- 2137
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 QY 2138 ---ATATACAAACTATCATCAGTATCGGTGCTGAGTGTGCTTGTAGACCATGTGA 2194
 Db 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
 QY 2195 GCATTTCTGATATPACCACTTATTTTCACCTG 2227
 Db 651 LysTyrPheLeuArgTyrIlySgluHisIle 661
 RESULT 9
 US-10-037-417-107
 ; Sequence 107, Application US/10037417
 ; Publication No. US20040052806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kekuda, Rameesh
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Liu, Xiaodong
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Patcurajan, Meera
 ; APPLICANT: Grose, William M
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine B
 ; APPLICANT: Verne, Corine A.M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Edinger, Shlomit R
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Maayan, Mark
 ; APPLICANT: Rothenberg, Mark
 ; APPLICANT: Stone, David J
 ; APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia
 APPLICANT: Shenoy, Sureesh G
 APPLICANT: Anderson, David W
 APPLICANT: Padigaru, Murallidhara
 APPLICANT: Taupier Jr, Raymond J
 APPLICANT: Miller, Charles E
 APPLICANT: Eileen, Andrew J
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-235
 CURRENT APPLICATION NUMBER: US/10/037,417
 CURRENT FILING DATE: 2002-09-20
 PRIOR APPLICATION NUMBER: 60/260,018
 PRIOR FILING DATE: 2001-01-05
 PRIOR APPLICATION NUMBER: 60/260,360
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: 60/272,411
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: 60/272,817
 PRIOR FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: 60/291,186
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: 60/303,231
 PRIOR FILING DATE: 2001-07-05
 PRIOR APPLICATION NUMBER: 60/305,060
 PRIOR FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: 60/318,405
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: 60/318,700
 NUMBER OF SEQ ID NOS: 227
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 107
 LENGTH: 661
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-037-417-107

Alignment Scores:
 Pred. No.: 1,57e-47 Length: 661
 Score: 597.50 Matches: 187
 Percent Similarity: 46.50% Conservative: 125
 Best Local Similarity: 27.87% Mismatches: 314
 Query Match: 10.05% Indels: 45
 Gaps: 15

US-09-396-985b-5 (1-3395) x US-10-037-417-107 (1-661)

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 10 LeuValAlaLeuPheLeuAlaSerCysArgAlaThrThrSerSerArgGlnLysCysAla 29
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 30 GlnLysGlnValAsnLysTrpTrpAsnCysGlnLysAsnGlnLysLeuAsnGlnLysProGly 49
 407 GACATCCCTTATTACCAAGCAAGCAAGCTAGATCTGAGCTTCAACCCCTGAGATCTTAA 466
 50 ThrLeuProAsnSerTrpGlnCysLeuGlnPheSerPheAsnValLeuProThrLileGln 69
 467 AGCTATAGCTTACCAATTTCTCAAACTTCAGTGGCTGATTTATTCAGAGGTGAAT 526
 70 AsnThrThrPheSerArgLeuLileAsnLeuThrPheLeuAspLeuThrArgCysGlnLile 89
 527 GAGCAATTTGAAGCAAGCAAGCAAGCTGATTAACAGCTCTCAACCTTGATGAC 586
 90 TyrTrpLileHisGlnAspTrpPheGlnSerGlnHisArgLeuAspTrpLileValLeuThr 109
 587 GAAAGCCCTATCAAGAGTTTCCCAAGAAAGTTTCTGAGCTAACAATTTAGAGAT 646
 110 AlaAsnProLeuLilePheMetAlaGlnThrAlaLeuSerGlyProLysAlaLeuLysHis 129
 647 CTGTGGCTGTGAGACAAAATGACCTCTTAGAGGTTTCATATTGACAGCTTATA 706

130 LeuPhePheLileGlnThrGlyLileSerSerLileAspPheLileProLeuHisAsnGlnLys 149
 707 TCCTTAAGAAACCAATAGGCGCTCATATCTTATACCTTAACTTGAAGCGCGAATAT 766
 150 ThrLeuGlnSerLeuLysLeuGlySerAsnHisLileSerSerLileLysLeuProLysGly 169
 767 TTTTCTTAATCTGACAAACCTAGAACATGTGAGATCTTTCTTAATACCTTAACTTAACTTAT 826
 170 PheProThr---GlnLysLeuLysValLeuAspPheLileAsnAlaLileHisLysLileu 188
 827 TCTGTCAAAGACTTACAGTTTCTACGTAAGAAATCCCAAGTCAATCTCTTGAAGCTG 886
 189 SerLysGlnAspLileSerSerLileGlnLile---AlaThrAsnLeuSerLileAsn 206
 887 TCTTTAAACCAATGTGATCTCATCAAGCCCAAGCTTTCAGGAAATTAAGCTCCATGAA 946
 207 AsnGlnAsnAspLileAlaGlyLileGlnProGlyAlaPheAspSerAlaValPheGlnSer 226
 947 TTGACTCTAAGAAAGTAATTTTAAATAGCTCAAAATGTACTGAAATATGCTCAAAAGATG 1006
 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuLeuValLilePheLysGlyLeu 242
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 243 LysAsnSerThrLileGlnSerLileLeuTrpLeuGlyThrPheGln---AspMetLysAspGln 261
 1067 AGTTTACCGCTTCTGTGATGAGAAAGCTATGCAATGTGAGCAATGATGAGTTCAGGTTA 1126
 262 AspLileSerProAlaValPheGlnGlyLeuLysGlnLysSerValGlnSerLileAsnLeu 281
 1127 ACATATATTAATCATTTTTCAGATGATGATTTATTAATCTCAATGCTTGCAAAATATTTCT 1186
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 1187 GCAATGCTTTTACAGGCTGATATTAACATACATAGCAAT----- 1228
 302 GlnLeuAspLeuThrAlaThrHisLileSerGlnLeuSerGlyLeuValGlyLeuSer 321
 1229 -----GTTCCTAGGCAATTTCAATGGCAATCCCTATCATCATTAAGTGT 1273
 322 ThrLeuLysLysLeuValLileSerAlaAsnLysPheLileAsnLeu---Cys 337
 1274 CATCTTAAGGCT-----TTTCCAAAGCTGAGCTTACCTTTTAAAGTTGAGACTTTA 1327
 338 GlnLileSerAlaSerAsnPheProSerLileThrHisLileSerLileLysGly----- 354
 1328 ACTACCAAGAGAGATATCAGCTTGTGTCAGTTGCT---CTGCCAAGCTTCAGATAT 1384
 355 AsnThrLysArgLeuGlnLileGlnLysGlyLeuGlnCysLeuGlnLysLeuGlnLysLeuArgGln 374
 1385 CTAGATCTTGTAGAAATGCGCATGAGCTTGAAGCTTGCTGCTTCTTATTCGATTTTGA 1444
 375 LeuAspLeuSerHisAspAspLileGlnThrSerAspLysCysAsnLeuGlnLysLeuArgAsn 394
 1445 ACAACAACTGTAAGTACTTACAGCTCAGCTTCAATGAGTGTATC---CTGATGAGAGGCC 1501
 395 LeuSerHisLileGlnSerLileAsnLeuSerLysTrpAsnLysLeuProLeuSerLysTrpGln 414
 1502 AACTTCATGAGGTGTAGAAAGCTGGAATACCTGAGACTTTGACAGCTTAAATAAG 1561
 415 AlaPheLysGlnCysProGlnLileGlnLysLeuLeuAspLeuAlaPheThrArgLysVal 434
 1562 GTACAGAAATTCAGAGTTCTTATCTCTTGAATAAACTTTTAACTTGAACATCTTAC 1621
 435 LysAspAlaGlnSerProPheGlnAsnLileLysLeuLysValLileAsnLysSerHis 454
 1622 ACTAATACCAAAATGTGACTTGTAGCAATTTCTTGAGCTTGAATGCTCAACACTTTA 1681
 455 SerLeuLeuAspLileSerSerGlnLysLeuPheAspLysLeuProAlaLysGlnHisLys 474
 1682 AAAATGCTGCGCAATCTTTCAAAGCAACACACCTT-----TCAATGTCTTTCACAAAC 1735
 475 AsnLeuGlnLysAsnHisPheProLysGlyAsnLileGlnLysThrAsnSerLysGlnThr 494

QY 1736 ACAACAACCTTAACATTCCTGATCTTTCTAATCCACATCGAACAAGATATCTAGGGGG 1795
DB 495 LeuGlyArgLeuGluIleValIleuSerPheCyaspLeuSerSerIleAerGlnHis 514
QY 1796 GTATTTGACACACTCTACAGACTCCAGTTATTAACAGTCAACAACACTCTGTCTT 1855
DB 515 AlaIleHisSerLeuIleuMetLeuHisIleValAspLeuSerHisAsnArgLeuThrSer 534
QY 1856 CTGAT-----CCATCCCATTAATTAACAGCTGTATCTCCACAGACTCTGTATTC 1906
DB 535 SerSerIleGluIleAlaLeuSerHisLeuIleGlyIleTy-----LeuAsnLeu 550
QY 1907 AGTTTACATCCCATAGACATCCCAAGATACTGCAACATTTCCAAAGACTAGCC 1966
DB 551 AlaSerHisIleSerIleIleuProSerLeuLeuProIleLeuSerGlnArg 570
QY 1967 GTCTTCAATCTGACTAATTAATTCGTGCTGTATATGTAATATCAGAAATTTCTTCAG 2026
DB 571 ThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyPheLeuGlu 590
QY 2027 TGGGTCAAGACCAAGAAATTTCTGTGTAATGTGAACAATGAATGTGCATCACT 2086
DB 591 TrpTyArgGluAsnMetGlnIleuGlnAspThrGluAspThrIleuCyGluAsnPro 610
QY 2087 ATAGACATGAAGGCTCCCTGCTGTGATTTTACGATTTCCACCTGTAT----- 2137
DB 611 ProLeuLeuArgGlyValArgLeuSerAspAlaThrLeuSerCysSerMetAlaVal 630
QY 2138 --ATATACAGACTATCATCATGATATCGGTGTCAGTGTCTGTGTAGCCACTGTA 2194
DB 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuIlePheAlaVal 650
QY 2195 GCATTTCTGATATACCACTTCTATTTCACTG 2227
DB 651 LysTyPheLeuArgTrpIleGlnHisIle 661

RESULT 10
US-09-954-987B-192
Sequence 192, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954, 987B
CURRENT FILING DATE: 2001-09-17
PRIORITY APPLICATION NUMBER: US 60/233,035
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 60/263,657
PRIORITY FILING DATE: 2001-01-23
PRIORITY APPLICATION NUMBER: US 60/291,726
PRIORITY FILING DATE: 2001-05-17
PRIORITY APPLICATION NUMBER: US 60/300,210
PRIORITY FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-192

Alignment Scores:
Pred. No.: 2,696-45 Length: 1032
Score: 575.00 Matches: 242
Percent Similarity: 40.93% Conservative: 153
Best Local Similarity: 25.08% Mismatch: 318
Query Match: 9.68% Indels: 252
DB: 10 Gaps: 40

US-09-396-985B-5 (1-3395) x US-09-954-987B-192 (1-1032)
QY 353 CTTCCTAATATTACCTTACCAATGATGATCAGAAAT---CTCAGCAAAATCCCTCATGAC 409
DB 120 LeuArgAsnLeuThrValIleuLeuLeuGluAspAsnGlnIleuTyThrIleProAlaGly 139
QY 410 ATCCCTTATTAACCAAGAACTAGATCTGAGCTTCAC--- 448
DB 140 LeuProGluSerLeuIleuGluLeuSerIleGlnHisAsnIlePheGlnValThrLys 159
QY 448 ----- 448
DB 160 AsnAsnThrPheGlyLeuArgAsnLeuGluArgLeuTyIleuGlyTrpAsnCytyrPhe 179
QY 449 -----CCCTGAG 457
DB 180 LysCyAsnGlnThrPheLysValGluAspGlyAlaPheLysAsnLeuIleHisLeuLys 199
QY 458 ATCTTAAGAGCTATAGCTTACCAATTTCC-----TCACA 493
DB 200 ValLeu---SerLeuSerPheAsnAsnLeuPheTyValProProLysLeuProSerSer 218
QY 494 CTTCAGTGTGCTGATTTATTCAGGTGTGAATTTGACAATTTGACAAGACGATGGCAT 553
DB 219 LeuArgLysLeuPheLeuSerAsnAlaLysIleMetAsnIleThrGlnIleAspPheLys 238
QY 554 GCGTTAAACACGCTTCAACCTTGCTGTGACAGCAAGAAC----- 592
DB 239 GlyLeuGluAsnLeuThrIleuLeuAspLeuSerGlyAsnCytyrAsnAla 258
QY 593 -----CCATCAAGAGTTTTC-----CCAGAAAGTTT 622
DB 259 ProPheProCysThrProCysLysGluAsnSerSerIleHisIleHisProLeuAlaPhe 278
QY 623 TCTGACATTAACAATTTAGAAATCTGTGCTGTGACCAAAATGACCTCTTAGAG 682
DB 279 GlnSerLeuThrGlnLeuLeuTyIleAsnLeuSerSerThrSerLeuArgThrIlePro 298
QY 683 GGTTCATATTGACAGCTTATATCTTAAAGAAATGATGGCTCAAT---CTT 739
DB 299 SerThrTrpPheGluAsnLeuSerAsnLeuIleGlnHisIleuGlnPheAspTyLeu 318
QY 740 ATACATTCCTTTAAGTTCGCTGAATATTTCTTAATCTGACAAACCTTAGAATGTGAT 799
DB 319 ValGlnIleIleAlaSerGlyAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAsp 338
QY 800 CTTCCTTATAC-----TATATCAAACTATTCTGTC----- 832
DB 339 LeuSerPheAsnPheGlnTyLysGluTyIleuGlnPheIleAsnIleSerSerAsnPhe 358
QY 832 ----- 832
DB 359 SerLysLeuArgSerLeuLysLysLeuHisIleuArgGlyTyValPheArgGlyLeuLys 378
QY 833 ---AAGACTTACAGTTTACAGTGAATCCCAAGCTCAATCTCTTAGACCTGTCT 889
DB 379 LysLysHisPheGlnIleuGlnSerLeuProAsnLeu---AlaThrIleAsnLeuGly 397
QY 890 TTAACCAATGATCTCATGACCCCAAGCTTTGAGGAATTAAGCTCATGAATG 949
DB 398 IleAsnPheIleGluLysIleAspPheLysAlaPheGln----- 410
QY 950 ACTTAAAGAGTAATTTTATAGCTCAAAATGTACTGAAATGTGCTTCAAAACATGACT 1009
DB 411 -----AsnPheSerLysLeuAspValIle-----TyLeuSer 421
QY 1010 GGTTCATGTCATCGGTGATCTTGGA---GAATTTAAATGAAGAACTG--- 1063
DB 422 GlyAsnArgIleAlaSerValLeuAspGlyThrAspTySerSerThrPheArgAsnArgLeu 441
QY 1064 -----GAAAGTTTTCAC----- 1075

Db 442 ArglyspProLeuSerThrAspAspArgLupheAspProHisValAsnPhenylrHisSer 461
 Qy 1076 ---GGTTGTCATGGAAGACTATGACATGACATGATGACGTTACGTTACATAT 1132
 Db 462 ThrlyspProLeuIlelyspProGlnCysThrAlaTyrGlyValAlaLeuAspSerLeu 481
 Qy 1133 ATAAATCATTTT-----TCAGATGATATTTATATCTC 1165
 Db 482 AsnAsnIlePheIleIleGlyLysSerGlnPheGlnGlyPheGlnAspIleAlaCysLeu 501
 Qy 1166 AATTGCTGGCAATATTTCTGCAATGTCCTTTCACAGGTGACATATATAACACATAC 1225
 Db 502 AsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGluPheSer----- 518
 Qy 1226 GATGTTCTAGGCAATTCGAATGCAATCCTTATCAATCATTTAGTCATCTTAAGCT 1285
 Db 518 ----- 518
 Qy 1286 TTTCGAAGCTGAGTCTACTTTTCTTAAAGTTGACCTTAACTACCAAGAGAGAT 1345
 Db 519 -----SerMetProHisIleIleLysTyrLeuAspLeuThrAsnAsnArgLeuAsp 534
 Qy 1346 ATC-----AGCTTGGTCAGTTGGCTCTGCCAAGCTGCAAGATCTAGATCTT 1393
 Db 535 PheAspAspAsnAlaPheSerAsp-----LeuHisAspLeuGluValLeuAspLeu 552
 Qy 1394 AGTGAATGGC-----ATGAGCTTTAGAGTGGCTGCTTCTTATCTGATTTTGAAACA 1447
 Db 553 SerHisAsnAlaHisTyrPheSerIleAlaGlyValThrHisArgLeuGlyPheIleGln 572
 Qy 1448 AAC-----AACCTGAAGTACTAGACTCAGCTTCATGAGTGTCAGCTGAGT--- 1498
 Db 573 AsnLeuIleAsnLeuArgValLeuAsnLeuSerHisAsnGlyIleTyrThrLeuThrGlu 592
 Qy 1499 -----GCCAATCTGAGGCTGTAGAGAGCTGGAATACCTGGACTTCACGACTCC 1549
 Db 593 GluSerGluLeuLysSerIleSerLeuLysGluValPheSerGlyAsnArgLeuAsp 612
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 Db 673 ThrLeuLeuGlnTyrPhe-----ProHisLeuHisLeuLeuAspLeuSerHisArgAsn 689
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 Qy 1832 ATGAGTCAACAACCTACTGTTCTGTGATCCATCCATTTAAACAGCTGTACTCCCTC 1891
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 Qy 2537 -----AGCCGCTCGCAATCATCTGATGCTT 2566
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 RESULT 11
 US-10-272-502A-31
 ; Sequence 31, Application US/10272502A
 ; Publication No. US20030139364A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Krieger, Arthur M.
 ; APPLICANT: Schetter, Christian
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Vollmer, Jörg
 ; APPLICANT: Bauer, Stefan
 ; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
 ; FILE REFERENCE: C01039, 70065, US
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/329,208
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1

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1 : SEQ ID NO 31
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3 : LENGTH: 1032
4 : TYPE: PRT
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6 : ORGANISM: Mus musculus
7 : US-10-272-502A-31
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[illegible]

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Qy 2006 GAATATTCAGAAATTTCTGCAAGTGGCTCAAGACAGAAATATGTC-----TTG 2053
Db 770 AspIleSerAspPheArgSerThrPheAsnGluAsnLeuAsnIleThrIleProLysLeu 789
Qy 2054 GTGATGTGTGAACAATGAATGTCATCACCTATAGACAGAAAGCCCTCCCTGGTGTG 2113
Db 790 ValAsnVal-----IleCysSerAsnProGlyAspGlnLysSerLysSerIleMet 806
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Db 807 SerLeuAspLeuThrThrCysValSerAspThrThrAlaValLeuPhePheLeuThr 826
Qy 2150 ATCATCAGTGTATGGTGGTGCAGTGGCTTGTGAGCCACTGTAGCATTTCTGATATAC 2209
Db 827 PheLeuThrThrSerMet-----ValMetLeuAlaIleValHisIlePhePheTyr 844
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Db 1010 LysAsnValValLeu 1014

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; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: CO1041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRN
; ORGANISM: Mus musculus
; US-10-407-952-32

Alignment Scores:
Pred. No.: 2,69e-45 Length: 1032
Score: 575.00 Matches: 242
Percent Similarity: 40.93% Conservative: 153
Best Local Similarity: 25.08% Mismatches: 318
Query Match: 9.68% Indels: 252
DB: 15 Gaps: 40

US-09-396-985b-5 (1-3395) x US-10-407-952-32 (1-1032)

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Qy 410 ATCCCTATTTCACCAACCAAGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 448
Db 140 LeuProGluSerLeuLysGluLeuSerLeuIleGlnAsnAsnIlePheGlnValThrLys 159
Qy 448 ----- 448
Db 160 AsnAsnThrPheGlyLeuArgAsnLeuGluArgLeuTyrLeuGlyTyrTrpAsnCysTyrPhe 179
Qy 449 -----CCCCTGAG 457
Db 180 LysCysAsnGlnThrPheLysValGluAspGlyAlaPheLysAsnLeuIleHisLeuLys 199
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Qy 494 CTTCAGTGGCTGATTTATTCAGGTGTGAATGGAATTTAGACAAATTTAGACAAAGCATGGCAT 553
Db 219 LeuArgLysLeuPheLeuSerAsnAlaLysIleMetAsnIleThrGlnGluAspPheLys 238
Qy 554 GGCCTTAACCAAGCTCTCAACCTTGCTGTGACAGAAAC----- 592
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Qy 593 -----CCATCAAGAGTTTTC-----CCAGAAAGTTT 622
Db 259 ProPheProCysThrProCysLysGluAsnSerSerIleHisIleHisPheLeuAlaPhe 278
Qy 623 TCTGCACTAACAAATTTAGAAATCTGTGCTGTGAGACAAATAGCACTGCTCTAGAG 682
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Qy 683 GGTTCATATTTGACAGCTTATATCTTAAAGAACTTAATATGGCTCATTAAT---CTT 739
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Qy 740 ATACATTCCTTTAAGTTCCTGAATATTTTCTAATCTGACAAACTGAAACATGATGAT 799
Db 319 ValGlnIleuIleAlaSerGlyAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAsp 338
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Db 339 LeuSerPheAsnPheGlnTyrLysGluTyrLeuGlnPheIleAsnIleSerSerAsnPhe 358

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RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication NO. US2003032074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan

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[illegible]

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QY	1832	ATGAGTCACAACAACCTACTGTTTCTGAGTCATCCCATTTATTAACAAGCTGTACTCCCTC	1891
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QY	1892	AGGACTCTTGATTCGACTTTCAATCCGATAGAG---ACATCCAAAGGAATATCTGCAACAT	1948
Db	730	ValhIsleuApleuSerPheAsnThrlleuYSerIleAenulYSerSerIeugInlThr	749
QY	1949	TTTCCAAAG---AGCTTAGCCGCTTTCGAATCTGACATAATTTGTTGCTTGATATGT	2005
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QY	2054	GTCGAATGTTGAACAAATGAATGTGCATCACCTATAGACATGAAGGCTCCCTGGTGTG	2113
Db	790	ValAsnVal-----IleCysSerAsnProIyAspInlYSerIySerIleu	806
QY	2114	GATTTTCAGAAATCCACTGT-----TATATATACAAGACT	2149
Db	807	SerIeApleuLeuThrlnCysValSerAspThrlhAlaValIleuPhePheLeuThr	826
QY	2150	ATCATCATGATCGATGGTCAGTGTGCTGTGGATGCCACTGATTCGATTTCTGATATAC	2209
Db	827	PheLeuThrlhTrhSerMet-----ValMetIleuAlaIleuValhIsIleuPheYr	844
QY	2210	-----CACTTCTATTTTCACTG-----ATACTATATGCTGGCTGTAAAAAGAC	2254
Db	845	TrpAspValTrpPheIleYrHIsEmetCysSerAlaYsleuYsGIYrYrArgThrSer	864
QY	2255	AGCAGAGAGAAGAACATCTATGATGACATTTGTGATCTAGCCAGCCAGAA-----	2305
Db	865	SerhTrhSerGIInThrPheYrAspAlaYrIleSerYrAspThrlYsAspAlaSerVal	884
QY	2306	GAGCACTGGTGAGAAACGACTGGTAAAGATTAGAGAAGAGAGTCCCGC---TTT	2362
Db	885	ThrlAspTrpValIleAenGIuLeuArgYrHIsIleuGIuInlSerGIuApleYsSerVal	904
QY	2363	CAGCTTTCCTTCATTCACGAGACTTATATTCCTGTGTAGCCATTCGCTCCAAACATATC	2422
Db	905	LeuLeuCylsleuGIuArgAspTrpAspProGIyLeuProIleIleAspAsnLeuMet	924
QY	2423	CAGAAAGCTCCCAAGAGCCGGAAGATTATTCGTGGTGCTAGACATTTATCCAG	2482
Db	925	GIIn---SerIleAenGIuSerIySerThrllePheValLeuThrlYsYr-----	941
QY	2483	AGCCGTTGATCTTGAATATGAGATTGCTCAGACATGCGACTTCTAGT-----	2536
Db	942	-----AlaYsSerTrpAsnPhelYrThrlAlaPhe	951
QY	2537	-----AGCCGCTTCGCAATCTTATGTTGCTT	2566
Db	952	TyrIleuAlaIeugInlArgIleuMetAspIuInleuMetAspValIleIlePheIleuLeu	971
QY	2567	GAGAAAGTGGAAAGTCTTCTGTAGGAGAGAGCTGCAATTGTATCGCTTCTTAGCGA	2626
Db	972	GIuPProValleuGIIn---TyrSerIInlYrLeuArgIleuArgGIuArgIleCysYs	989
QY	2627	AACAGCTCATCGATGGAGAGACAAATGCTCGGGAGAGCAGATCTTCTGAGAAAGATC	2686
Db	990	SerSerIleIeugInlTrpProAsnAsnProYsAlaGIuAenleuPheTrpGIuSerIeu	1009
QY	2687	AAAAAGCCCTGTTG	2701

[illegible]

OY	887	TCCTTAAACCCAAATTGACTCCATTCATCAACCCCAAGCCTTTCAGGGAAATTAGGCTCCATGAA	946
Db	348	SerPheAn-----TyrGluLeuGlnValTyrHisAla-----Ser	359
OY	947	TTGACTCTTAACAAGTAATTTTAATTAAGTCCAAATGACTAGTAAAAATGTC-----	994
Db	360	IleThrLeuProHisSerLeuSerSerSerLeuGluGlnLeuValTyrGlySerGly	379
OY	995	-----CTTCAAAACATGACCTGGTTTACATGTCCTCATCGCTTG-----	103
Db	380	TyrValPheIlysgIuLeuIlyAsnSerSerLeuSerValLeuHisIlyLeuProArgLeu	399
OY	1031	-----ATCTGGACAAATTTTAAAAAT	105
Db	400	GluValLeuAspLeuGlyTyrAsnPheIleIyValAlaAspLeuAsnIlePheIlyHis	419
OY	1052	GAAGAAGATCTGCAAGATTGTGACCGTTCGTGCATGAA-----	109
Db	420	PheGluAsnLeuIyValAspLeuSerValAsnIyIleSerProSerGluIuSer	439
OY	1091	-----GGACTATGC-----AATGTGACCATGATGAGTTCAGG-----	112
Db	440	ArgGluValGlyPheCysProAsnAlaGlnThrSerValAspArgHisGlyProGlnVal	459
OY	1124	TTAACATATTAATTAATCATTTTTCAGATGATATTTTAATTCGAAATTCG---TTGGCAAT	118
Db	460	LeuGlnAlaLeuHisIeTyrPheArgTyrArgGlnTyrIlaArgSerCysArgPheIyAsn	479
OY	1181	ATTCTCGCAATGTCTTTACAGAGTGATCATATTAACAACATAGACAGATGTTCTTAGCAT	124
Db	480	LysGluProProSerPheLeuProLeuAsn-----AlaAspCys-----His	493
OY	1241	TTCAAAATGCGACTCTTATCATCATTTAGATGTCAT-----CTTAAGCTTTTCCA	129
Db	494	IleTyrGlyGlnThrLeuAspLeuSerArgAsnAsnIlePhePheIleIySerProSerAsp	513
OY	1292	AAGCTGAGCTACACTTTTCTTAATAAGTTGAGCATTTATACCAAGAGAGATATACAG	135
Db	514	PheGlnHisLeuSerPheLeuIlyCysLeuAsnLeuSerGlyAsn-----Thr	529
OY	1352	TTTGTCACGTTG-----GCTTGCCAAAGTCTCAGATATCTAGAT	139
Db	530	IleGlyGlnThrLeuAsnGlySerGlnIuLeuTyrProLeuArgGlnIuLeuArgTyrLeuAsp	549
OY	1391	CTTAGTGAATTGCATAGACGCTTAAAGAGTTCGTCTTATTCGATTTTGGAAACAAC	145
Db	550	PheSerAsnAsnArgLeuAsp-----	556
OY	1451	AACCTGAAGTACTTAGACCTCAGCTTCAATGGTGCATCCTGATGAGTGCSCAACTTCATG	151
Db	557	-----LeuLeuTyrSerThrAlaPheGlu	564
OY	1511	GGTCTAGAAGACTGGAAATCTGAGAC-----TTTCAGCACTCC	154
Db	565	GluLeuGlnSerLeuGlnValLeuAspLeuSerSerAsnSerHisIyTyrPheGlnAlaGlu	584
OY	1550	ACTTTAAAAAAGTGACAGATTCCTCAGATGTTCTATCT---CTTGAAAACTTCTTAC	160
Db	585	GlyIleThrHisMetLeuAsnPheThrIySlyIyValArgLeuLeuAspIyIyLeuMetC	604
OY	1607	-----CTTGACATCTCTTACATTAATCAAA---ATTGACTTTGGCATATTTCTT	165
Db	605	AsnAspAsnAspIleSerThrSerAlaSerArgThrMetGluSerAsp-----	620
OY	1658	GGCTTGATCAGTCTCACAACCTTTAAAAAATGGCTGGCAATTTCTTTCAA-----	170
Db	621	-----SerLeuArgIleLeuGlnPheArgGlnAlaAsnHisIyLeuAspValLeuTyrArg	637
OY	1706	-----GACACACACCCCTTTCAAAATCTTTTCAACAACAACAACCTTAATCTCGAT	175
Db	638	AlaIyAspAsnAlaGlyTyrLeuAspPhePheIyAsnLeuPheAsnIuLeuGlnValLeuAsp	657

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QY 1760 CTTTCTAATGCGCAATGGAACAGATATCTAGGGGGATTGATGAC----- 1804
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Db 658 TLeSerArgAnSerLeuAnSerLeuProGluValPheGluGlyMetProProAsn 677
QY 1804 ----- 1804
Db 678 LeuValAnLeuSerLeuAlaValAnGlyLeuValSerPhePheTrpArgLeuGln 697
QY 1805 ACACCTACAGACATCCAGATTATAACATAGACACAAACCA----- 1849
   |||:||||: |||:||||: |||:||||: |||:||||:
Db 698 LeuLeuValSerLeuGluLeuLeuAnSerLeuValAnGlnLeuThrValProGlu 717
QY 1850 ----- 1850
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Db 718 ArgLeuAlaAnCySerLeuValThrThrLeuLeuValSerLeuValAnGlnLeuValArg 737
QY 1877 CAGCTG----- 1912
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Db 738 GlnLeuThrValThrPheLeuGluAspAlaLeuGlnLeuValGlyLeuAspAlaSerSer 757
QY 1913 AATGCGCATAGACATCCAAAGAAATCTGCA----- 1957
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Db 758 AsnValIleGln----- 1957
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QY 1958 ---AGTCTAGCGCTTCAATCTGACATATATCTGTGCTTGTATATGATATATCAG 2014
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Db 774 AsnAnLeuGluMetLeuValLeuValSerValAnGlyPheLeuValCyAnCyAspAlaVal 793
QY 2015 AATTCTTGACAGTGGGTCAAGACCAAGAAATGTTCTTGATGAAATGTT--GAACAAATG 2071
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Db 794 TrpPheValTrpTrpValAnSerLeuThrAspValThrLeuProGlyLeuAlaThrAspVal 813
QY 2072 AAATGTCGATCACTATAGACATAGACGCTCCCTGCGTGGATTTTACAAATCCACC 2131
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Db 814 ThrCyValGlyProGlyAlaValSerGlyGlnSerValIleSerLeuAspLeuValThr 833
QY 2132 TGTTATATATACAGACT-----ATCATCAGATGATGCGTGCAGTGCCTT-- 2179
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Db 834 CysGlnLeuAspLeuThrAnLeuValLeuValSerLeuValSerLeuValLeuPhe 853
QY 2180 -----GTGAGCACTGATGATTTGTGATA-----TACCACTTCTAT 2218
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QY 2219 TTTTACCTGATACCTATATGCTGCGCTGTAAGAAAGACAGACAGAAAGATATGAT 2278
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Db 874 PheTrpValAlaValSerLeuGlyValGlnLeuGlnSerMetGluSerCysValAsp 893
QY 2279 GCATTTGATCTACTGCGACGCAAGATGAG-----GACTGGGTGAGAAAGAGCTG 2329
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Db 894 AlaPheIleValGlyThrPheThrLeuValAnSerLeuValThrGluTrpValLeuGlnGlu 913
QY 2330 GTAAAGAAATTGAAGAAAGAGTGGCCGC-----TTTCACTTTGCTTCATTAAC 2380
   |||:||||: |||:||||: |||:||||: |||:||||:
Db 914 ValAlaValSerLeuGluAsp-----ProArgGluValSerPheAnLeuValLeuGluGln 931
QY 2381 AGGAGCTTATCTGCTGCTGATGCACTGCTGCAATCAGATCAGAAAGCTTCCACAG 2440
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Db 932 ArgAspTrpLeuProGlyGlnProValLeuGlnValAnSerLeu--SerIleGlnLeu 950
QY 2441 AGCGGAAAGTATATGCTGCTGCTGATGCACTTATCCAGAGCGCTTGATGATCTTT 2500
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Db 951 SerValSerThrValPheValMetThrGlnValGlyAlaValThrGlnValSerPheValMet 970
QY 2501 GAATATGAGATGCTCAGACATGCGATTTCTGATGACCGCTTGCGATCATCTTCAAT 2560
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Db 971 AlaPheValLeuSerValIleGln--ArgLeuLeuAspGluValValAspValIleIleLeu 989
QY 2561 GTCCTGAGAAAGTGAAGAAATCTGCTGAGGACGAGC---GTGCAATTTGATGCGCTT 2617
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Db 990 IlePhe-----LeuGlnValProLeuGlnValSerLeuPheLeuGlnLeuAlaValArg 1007
QY 2618 CTTAGCAGAAACACTACCTGAGTGGAGGAGCAATGCTTGAGGAGGACATCTTGTG 2677

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Db 1008 LeuCyArgSerSerValLeuGluTrpProAlaAnProGlnAlaHisProValTrpPheTrp 1027
QY 2678 AGAAGACTCAAAAAGCCCTG 2698
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RESULT 15
US-10-407-952-26
; Sequence 26, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G, U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 1050
; TYPE: PRN
; ORGANISM: Mus musculus
US-10-407-952-26

Alignment Scores:
Pred. No.: 9,18e-44 Length: 1050
Score: 559.00 Matches: 265
Percent Similarity: 38.45% Conservative: 153
Best Local Similarity: 24.38% Mismatches: 327
Query Match: 9.41% Indels: 342
Gaps: 52
DB: 15

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Db 13 LeuIlePheLeuAnMetLeuLeuValSerArgValPheGlyPheArgTrpPheProVal 32
QY 329 AGCTGAATCCCTGCATAGAGTACTTCCATATATT-----ACCTACCA 373
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Db 33 ThrIle--ProCys--GluValValSerValAnIleProGluAlaHisValIleValAsp 50
QY 374 TGCATGATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGACCTA 433
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Db 51 CysThrAspValSerLeuThrGluIleProGluGlyIleProThrAnSerThrAnLeu 70
QY 434 GATTCAGCTTCAACCCCTGAAGATCTTAAGAACTATAGCTTACCAAAATTCTCAAA 493
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Db 71 ThrLeuThrIleAnHisIleProSerIleSerProAspSerPheArgValGlnHis 90
QY 494 CTTCAAGGCTGATTTA-----TCCAGGTGAG 523
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Db 91 LeuGlnIleLeuAspLeuArgCysAnCysValProValLeuLeuGlySerValAnAsn 110
QY 524 ATTGAGCA-----ATTGAAGACAGGATGAGCTTAAACAGCTTCA 571
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Db 111 ValCysThrValArgLeuGlnIleArgProGlySerPheSerGlyLeuSerAspLeuVal 130
QY 572 ACCTTGATGACAGAGAAACCTATCAGAGTTTTC-----CAGAAATTTT 622
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Db 131 AlaLeuValLeuAspGluAnGlnLeuGluIleProGlnAspLeuProSerSerLeu 150
QY 623 TCTGAGTAACAATTTAGN-----AATCGGTGCTGTGAG-----ACA 664
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Db 151 His-----LeuLeuSerLeuGlnAlaAnAnIlePheSerIleThrValGluAnLeuThr 169
QY 665 AAATGACCTCTCTAGAGGCTTTCATATATGACAG----- 700

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Qy      701 -----CTTATA 706
Db      190 AsnValSerTyrSerIleGluLysAspAlaPheLeuValMetArgAsnLeuLysValLeu 209
Qy      707 TCTTAAAGAACTAATATGTGGCT----- 730
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Qy      731 -----CATATCTT 739
Db      230 LeuTyrLeuTyrAsnAsnIleIleLysLysIleGlnGlnAsnAspPheAsnAsnLeuAsn 249
Qy      739 ----- 739
Db      250 GluLeuGlnValLeuAspLeuSerGlyAsnGlyProArgGlyTyrAsnValProTyrPro 269
Qy      739 ----- 739
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Qy      740 -----ATACATTCCTTAAATTG-----CTGAATAT 766
Db      290 ThrGluLeuLysValLeuArgLeuHisSerAsnSerLeuGlnHisValProProThrTyr 309
Qy      767 TTTTCTATCTGACAAACCTTGAAACATGTGATCTTTTATTAACATAATTCAAACTATT 826
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Qy      827 TCTGTCAAGACTTACAGTTCTACGTGAATAATCCCAAGCATCTCTCTTGAACCTG 886
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Db      348 SerPheAsn-----TyrGluLeuGlnValTyrHisAla-----Ser 359
Qy      947 TTGACTCTAGAGACTAATTTTAAATGCTCAAAATGACTGAAATATGTC----- 994
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Qy      995 -----CTTCAAAACATGACGTGTTTACATGTCATCGGTG----- 1030
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Qy      1052 GAAAGAAATCTGAAAGTTTGCACCGTTCTGTCATGAA----- 1090
Db      420 PheGluAsnLeuLysLeuIleAspLeuSerValAsnLysIleSerProSerGluGlnSer 439
Qy      1091 -----GGACATATGC-----AATGAGCATGATGATGATGAGC----- 1123
Db      440 ArgGluValGlyPheCysProAsnAlaGlnThrSerValAspArgHisGlyProGlnVal 459
Qy      1124 TTAACATATATATCAATTTTTCAGATGATATTTATATCAATTCG-----TTGCAAAAT 1180
Db      460 LeuGluAlaLeuHisTyrPheArgIleTyrAspGluTyrHisAlaArgSerGlyAspPheLysAsn 479
Qy      1181 ATTTCTGCATGTCTTTTCACAGGTGTACATATTAACAACATAGCATGTTCTTAGGCAT 1240
Db      480 LysGluProProSerPheLeuProLeuAsn-----AlaAspCys-----His 493
Qy      1241 TTCAAAAGCAATCCTTATCAATCATATGATGTGAT-----CTTAACCTTTTCCA 1291
Db      494 IleTyrGlyLysIleThrLeuAspLeuSerTyrAsnAsnIlePhePheIleLysProSerAsp 513
Qy      1292 AAGCTGAGTCACTTTTCTTAAAGTTGAGCTTTAACTACCAACAGAGAGATATCAAC 1351

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Db      514 PheGlnHisLeuSerPheLeuLysCysLeuAsnLeuSerGlyAsn-----Thr 529
Qy      1352 TTTGTCAGATTG-----GCTTGCCAACTCTCAGATATCTGAT 1390
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Db      550 PheSerAsnAsnAlaGluLeuAsp----- 556
Qy      1451 AACCTGAAGTACTTGAACCTTCAAGCTTCAATGCTGTCAATCTGATGATGCGCAACTTCATG 1510
Db      557 -----LeuLeuTyrSerThrAlaPheGlu 564
Qy      1511 GGTCTGAAGAGCTGAATACCTGGAC-----TTTGACAGCTCC 1549
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Qy      1550 ACTTTAAAAAGGTCACAGAAATTCAGATGTTCTATCT-----CTTGAAAACTTTTAC 1606
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Qy      1658 GGCCTTATCAGTCTCAACACTTTTAAATAGCTGGCAATCTTTCAAA----- 1705
Db      621 -----SerLeuArgIleLeuGlnPheArgGlyLysAsnIleLeuAspValLeuTyrArg 637
Qy      1706 -----GACAAACACCTTTCAAAATATGCTTTTAAACAACCAACAACTTACCTGAT 1759
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Qy      1760 CTTTCTAATGCGCAACTGGAACAGATATTAAGGGGATTTTGAAC----- 1804
Db      658 IleSerArgAsnSerLeuAsnSerLeuProGluValPheGlnGlyMetProProAsn 677
Qy      1804 ----- 1804
Db      678 LeuLysAsnLeuSerLeuAlaLysAsnGlyLeuLysSerPhePheTyrAspArgLeuGln 697
Qy      1805 ACACTTACAGACTCCGATTTTAAACATGATGCAACAACCTA----- 1849
Db      698 LeuLeuLysHisLeuGluIleLeuAspLeuSerHisAsnGlnLeuThrLysValProGlu 717
Qy      1850 -----CTGTTTCTGATTCATCCATTAATAA 1876
Db      718 ArgLeuAlaAsnGlySerLysSerLeuThrThrLeuIleLeuLysHisAsnGlnIleArg 737
Qy      1877 CAGCTG-----TACTCCCTCAGACTCTTTGATGAGATTTC 1912
Db      738 GlnLeuThrLysTyrPheLeuGlnAspAlaLeuGlnIleuLysTyrLeuAspIleSerSer 757
Qy      1913 AATGCAATAGACATGCAAAAGAACTAGTCAAA-----CATTTCCAAAG----- 1957
Db      758 AsnLysIleGln-----ValIleGlnLysThrSerPhePheProGlnAsnValLeu 773
Qy      1958 ---AGTCAACCGCTTCAATCTGACTAATATTTCTGCTTGTATATGTAATATCAG 2014
Db      774 AsnAsnLeuGlnMetLeuValLeuHisGlnIleAsnArgPheLeuCysAsnGlyAspAlaVal 793
Qy      2015 AATTTCTGACAGTGGGTCGAAGACACCAAAATGTTCTTGGAATGTT---GAAACAATG 2071
Db      794 TyrPheValIleTyrPheValAsnHisThrAspValThrIleProTyrLeuAlaThrAspVal 813
Qy      2072 AAATGTCATCACCCTATAGACATGAGGCTCCCTGGTGTGATTTTACGAATTTCAAC 2131
Db      814 ThrCysValGlyProGluAlaHisLysGlyGlnSerValIleSerLeuAspLeuTyrThr 833
Qy      2132 TGTATATATACAAAGCT-----ATCATCAGTATATCGGTGAGTGTGCTT--- 2179
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